

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



Applicant : Forsyth, et al.
Appl. No. : Unknown
Filed : Herewith
For : GENES IDENTIFIED AS REQUIRED FOR
PROLIFERATION OF E. COLI

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

A copy of the Sequence Listing in computer readable form as required by 37 C.F.R.

§ 1.821(e) is submitted herewith.

As required by 37 C.F.R. § 1.821(f), the data on the enclosed disk is identical to the
Sequence Listing in the application filed herewith.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: December 19, 2000

By: Daniel Hart
Daniel Hart
Registration No. 40,637
Attorney of Record
620 Newport Center Drive
Sixteenth Floor
Newport Beach, CA 92660
(619) 235-8550

SEQUENCE LISTING

<110> Forsyth, R. Allyn
Ohlsen, Kari L.
Zyskind, Judith W.

<120> Genes identified as required for
proliferation of E. coli

<130> ELITRA.009A

<150> US 60/173005

<151> 1999-12-23

<160> 481

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 142

<212> DNA

<213> Escherichia coli

<400> 1

```
cgctccttag agtacttctg gtgccagaga gataattttc atgaacttct cactacgaag 60
ctcacgagtt accggcccaa aaatacgcgt accgataggc tgctcgctgt gttgttcag 120
aagaacacaa gcattaccat cg                                     142
```

<210> 2

<211> 154

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(154)

<223> n = A,T,C or G

<400> 2

```
gctccttaga gtacttntgg tgccggagag ataattttca tgaacttctc actacnaagc 60
tcacgagtta ccggcccaaa aatacgcgta ccgataggct gctcgctggt gttgttcacg 120
aagaacacaa gcattaccat cgaagcgaat gaca                                     154
```

<210> 3

<211> 140

<212> DNA

<213> Escherichia coli

<400> 3

```
tacttctggt gccagagaga taattttcat gaacttctca ctacgaagct cacgagttac 60
cggcccaaaa atacgcgtac cgataggctg ctcgctgttg ttgttcagaa gaacacaagc 120
attaccatcg aagcgaatga                                     140
```

<210> 4
<211> 177
<212> DNA
<213> Escherichia coli

<400> 4
cgctccttag agtactttctg gtgccagaga gataattttc atgaacttct cactacgaag 60
ctcacgagtt accggcccaa aaatacgcgt accgataggc tgctcgctgt tgttgttcag 120
aagaacacaa gcattaccat cgaagcgaat gacagaaccg tccgggcgac gaacacc 177

<210> 5
<211> 255
<212> DNA
<213> Escherichia coli

<400> 5
ctctttttct tcgagatgga cgcagtgagc aaagacacag tttttaccgg tcaggccgta 60
ctgatggtaa acatccagat aaccatcatg gtcaggataa agcgatttca cccaggcaat 120
ttcatctttg ttttcacaga gatgggtatg taccacgta tccggatatt cttctttcag 180
gcggttgcgcc atcgccatct gttcaggaga tgaggtcggg gcgaagcgtg gcgtaatcgc 240
atatagcaga cgacc 255

<210> 6
<211> 395
<212> DNA
<213> Escherichia coli

<400> 6
tccgcgatcg cggataaaaa ggaggattta aataaggcgt tgatgcgccg tttgaagtcg 60
gcaatattaa gccgcattgc atctcgacat gcggcttata cggtttacca gctatatattc 120
actcccagca tgccctgagt atcgctatag cttttatcac ctagttgcac accgacattc 180
ccccacaggc taaggtttgt atttactttc gcctcaaccc cggtagctac ttcaccgaga 240
ttacgcgcac cttcacggcc tacggtttga ccattcatct tcacggcgta gactttgcta 300
ttgttgatcc agttcgcttc aatgtaaggc tggaactcac gctgtttacc atcgtcacgc 360
tggtgatggc tgttcaggta ggttttcacc ccaag 395

<210> 7
<211> 280
<212> DNA
<213> Escherichia coli

<400> 7
tgatcgatca ggtaatttgc cagcggtaga taattagtga tgatttgcac tggettgcc 60
cacattttcc gcccaagcag aaacgcggtg gagccgcagt tgatgactac gctttcgccc 120
ggattaacca gctgcgaggc cgctttagcg atacgtactt tttcatcgtg attctgcgcc 180
tgatgcagat tcatcggcgt ccagcgcggg cgctgttggg taatagcttc tgcgccattg 240
cgcacttttt tcagtttgcc gctttcgtca agtttattga 280

<210> 8
<211> 363
<212> DNA
<213> Escherichia coli

<400> 8
agtaaaggat atacaaattt aaaggaagt gcggcgaagt caaaacttac agatacaacg 60
gtttcaattc cgataacagc cagttactac gtctacgata caaacaaggt taaatctggc 120

gcactggagg caaccgcatt aatcaacgtg aaatacagact aataacaagc aagacgagca 180
 agtgggctaata aataaaaaaat aacaaggtgt ctgcatttcc ccctcatgat gaggggggctt 240
 ttttttagcga tgataaaaaaa tctcaccgtc gtagggcttta atgatttttac cgtcgggtgtc 300
 gctgatcaac acgtacgcgc caccatata ggtccagtgc gtcccggcat caggcgcgagg 360
 cag 363

<210> 9
 <211> 295
 <212> DNA
 <213> Escherichia coli

<400> 9
 ttacagatac aacggtttca attccgataa cagccagtta ctacgtctac gatacaaaca 60
 aagttaaatac tggcgactg gaggaacacg cattaatcaa cgtgaaatac gactaataac 120
 aagcaagacg agcaagtggc taataataaa aaataacaag gtgtctgcat ttccccctca 180
 tgatgagggg gcttttttta gcgatgataa aaaatctcac cgtcgtaggc tttaatgatt 240
 ttaccgtcgg tgctcgtgat caacacgtac gcgccacca tatagggtcca gtgcg 295

<210> 10
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 10
 acgactaata acaagcaaga cgagcaagtg gctaataata aaaaataaca aggtgtctgc 60
 atttccccct catgatgagg gggctttttt tagcgatgat aaaaaatctc accgtcgtag 120
 gctttaatga ttttaccgtc ggtgtcgtg atcaacacgt a 161

<210> 11
 <211> 290
 <212> DNA
 <213> Escherichia coli

<400> 11
 tgcggcgaag tcaaaactta cagatacaac ggtttcaatt ccgataacag ccagttacta 60
 cgtctacgat acaaacaaaag tttaatctgg cgactggag gcaaccgcat taatcaacgt 120
 gaaatacgac taataacaag caagacgagc aagtggctaa taataaaaaa taacaagggtg 180
 tctgcatttc ccctcatga tgagggggct ttttttagcg atgataaaaa atctcaccgt 240
 cgtaggcttt aatgatttta ccgtcgggtg cgctgatcaa cacgtacgcg 290

<210> 12
 <211> 137
 <212> DNA
 <213> Escherichia coli

<400> 12
 ctgggttttag cttttgcttc gtaaacacgt aataaaacgt cctcacacaa tatgaggacg 60
 ccgaatttta gggcgatgcc gaaaaggtgt caagaaatat acaacgatcc cgccatcacc 120
 aggccatctg gctgggg 137

<210> 13
 <211> 275
 <212> DNA
 <213> Escherichia coli

<400> 13
 cgtcatgtac gtgcagtttg gtcgtacgct tgatgaattt accgtagatc ggggtgtttca 60

caaaacgttc gatagcaaca acaatggatt tctccatttt gtcgctaaca acgcgacctt 120
gcagagtacg gattttatcg gtcattacgc acccgccctc tcgttcagta aagtcttaac 180
gcgtgcgaca tcgcgacgca cttgcttcaa caggtgagac tgttgcagct ggccacttgc 240
agcctgcata cgcaggttga actgctcacg cagca 275

<210> 14
<211> 239
<212> DNA
<213> Escherichia coli

<400> 14
tgtcggtaaa caatgacaat ttgagacaga gtgaaagggtc agatttgctg agtaatgcac 60
ataatgggta tttaaataaa ccacatgaat cattaatggg ttattcatta tttttgtgat 120
ttactcacia tgtatcaggg aaatataact taccgggaga tgtaatatgt ttaatttttc 180
aaatcgaaat ttaaaatatt gtgccggagg catctctggc acattgggca attacggca 239

<210> 15
<211> 114
<212> DNA
<213> Escherichia coli

<400> 15
cgatgttctg aatctgctcg cgcattctgct caatcaacac tttcagctcg atggcggagt 60
ttgtcacttc ggcatgata gacttcgacg caagagtgtt cgactcgcgg ttga 114

<210> 16
<211> 290
<212> DNA
<213> Escherichia coli

<400> 16
acgggaagta attgtaactt agtttgtaaa ggtcatatgc ttgttgatat ttcttttttg 60
gctgacatac tgatgcaaaa tcttttagat actcatgatt ttcgaacgca taaatgcaca 120
agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggtg tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattattg 290

<210> 17
<211> 444
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

<400> 17
acgggaagta attgtaactt agtttgtaaa ggtcatatgc ttgttgatat ttcttttttg 60
gctgacatac tgatgcaaaa tcttttagat actcatgatt ttcgaacgca taaatgcaca 120
agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggtg tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattantg aatatttcaa 300
ttgtttctgt gtcataata ttcctctgng atgtgntcgc ngatgccnaa cnattatttg 360
antgactcat ngnnatnttt atatnnatcc nntnntaant natnantntn aagccngcnt 420
tgcttatggg ntantntnat ttat 444

<210> 18
 <211> 250
 <212> DNA
 <213> Escherichia coli

<400> 18
 cgctggaaaa aacctaaaat attcatctta ttccccctac gagaacccta tttggctcgt 60
 ttcaagccgt atttttatatt tgctgcaaatt tgtactgccg atgttctgta atcagattgt 120
 tagatcatct gctacagagt gtgtgaaaaat ttaattcgta tcgcaaatta aacgcgtgtc 180
 ttttgtgagt tttgtcacca aatatcgta ttatcactcc cttttactgg ctaaaccaga 240
 aaacttatatt 250

<210> 19
 <211> 237
 <212> DNA
 <213> Escherichia coli

<400> 19
 gtattacaac aagaatacag tgctaaaaaa agaatgtacc tgaagatagt cttcattttt 60
 actccaatgt ttctttattg ttatggtttg cgctgttttt gtttgttatt cgtagtaaat 120
 atccactaac acatggctca taagtgtgacc agatgtaaca ctcaatgcag gatcgatttt 180
 ttgcatcggg gtgctaaatt tccaggatga accattcatg tcatccgaca ttactgg 237

<210> 20
 <211> 237
 <212> DNA
 <213> Escherichia coli

<400> 20
 catcatcaca gcggcagcca tgtacagcag atccatattc aggtttttcca tgacagtctc 60
 cagtttgttt cagttaaaac gtagtagtgt tggtaaatta atgttcttca gacgccatcg 120
 acagatagac gatcgtcaga accatgaaga tgaaggcttg cagcgtaatg atcaggatgt 180
 ggaaaaatggc ccacggcaca ttcaggatcc actgtgacca ccacggcaac agaccag 237

<210> 21
 <211> 139
 <212> DNA
 <213> Escherichia coli

<400> 21
 cccgcgacgt tatccgogtg taggcacgt catgacgtaa acggcgatcg gcggtataac 60
 gggtgatcat cgaatccatg ttgccagcag taacaccgaa aaacagattc ggtttaccga 120
 gacgcataaa gtcgtcttt 139

<210> 22
 <211> 211
 <212> DNA
 <213> Escherichia coli

<400> 22
 ggagagcgaa gggctatccg gccaggggtga aattatcgcc gcgaacgcac aatttgatat 60
 cgacgagtaa agtactcaaa cggcgcgctc cacacatgca ccagtcgggt gaacgggaag 120
 agcaggaaga tggtcattcc caacaccaga tgcaggcgga agacgaacgc tacgccgttg 180
 agcatctctg acgatccacc acggaaagtg a 211

<210> 23
 <211> 154

```

<212> DNA
<213> Escherichia coli

<400> 23
cacgacggat tttegtgccc atgattcgct ccttagagta cttctgggtgc cagagagata 60
attttcatga acttctcact acgaagctca cgagttaccc ggcccaaaaa tacgcgtacc 120
gataggctgc tcgtgttgtg tgttcagaag aaca 154

<210> 24
<211> 160
<212> DNA
<213> Escherichia coli

<400> 24
acttgcgtcat cacgacggat tttegtgccc atgattcgct ccttagagta cttctgggtgc 60
cagagagata attttcatga acttctcact acgaagctca cgagttaccg gcccaaaaat 120
acgcgtaccg ataggctgct cgctgttgtt gttcagaaga 160

<210> 25
<211> 244
<212> DNA
<213> Escherichia coli

<400> 25
aatgaccttg ccggaagaca ggacattctt aactttaccg cgtttacctt tatctttacc 60
ggttaacacg ataacttcgt catcacgacg gattttcgct gccatgattc gtccttaga 120
gtacttctgg tgccagagag ataattttca tgaacttctc actacgaagc tcacgagtta 180
ccggcccaaa aatacgcgta ccgataggct gtcgctggtt gttgttcaga agaacacaag 240
catt 244

<210> 26
<211> 108
<212> DNA
<213> Escherichia coli

<400> 26
tgttcgatct cgaaacttac acctttctca gccagcacia tgcggacctg atggctatag 60
atgtcagtag gaccggaaaa cagcgtcatt acccgaacgt ttgttggc 108

<210> 27
<211> 369
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 27
tccagacgct ctttcttggc gtcgtagtca aagatacccc ctaagaacgt cggagcggttc 60
cgtgagtcct gaatgcgatt atttaccgga ttaatttcaa acatggctctg atttctttta 120
ttgagctagt caaaatgcgg tgataagagc gggattgtac ccaatccacg ctctttttta 180
tagagaagat gacgctaaat tggccagata ttgtcgatga taatttgcag gctgcgggttc 240
cacgaaactc gttgatatcg agcttataag ccagttgcac ttngcgcacc cgttatccgg 300
ccagagggcg gtatcgacat taaaagcaat accatccagc agtggaccgc cggccgaccg 360
gttcgacca 369

```

<210> 28
 <211> 457
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(457)
 <223> n = A,T,C or G

<400> 28
 accccctaag aacgtcggag cgttcogtga ggtcctgaat gcgattatatt accggattaa 60
 tttcaaacat ggtctgattt cttttattga gctagtcaaa atgcggtgat aagagcggga 120
 ttgtacccaa tccacgctct tttttataga gaagatgacg cttaaattggc cagatattgt 180
 cgatgataat ttgcaggctg cggttgccgc gaaactcgtt gataatcgagc ttataagcca 240
 gttgcacttc gcgcacgccg ttatccggcc agagggcggt atcgacatta aaagcaatac 300
 catccagcag tggaccgccg ccgaccggtt cgaccatnac cttcaaatac cgttcgccca 360
 ccagccgctg ttgcancaga cggaaatgac cgtcaaacag cggctccggg aacatctgcc 420
 cccacgggccc agcatcgcgc agcagctgcg ccacttc 457

<210> 29
 <211> 729
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 29
 ctttttacgg acaaacaatc atgcaaccag aagttgaagt attaacccgat cataatgagc 60
 taatttggtc gagctttatt gaacacattg ccaacacatt aaatttagga gtggtgtaca 120
 actaaacctg cagccaagga tgtatagtga gcgaagccct atcaggcctt tttggtcagt 180
 agataagatt gatcttcggt gatagaattt acttacacca gctgttacat taagataatt 240
 ttttggtggg agaatgataa gatcttacgt aacaatttga ttttaattgt gccgataata 300
 ggagtcgaac ctacgacctt cgcattacga atgcgctgct ctaccaactg agctatatcg 360
 gccctgaaag gacatgttca cgaacgtgaa tcacgggtgga caagggttaa actaaccggg 420
 cgatgcgtca atggccttgt gaatcaaata gctacttttg catcaccggt ttttatttac 480
 gcacgaatgg tgtaatcacc aatgccgcat cacttgtaag tgggtcaagt cttncagccc 540
 cattgggcca cgcgcggtgg agttttttgt tgettaccgg cactttcgca cccagaccaa 600
 actggccgcc gtcggtaaaa cgcgtagagg cgttacgtaa acagcggacg aatccacttc 660
 gtnacaaaac gcttggcgtt ggcataatcg gggtcangat cgcaatcgga gtgttgtgtg 720
 cccgggttn 729

<210> 30
 <211> 305
 <212> DNA
 <213> Escherichia coli

<400> 30
 agccattgtc cggagaattt tcgtctttct cgagggtatt atctgaaagt aactcttctg 60
 agctagagtc ttctatgttt aaatccatag tataattaat ttgggggacg accagataag 120
 cattttcttt ggtattttca taatcttcaa tgattatata cgatgtaatc atatattttt 180
 tctgatgaga attctttcat ctctgttaat ttaattctgt tcaagcaatt gatgattttc 240
 gatgagcttt tatatatattc ttttggttaat tcattttcta atttatctgt aagagttgcc 300

cttgg

305

<210> 31

<211> 425

<212> DNA

<213> Escherichia coli

<400> 31

```
aggttactgg cgaggttatc gagaaacgcc agactgatac ccataaaaaa gagaataagg 60
taaaccatcc agcttaatag ctgattaata acttttaacg cagcttggtg gcgaagcgga 120
atgaggtaac ccacaatcag ggaaccaga atgattaaca gccagaaaaa catgaaaacc 180
cagtccttgc aaagatgaag tcgaaatgcg cgatgacaca ctactgaaag cggaaggacg 240
agtaaagttg caattaaaag gaaatgttat gcataaggag cagtagagta ttcgttttca 300
tttaaagata ttcttgcgct ttaattacaa actgcaccga tgttggtggc gtcaaaatcg 360
ccgaggcgtt ccctgaaggc cggggcagcc cacatggatg tgggctgagg gcgcgtttta 420
caggg 425
```

<210> 32

<211> 381

<212> DNA

<213> Escherichia coli

<400> 32

```
aaaagagaat aaggtaaacc atccagctta atagctgatt aataactttt aacgcagctt 60
gttggcgaag cggaatgagg taaccacaaa tcaggggaac cagaatgatt aacagcccag 120
aaaacatgaa aaccagctcc ttgcaaagat gaagtcgaaa tgcgcgatga cacactactg 180
aaagcggaag gacgagtaaa gttgcaatta aaaggaaatg ttatgcataa ggagcagtag 240
agtattcggt ttcatTTaaa gatattcttg cgctttaatt acaaactgca ccgatgttgg 300
tggcgctcaaa atcgccgagg cgttccctga aggccggggc agcccatg gatgtgggct 360
gagggcgcggt ttacaggga t 381
```

<210> 33

<211> 329

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(329)

<223> n = A,T,C or G

<400> 33

```
gtcgatgttg tgcccgaact tgccatgctc cagtcctttt cttctggggc gactttccgg 60
gaggtgctta aacgaaaaac cccgcccggt ttgcgccggc ggggttttgg aatcgtgtgt 120
tgttccagtc cctacggcgc attgccgacg accaccacca cacgcacgac gaccactgcg 180
gcgatgggc gcagttggta gtagttttgc gttgagcatg gaagtagtca ttggggacct 240
tgttggtttt gtgtttaaca atatttatac aagcacagct ttacaggga gacaatggaa 300
aatttttcag caaggga aaa ttgaggggn 329
```

<210> 34

<211> 442

<212> DNA

<213> Escherichia coli

<400> 34

```
gatgttgtgc ccgaacttgc catgctccag tccttttctt ctgggccgac tttccgggag 60
gtgcttaaac gaaaaacccc gcccggtttg cgccggcggg gttttgaat cgtgtgttgt 120
```


<212> DNA
<213> Escherichia coli

<400> 39
tcgcaaggaa aggcgtcagc gcaaaaaacca gctccggctt gtgggttagga tctttatagt 60
tacgctcggc ggcatccatc gggatacctg cggcattttc tttggcaaaa cggatttcag 120
aattgtgttt gtttggatga acctgaatgg agagtggctg tgctgcgcat aatactttga 180
acaggaaagg c 191

<210> 40
<211> 158
<212> DNA
<213> Escherichia coli

<400> 40
ccggcttggtg gttaggatct ttatagttac gctcggcggc atccatcggg atacctgcgg 60
cattttcttt ggcaaaaccg atttcagaat tgtgtttgtt tggatgaacc tgaatggaga 120
gtggctgtgc tgcgcataat actttgaaca gaaaaggc 158

<210> 41
<211> 184
<212> DNA
<213> Escherichia coli

<400> 41
tcgaagaatt taacggaggg taaaaaaacc gacgcacact ggcgtcggct ctggcaggat 60
gtttcgtaat tagatagcca ccggcgcttt aatgcccgga tgcggatcgt agccttcaat 120
ctcaaagtct tcgaaacggt agtcgaagat ggattcgggt ttacgtttga taatcaactt 180
cggc 184

<210> 42
<211> 122
<212> DNA
<213> Escherichia coli

<400> 42
gtagaagtgc aaattacgaa cctgaatttt actcggggca gtttcaacca tactcattgc 60
aatcttttcc tcatcgtgcc tgatgcactt cgctaatacag gcttaccgta ggccggatca 120
gg 122

<210> 43
<211> 163
<212> DNA
<213> Escherichia coli

<400> 43
taaatccgc gtatagcgtg ggcgctttgg ctccggtcgc ttcgacgagg tccgcaagag 60
aagtcgcttc ataaccgtgt tgccagaaca atttcatggc cttatcaagc gcggcatccc 120
tgtcgaacac ttttggggcg ccacggcttt tttttacaca ttg 163

<210> 44
<211> 161
<212> DNA
<213> Escherichia coli

<400> 44
gcaaattgttt tcgtaattca ggagaaatgg caaataaagc attaaaaatt tgaatgcttt 60

gtgtaataaa aaagcagaca ggcgacggag tgaccactcc gtcgctttac aaagagagga 120
 aaatcatagg ttgccggtgt agtgccacgc taaataacgc a 161

<210> 45
 <211> 251
 <212> DNA
 <213> Escherichia coli

<400> 45
 ggctgtaacg gtaaagccct caccgaagcg agggcttgaa ggagaagggt tatgatgcga 60
 cttgtcatca tactgattgt actgttactc ataagtttca gcgcttatta acagtcagtc 120
 tcaggggagg agcaatcctc ccttaccctt actcactaaa ttaggtcaaa gaatcaacga 180
 tgtcaatcag ggcgatgcgg ttgtatcgcc cttaccactc ccagactttc gacggtgtaa 240
 ccaccgcagg a 251

<210> 46
 <211> 286
 <212> DNA
 <213> Escherichia coli

<400> 46
 caccgaagcg agggcttgaa ggagaagggt tatgatgcga cttgtcatca tactgattgt 60
 actgttactc ataagtttca gcgcttatta acagtcagtc tcaggggagg agcaatcctc 120
 ccttaccctt actcactaaa ttaggtcaaa gaatcaacga tgtcaatcag ggcgatgcgg 180
 gtgtatcgcc cttaccactc ccagactttc gacggtgtaa ccaccgcagg aagagggata 240
 tcccactctt caacggggag tttttccacc aactgacaat catgcg 286

<210> 47
 <211> 180
 <212> DNA
 <213> Escherichia coli

<400> 47
 ccggggctga cgtgggcat aatcgggtcg ccaggaatag ggcggcagca tttcgcaaag 60
 gtgatcagca cgccatcggc acctttaatg ggcagatgtc cgtggctttg ggttgccggt 120
 ggaatggagg cgtcccatg ttgcagattt ttcgcgacca ccacgctcat tgcgttacca 180

<210> 48
 <211> 254
 <212> DNA
 <213> Escherichia coli

<400> 48
 tgtcgagcat acgcggcagc gccgactcgg aagatgaagt ccccagtaca atcagcagtt 60
 cttcacggat gtagcggata aatttgaaga tactgaaacc agtcgcttta gcgattgaac 120
 ccaataccag caccacaaac aggatacagg taatgtagaa acagataatc agctgcccc 180
 gttgcaccag tgtgccgacg ccgtatttac cgatggtaaa cgccattgcc ccgaacgcac 240
 caataggtgc caga 254

<210> 49
 <211> 300
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature

<222> (1)...(300)
<223> n = A,T,C or G

<400> 49
agctgacgca tgggtgtttgc caacgcacac gccaccgagg cgggcgcaaa caccancgta 60
ccgccgagca ccaccggctt acgcccgaag ctgtctgccca tcggcccgtg gattaactgc 120
cccaacgcaa agcccagaat ataagtactg aggggtcatct gcgtactgcc cgcgcgtacg 180
ccaaactgcg ctgaaattac cggtagcgcg ggcagatata tatcaatcga cagcggcatc 240
aacatggcca gcaggccaag gataaaaaca atagcaaacg acgaatgctg tcgggtggtc 300

<210> 50
<211> 207
<212> DNA
<213> Escherichia coli

<400> 50
caacatctca tgtctggatt tgtagatata cgtggaattc caattgggtat cttttgtagg 60
attcaacata tcatgtaagc gctgggagct taccaccata actggcccat catcgactga 120
ggagaacagg ataaagatat tatcgtttcg tgttaattca ttcgtgttaa aggttcttaa 180
attatcttca gtttctataa atatagg 207

<210> 51
<211> 213
<212> DNA
<213> Escherichia coli

<400> 51
ttctgtaatc agaaaaagaa gaactggaat ttttaataaat attatttctc tgggaacggg 60
gggggtataat caatatgacg agttgaatat tatatttttt ataagaatta tatgagatta 120
aagaaatctg ccgtaaagac agatttcttt aaaagataat tagagatttg cgacgttatg 180
ataaactttt tgtacatcgt cgtcatcttc aag 213

<210> 52
<211> 381
<212> DNA
<213> Escherichia coli

<400> 52
tctgttagtg tattatccac tgcggccctt tccgccgtct cgcaaacggg cgctggcttt 60
aggaaaggat gttccgtggc cgtaaatagca ggtgtttcac agcgcttgct atcgcggcaa 120
tatcgccagt ggtgctgtcg tgatgcggtc ttcgcatgga ccgcacaatg aagatacggg 180
gcttttgtat cgtacttatt gtttctgggt cgctgttaac cgaggtaaat aataaccgga 240
gtctctccgg cgacaattta ctggtgggta acaaccttca gagcagcaag taagcccga 300
tgccgccctt tgggcggcat attttagatt atccgattct gtttaaagtc acgcaaaaaa 360
ccaccccgag gacgttcata g 381

<210> 53
<211> 154
<212> DNA
<213> Escherichia coli

<400> 53
aaatagaccg gcatactttc gtgcggcagc ataatacaaca gtacgagcgc agcgggtacta 60
atgataaagg ttagcatag atatttactt ggcgatttca ggatcttata tgaaatcatg 120
ccaccaatcg gtccaccaat cattttcaga cagt 154

<210> 54
 <211> 191
 <212> DNA
 <213> Escherichia coli

<400> 54
 tccttagtca ggtactgacg tactttaaaa tcgctgtcca ggttgtcagc gaattctttg 60
 gtgttcgcaa accaggtaga gttccatggg ttacaatac ccaggcgaat accattagga 120
 tgtactttct gaccattgc tagtctccag agtctcagcg atcggacaca accacagtga 180
 tgtggctggg g 191

<210> 55
 <211> 190
 <212> DNA
 <213> Escherichia coli

<400> 55
 gctggtgccc gttttccatg ccagtggggc gacgcgcggc aaggcactat ccggcaaggg 60
 ttgcgcttca tcagccataa tccggcgaat gatccacgcc gccccgacg acattaaagg 120
 ccgttcaagc agcggatcgt caggctgtaa gcgcaatttg cctgccttgc cgtggcgagc 180
 aaacgcggtg 190

<210> 56
 <211> 402
 <212> DNA
 <213> Escherichia coli

<400> 56
 aaaaaatgaa attcctcttt gacggggccaa tagcgatatt ggccattttt ttagcgcaac 60
 atttgcggca aattcccttc tccatacagg tgtagtgcac cgaccgcgac cacatatcgc 120
 cccggcggca tggcgcgtaa tttatccgcg caggcgagat ttcgctgatg catcagcaca 180
 tcgtacagcg actgactgaa cgtattgggc agcgttatat cattatcttg cggcgggtgca 240
 ttcagccacc agctcatcat ttgttgcagc aaccgtgcgt tggatatgcca gtgggtcagc 300
 gtatcgtcca gcagcgcag tcctttgtca gggagctgga gcaacatggc aatctggttt 360
 tcagccctt ccagttcaat cacgggttta tgttgttgc t 402

<210> 57
 <211> 595
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 57
 aattaatcag agcaacggta aaacaatgaa agtgtaaaaa acacttttgc gccattatg 60
 gagaaaaaaa gaaaatttga tggagagtga tgagagaata ttacaacacg atgattttgc 120
 agagattatg aagaactata ccggatgact ggtgataaat aaagcaaata accaggatta 180
 atctgtatta atttataaga aagcaactta ataccgcgag aatgatttct gcgggtaagt 240
 attagcttat tttttcgagc attaatcccg cgcgtaatcc caacgctacc aacggattag 300
 ggaataaac atactctaca tcatgggtta cggtaaaacg ttctctccg tcctgcgcca 360
 gcaatgttcc tttctcaaac ggcataaaat tcagcgtgtc acttgccata tgcatttcga 420
 aggacggcga gtggcgagta atttgcgaaa ccacccgata acggagcggc ggtgttctca 480
 cgataccgac actctcacca gatagcagcg cagcaattgc gctggcagtt actgcaaact 540
 ggcgaagatc gttttgcccc aagggaacg ctttgccaag ttncagccgt acang 595

```

<210> 58
<211> 250
<212> DNA
<213> Escherichia coli

<400> 58
gaaactcagt ggaatggggg agccgcaata gcgaacatgt tccatgccgc caataatctg 60
tgcgcggtga atatgcccga gcgcgatgta gtcggctggt ggaaagtttt gtgccggaaa 120
cgcgtccagc gtgccaatat aaatgtcacg cacggcgta cttttactgg cccccacgg 180
cgttaaatgt cccgtggcga tgatgggcag aggctgatcg ccgcgcagtt tgcaggcatc 240
ggcatagtgt                                     250

<210> 59
<211> 236
<212> DNA
<213> Escherichia coli

<400> 59
aaaggttcgg caaaagccat aaccttttcg tcagctttgg cgggataagg gacacattgc 60
gacgtttcga ccattttata acgggtaaaa ccaccatcaa catgagggaa atacatggca 120
ctgccaaaaa aacgcatatc tgtacactga ttctcgttat gttcaatgca gtatttgcag 180
tgaccgcacg gtttagacgg attaatggct accgtttgcc cttcatgtaa ttctga      236

<210> 60
<211> 92
<212> DNA
<213> Escherichia coli

<400> 60
gaagagatgt tcaggttttc gttatcggca atggatatga acttgatatt ctcatacttc 60
tcgtcaggcg tggagtacgc cgcgccacgg aa                                     92

<210> 61
<211> 62
<212> DNA
<213> Escherichia coli

<400> 61
tgtcgacatt cagcaattcc gggatattcgt cgcgcagggc aaatgtacag gttgaggagg 60
tg                                                62

<210> 62
<211> 72
<212> DNA
<213> Escherichia coli

<400> 62
acttatcaaa ccatttttcc gtttcaacgg aggtctgcac ctgagcgatg gtgtcatcca 60
tcagcttttt ga                                     72

<210> 63
<211> 66
<212> DNA
<213> Escherichia coli

<400> 63

```

aaacgcatgg cgcgtaaagg ttcaatcagt ccgatttcag cgggtgctgaa ctcgctaaat 60
tcttca 66

<210> 64
<211> 143
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(143)
<223> n = A,T,C or G

<400> 64
tataggggnc tatttcatta acccgacact ggattaattc aacaggaata ttatgattct 60
gacacaactc ttttaattttc tccgcgcgca tcgtagaggt cgcaaccgcg cctccgcaag 120
cgacaataat cttgcgtttc ata 143

<210> 65
<211> 210
<212> DNA
<213> Escherichia coli

<400> 65
gaggaaccgt gtgacacaca aagggtgatt attttccatt gcggcgtata atcctggctc 60
accatcatgt attttcatgg ctaaaatact catcaccagt tttttgttta aaagctcttg 120
tgctattgga gtggttaatg cattcagaaa gatatcgatt atttcatcga atccatacaa 180
catggagata taaagtccag gtgtttcgtt 210

<210> 66
<211> 118
<212> DNA
<213> Escherichia coli

<400> 66
agagctgtga aggagaaaat acgaccacct ttaacggttt tagatacgcg gtttaccgcg 60
atcagctttt cctgcagttc gccagcttgt ttttcgatgt gagccatctt acacctct 118

<210> 67
<211> 531
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(531)
<223> n = A,T,C or G

<400> 67
cctttcaacg cagtagaggg gaatgncnc tacggcatcg gcaccgcgct caattttctgc 60
cagcatatag cccattccgt cttgatcggg cggaacatag gtgtcggcat cacttaaaaa 120
aacctggctg caggtggcgt aattgaggcc attcatcagc gcaccacctt taccggtatt 180
tttttgctg acggcaacaa agcggtcgcc ccatttgcgt ttgacttccg ccatgaccgc 240
ttcgggtattg tccgtggagc cgtcggttaac gcaaattacc cggcaaaaat aanggggttcg 300
cagtaantta tccagtgact ggcgccagac acgggccttt tttntncgca gntttaatgg 360
cgtcnaatac agcctttttt tttantgggt ttacctnta nccgtnttta aaaaccata 420
gcaaccattg ttttngacct tcanaatnaa aaattcnggg ttttaaaaagc gcgttttccg 480

gcaacttgnt ggacagggca aaaaattcct gcctgggtcg ccgnatctgn g 531

<210> 68

<211> 102

<212> DNA

<213> Escherichia coli

<400> 68

agcgccggta acgcccgtta aatgtttctcg ttcggcttcc cgatcgttat tcaacagggt 60
gcgtaccgta gcggcatatt tcttccctgc ttcacgcgca tc 102

<210> 69

<211> 167

<212> DNA

<213> Escherichia coli

<400> 69

aaaactcacc ttttttgttg ttatccctca attaccacaa gtaaaaggag ataaaccgac 60
aatgacctag acgtaattat gtaaaaatac tgatgttcgt cactgactat ttccgatatt 120
cagctgttga aaaatcaaaa aactggaaaa ataattttta atatcat 167

<210> 70

<211> 83

<212> DNA

<213> Escherichia coli

<400> 70

gccacgcca gcataaacag cgggatcgag ccttcaatcg gtacgccag tacacctttc 60
accatcagca ccagcgataa tcc 83

<210> 71

<211> 103

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(103)

<223> n = A,T,C or G

<400> 71

gccnggcggg aaccgacatg ttcccaactct acgcccggctg gcgcgggttt catttttgcg 60
cacctgatag ccgcacgatt gcagatcaac aacgcctttt ttg 103

<210> 72

<211> 121

<212> DNA

<213> Escherichia coli

<400> 72

tagctttcttc cacattgtcg aactgaacgt ccagacgggtg tttagaaacg ttgatgctcg 60
ggatttttttc cgcacccagg caaacgcgcg ccatggctgc aacggtttct gacggatact 120
g 121

<210> 73

<211> 163

<212> DNA

<213> Escherichia coli

<400> 73

```
tagttattgg ctgttttgag aatgtaatct tccaactgct tataactcct cagatgcaat 60
aatccgagaa tcacatgcaa ttatttcata aattcgtggg atcgttcacg aagtgcgtca 120
gcatagttga ccagaccgtc gagtcgctgc atcagtttac gta 163
```

<210> 74

<211> 106

<212> DNA

<213> Escherichia coli

<400> 74

```
aaaaccatga gggtattatg gccgatttga ggagggaag agtaagagca gtttggttaa 60
tgtacaacga cgattctccc accgggcgcg ttttaaagcg acggtg 106
```

<210> 75

<211> 319

<212> DNA

<213> Escherichia coli

<400> 75

```
ctggagattg agtagatatt cttgttcaga atgtatcagc ccgatgggtc tacgattcct 60
aagccacgaa gagttcagat agtacaacgg catgtctctt ttgactatct ggcaaccggg 120
cagtgtgttc tctcacgcat cacaaaagca gcaggcataa aaaaaccggc ttgcgcgggt 180
ttttcacaaa gtttcagcaa attggcgatt aagccagttt gttgatctgt gcagtcaggt 240
tagccttatg acgtgcagct ttgtttttgt ggatcaaacc tttagcagcc tgacgggtcca 300
cgatcggttg catttcggt 319
```

<210> 76

<211> 237

<212> DNA

<213> Escherichia coli

<400> 76

```
cgaaccaacg acccccacca tgtcaagggt gtgctctaac caactgagct atgaacgcaa 60
cgttgtaggt gacaacgggg acgaatatta gcggcagagt gggaagggtg caagaggcaa 120
aacgtaattt tctgcgctat ttcgaccggt tgcagagctt ttaagcaaatt tggctatatt 180
ttgttgattt gcaagggtga tttttattca ggatcgcatt tacatctgat acaacct 237
```

<210> 77

<211> 241

<212> DNA

<213> Escherichia coli

<400> 77

```
tgtgacagag tggttatcgt taatcaggca aagagggaag aacatattat ttaaaccatt 60
atagcgcata aaatatcctt ataattaaca agaaagaaaa ggcattattct ctgcattatc 120
attttctacg actgtcaaaa atcgctcatt ttttaatgag tttatttgtt taatattatg 180
ggaaaagggt atgcatttgg gagaggaaga gtattccccg gtcagacgac cggggaagggt 240
g 241
```

<210> 78

<211> 89

<212> DNA

<213> Escherichia coli

<400> 78
cccggctggg ttttttcaag tttacgcagg ggtgcgggag atcacttccg ggttgctggc 60
agcttcgcct ttcggcgaaa tgctgtggt 89

<210> 79
<211> 140
<212> DNA
<213> Escherichia coli

<400> 79
tcgcgaacac cgtagtggat gtagttaccc gcagcatctt cgttgattgc tttagaacca 60
gaccacaggg tcagggttaga cggcgccagg tcagcagaac cgccgaggaa ttccggcaac 120
agcggaccga acgcttcgat 140

<210> 80
<211> 189
<212> DNA
<213> Escherichia coli

<400> 80
gttagtaaag ccgatgaggg gagcagtcac ttgcgccgac ggatagtaac ggcgagactc 60
ttcacgcaga tgaatccccg gcagtttcag ttttttgatg tagtccgcca tgtcagggtt 120
cacctgacgc gccagataaa taaagcgccc tttcgggttg gcgttaatgc gggctgaaag 180
ctgatccag 189

<210> 81
<211> 347
<212> DNA
<213> Escherichia coli

<400> 81
gcagttcacc ggcacgcgct ttcttatata agcctttggg atcgcgggct tcgcaaatac 60
ccagcggcgt atcgacaaac acttcgataa agcgcccttc tcctacgcgt tcgcgaacca 120
totggcggtt ggcgcgggtg ggcgagataa atgcgggtcag caccaccagt ccggcttcaa 180
ccatcaaatt cgccacttca ccgacgcgac ggatattctc tttacgatcg gcacgcgtaa 240
aaccgagatc gctgcataat ccgtggcgaa cattgtcgcc atccagcaga tacgtactga 300
cgccgagttt atgtaacgcc tcctccagcg ccccggcgac cgttgat 347

<210> 82
<211> 67
<212> DNA
<213> Escherichia coli

<400> 82
ccctgacgat cagtgatagt cacgatggtg ttgttgaaaag aagcatggat atgagccacg 60
ccgtcag 67

<210> 83
<211> 176
<212> DNA
<213> Escherichia coli

<400> 83
agcaaagcga gccgaacatg gtggcgaggc tgccgtaaag taaaaactgg gtcgccaact 60
ccgggtgatc catcacgtat ttcacgaagt agagcgtcgc cccgccgcgc accacgttgg 120
agcaggtcgc catcatcttg aacgcgcaca tgatgcgcca ctggctgttg ccacagc 176

<210> 84
 <211> 632
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(632)
 <223> n = A,T,C or G

<400> 84
 tnncannnnnc nnnnnnnnnn nnnnnnnncn ntncctagan tntcnangtc tncnncnncn 60
 tnncnnnncc cttcnnnncc nnnnanangn ncnncncccc cnnnccnnt tttgttttgg 120
 aaantccgtt tcaggaanag cttctgaatc ccganccgntt gataactgnn ggccagagtc 180
 ataatgcgca ccaataataa tcagcgggcc atcggcgagga ccataatcag caacaatgnn 240
 nnggtagggg ccacccgtaa tggggaccgt cctgcgaggt aactctggca ccgctactga 300
 caaagacctc ttttatatat tctgcgggac ctattcagat tatcaatatt gtcnnggcact 360
 acgtggatgc acaagtttgt gtaagataac gaactgnttt ttctaattgc tcaggacttt 420
 gcgtgtcggg gccgttgacg gtaatgcatt gacccagggg tggtaaaaaa taatcatagg 480
 gagtaaaaac acaataataa taataaaagc caagattatt tttttcatat gcaaaaattat 540
 taatgggggt gcgtttggtg aatcattatn ttgctatggg ttctgatatt gngattttta 600
 ttaaagatta agcangggat tataccaaaa ga 632

<210> 85
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 85
 gcgctattca gcgtaattgg cagcagctgc ggatcgctcat caatcttctc tgacagcggc 60
 tgatgtactt caaccagacg cgcaccgttt ggttcggcag agacttttat cggagtgttg 120
 atgatattca ctttggtgcc tggggtgacc tggctaaaga g 161

<210> 86
 <211> 188
 <212> DNA
 <213> Escherichia coli

<400> 86
 caaggggtgag catttgcagc gaatcagaaa gggcgcagaa cagtgaagac aacagaaaaa 60
 cgaccagacc gcatttataa atacgtcgat agccaaacat atcgcccaga aacgaaaacg 120
 agagcagggg gatgacaatg gcgatttgat aggcgttcac taccagatg gaactggctg 180
 gcgtggca 188

<210> 87
 <211> 175
 <212> DNA
 <213> Escherichia coli

<400> 87
 tgagcatttg cagcgaatca gaaagggcgc agaacagtga agacaacaga aaaacgacca 60
 gaccgcattt ataaatacgt cgatagccaa acatatcgcc cagaaacgaa aacgagagca 120
 gggagatgac aatggcgatt tgataggcgt tcactacca gatggaactg gctgg 175

<210> 88
 <211> 194
 <212> DNA

<213> Escherichia coli

<400> 88

cgcaagggtg agcatttgca gcgaatcaga aagggcgag aacagtgaag acaacagaaa 60
aagcaccaga ccgcatttat aaatacgtcg atagccaaac atatcgccca gaaacgaaaa 120
cgagagcagg gagatgacaa tggcgatttg ataggcggtc actacccaga tggaactggc 180
tggcgtggca tgaa 194

<210> 89

<211> 272

<212> DNA

<213> Escherichia coli

<400> 89

ccttgataaa ggaaagggtt atgatgaagc tcgtcatcat actggttggtg ttgttactgt 60
taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
tctgtgaacc gctttccggt tagccttttt tatcctgttg gatcttcttg atgatgttgg 240
tcgtcgagca accgtcttca aagttgagca cc 272

<210> 90

<211> 245

<212> DNA

<213> Escherichia coli

<400> 90

ccttgataaa ggaaagggtt atgatgaagc tcgtcatcat actggttggtg ttgttactgt 60
taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
tctgtgaacc gctttccggt tagccttttt tatcctgttg gatcttcttg atgatgttgg 240
tcgtc 245

<210> 91

<211> 203

<212> DNA

<213> Escherichia coli

<400> 91

taccaaaaaa agccacgtta tcttggtgat gcaaaagagt gaacgtggcg ttaaatgtaa 60
ccagttatat cagtagaaaa cctgggtggt gttacagtc taaccggtca attttttatg 120
atttttttga taaaaattaa attttatgtg ctttaatac caccagatga cgttcgccat 180
ccagggtctg aacctgaagt tta 203

<210> 92

<211> 189

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(189)

<223> n = A,T,C or G

<400> 92

ctaataactt attttctgct taccaaaaaa agccacgtta tcttggtgat gcnaaagagt 60
gaacgtggcg ttaaatgtac cagttatatc agtagaaaac ctggttgntg ntaacagtct 120
aacgggcaat tttttatgat ttttttgata aaaattaaat tttatttgct ttaatcacca 180

ccagatgac 189

<210> 93
<211> 221
<212> DNA
<213> Escherichia coli

<400> 93
agcgcaacag cggaaaccag ggtagccagt tttttcatgt tcatattcaa gatgtcctgt 60
agtcgttatt actgcttttt gttgtctacc agcaccgcca gcaaaatcac caccgctttg 120
acgatcatct ggtaatagga ggaaacacct aacaaattca atccattatt aaggaagcca 180
agaattaatg cgccgatcaa cgtcccaaca atgcgacctt t 221

<210> 94
<211> 117
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(117)

<400> 94
atg aaa gtt cgt gct tcc gtc aag aaa tta tgc cgt aac tgc aaa atc 48
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1 5 10 15
gtt aag cgt gat ggt gtc atc cgt gtg att tgc agt gcc gag ccg aag 96
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
20 25 30
cat aaa cag cgc caa ggc tga 117
His Lys Gln Arg Gln Gly *
35

<210> 95
<211> 1332
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1332)

<400> 95
atg gct aaa caa ccg gga tta gat ttt caa agt gcc aaa ggt ggc tta 48
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1 5 10 15
ggc gag ctg aaa cgc aga ctg ctg ttt gtt atc ggt gcg ctg att gtg 96
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
20 25 30
ttc cgt att ggc tct ttt att ccg atc cct ggt att gat gcc gct gta 144
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
35 40 45

ctt gcc aaa ctg ctt gag caa cag cga ggc acc atc att gag atg ttt	192
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe	
50 55 60	
aac atg ttc tct ggt ggt gct ctc agc cgt gct tct atc ttt gct ctg	240
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu	
65 70 75 80	
ggg atc atg ccg tat att tcg gcg tcg atc att atc cag ctg ctg acg	288
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr	
85 90 95	
gtg gtt cac cca acg ttg gca gaa att aag aaa gaa ggg gag tct ggt	336
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly	
100 105 110	
cgt cgt aag atc agc cag tac acc cgc tac ggt act ctg gtg ctg gca	384
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala	
115 120 125	
ata ttc cag tcg atc ggt att gct acc ggt ctg ccg aat atg cct ggt	432
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly	
130 135 140	
atg caa ggc ctg gtg att aac ccg ggc ttt gca ttc tac ttc acc gct	480
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala	
145 150 155 160	
gtt gta agt ctg gtc aca gga acc atg ttc ctg atg tgg ttg ggc gaa	528
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu	
165 170 175	
cag att act gaa cga ggt atc ggc aac ggt att tca atc att atc ttc	576
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe	
180 185 190	
gcc ggt att gtc gcg gga ctc ccg cca gcc att gcc cat act atc gag	624
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu	
195 200 205	
caa gcg cgt caa ggc gac ctg cac ttc ctc gtg ttg ctg ttg gtt gca	672
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala	
210 215 220	
gta tta gta ttt gca gtg acg ttc ttt gtt gta ttt gtt gag cgt ggt	720
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly	
225 230 235 240	
caa cgc cgc att gtg gta aac tac gcg aaa cgt cag caa ggt cgt cgt	768
Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg	
245 250 255	
gtc tat gct gca cag agc aca cat tta ccg ctg aaa gtg aat atg gcg	816
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala	
260 265 270	

```

ggg gta atc ccg gca atc ttc gct tcc agt att att ctg ttc ccg gcg 864
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
275 280 285

acc atc gcg tca tgg ttc ggg ggc ggt act ggt tgg aac tgg ctg aca 912
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290 295 300

aca att tcg ctg tat ttg cag cct ggg caa ccg ctt tat gtg tta ctc 960
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305 310 315 320

tat gcg tct gca atc atc ttc ttc tgt ttc ttc tac acg gcg ttg gtt 1008
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325 330 335

ttc aac ccg cgt gaa aca gca gat aac ctg aag aag tcc ggt gca ttt 1056
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340 345 350

gta cca gga att cgt ccg gga gag caa acg gcg aag tat atc gat aaa 1104
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355 360 365

gta atg acc cgc ctg acc ctg gtt ggt gcg ctg tat att acc ttt atc 1152
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370 375 380

tgc ctg atc ccg gag ttc atg cgt gat gca atg aaa gta ccg ttc tac 1200
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385 390 395 400

ttc ggt ggg acc tca ctg ctt atc gtt gtt gtc gtg att atg gac ttt 1248
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405 410 415

atg gct caa gtg caa act ctg atg atg tcc agt cag tat gag tct gca 1296
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420 425 430

ttg aag aag gcg aac ctg aaa ggc tac ggc cga taa 1332
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg *
435 440

```

<210> 96
 <211> 435
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(435)

```

<400> 96
atg cgt tta aat act ctg tct ccg gcc gaa ggc tcc aaa aag gcg ggt 48
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly

```

1	5	10	15	
aaa cgc ctg ggt cgt ggt atc ggt tct ggc ctc ggt aaa acc ggt ggt				96
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly	20	25	30	
cgt ggt cac aaa ggt cag aag tct cgt tct ggc ggt ggc gta cgt cgc				144
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg	35	40	45	
ggt ttc gag ggt ggt cag atg cct ctg tac cgt cgt ctg ccg aaa ttc				192
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe	50	55	60	
ggc ttc act tct cgt aaa gca gcg att aca gcc gaa att cgt ctg tct				240
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser	65	70	75	80
gac ctg gct aaa gta gaa ggc ggt gta gta gac ctg aac acg ctg aaa				288
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys	85	90	95	
gcg gct aac att atc ggt atc cag atc gag ttc gcg aaa gtg atc ctg				336
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu	100	105	110	
gct ggc gaa gta acg act ccg gta act gtt cgt ggc ctg cgt gtt act				384
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr	115	120	125	
aaa ggc gct cgt gct gct atc gaa gct gct ggc ggt aaa atc gag gaa				432
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu	130	135	140	
taa				435
*				

<210> 97
 <211> 180
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(180)

<400> 97	
atg gca aag act att aaa att act caa acc cgc agt gca atc ggt cgt	48
Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg	
1 5 10 15	
ctg ccg aaa cac aag gca acg ctg ctt ggc ctg ggt ctg cgt cgt att	96
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile	
20 25 30	

ggt cac acc gta gag cgc gag gat act cct gct att cgc ggt atg atc 144
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
35 40 45

aac gcg gtt tcc ttc atg gtt aaa gtt gag gag taa 180
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu *
50 55

<210> 98

<211> 504

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(504)

<400> 98

atg gct cac atc gaa aaa caa gct ggc gaa ctg cag gaa aag ctg atc 48
Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
1 5 10 15

gcg gta aac cgc gta tct aaa acc gtt aaa ggt ggt cgt att ttc tcc 96
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
20 25 30

ttc aca gct ctg act gta gtt ggc gat ggt aac ggt cgc gtt ggt ttt 144
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
35 40 45

ggt tac ggt aaa gcg cgt gaa gtt cca gca gcg atc cag aaa gcg atg 192
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
50 55 60

gaa aaa gcc cgt cgc aat atg att aac gtc gcg ctg aat aac ggc act 240
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65 70 75 80

ctg caa cac cct gtt aaa ggt gtt cac acg ggt tct cgc gta ttc atg 288
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
85 90 95

cag ccg gct tcc gaa ggt acc ggt atc atc gcc ggt ggt gca atg cgc 336
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
100 105 110

gcc gtt ctg gaa gtc gct ggg gtt cat aac gtt ctg gct aaa gcc tat 384
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
115 120 125

ggt tcc acc aac ccg atc aac gtg gtt cgt gca act att gat ggc ctg 432
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
130 135 140

gaa aat atg aat tct cca gaa atg gtc gct gcc aag cgt ggt aaa tcc 480
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser

145	150	155	160	
gtt gaa gaa att ctg ggg aaa taa				504
Val Glu Glu Ile Leu Gly Lys *				
	165			

<210> 99
 <211> 354
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(354)

<400> 99	
atg gat aag aaa tct gct cgt atc cgt cgt gcg acc cgc gca cgc cgc	48
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg	
1 5 10 15	
aag ctc cag gag ctg ggc gca act cgc ctg gtg gta cat cgt acc ccg	96
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro	
20 25 30	
cgt cac att tac gca cag gta att gca ccg aac ggt tct gaa gtt ctg	144
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu	
35 40 45	
gta gct gct tct act gta gaa aaa gct atc gct gaa caa ctg aag tac	192
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr	
50 55 60	
acc ggt aac aaa gac gcg gct gca gct gtg ggt aaa gct gtc gct gaa	240
Thr Gly Asn Lys Asp Ala Ala Ala Ala Val Gly Lys Ala Val Ala Glu	
65 70 75 80	
cgc gct ctg gaa aaa ggc atc aaa gat gta tcc ttt gac cgt tcc ggg	288
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly	
85 90 95	
ttc caa tat cat ggt cgt gtc cag gca ctg gca gat gct gcc cgt gaa	336
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu	
100 105 110	
gct ggc ctt cag ttc taa	354
Ala Gly Leu Gln Phe *	
115	

<210> 100
 <211> 534
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1)...(534)

<400> 100

atg	tct	cgt	ggt	gct	aaa	gca	ccg	gtc	ggt	ggt	cct	gcc	ggc	ggt	gac	48
Met	Ser	Arg	Val	Ala	Lys	Ala	Pro	Val	Val	Val	Pro	Ala	Gly	Val	Asp	
1				5				10						15		

gta	aaa	atc	aac	ggg	cag	ggt	att	acg	atc	aaa	ggg	aaa	aac	ggc	gag	96
Val	Lys	Ile	Asn	Gly	Gln	Val	Ile	Thr	Ile	Lys	Gly	Lys	Asn	Gly	Glu	
			20					25					30			

ctg	act	cgt	act	ctc	aac	gat	gct	ggt	gaa	ggt	aaa	cat	gca	gat	aat	144
Leu	Thr	Arg	Thr	Leu	Asn	Asp	Ala	Val	Glu	Val	Lys	His	Ala	Asp	Asn	
		35					40					45				

acc	ctg	acc	ttc	ggg	ccg	cgt	gat	ggg	tac	gca	gac	ggg	tgg	gca	cag	192
Thr	Leu	Thr	Phe	Gly	Pro	Arg	Asp	Gly	Tyr	Ala	Asp	Gly	Trp	Ala	Gln	
	50					55					60					

gct	ggg	acc	gcg	cgt	gcc	ctg	ctg	aac	tca	atg	ggt	atc	ggg	ggt	acc	240
Ala	Gly	Thr	Ala	Arg	Ala	Leu	Leu	Asn	Ser	Met	Val	Ile	Gly	Val	Thr	
65					70				75						80	

gaa	ggc	ttc	act	aag	aag	ctg	cag	ctg	ggt	ggt	gta	ggg	tac	cgt	gca	288
Glu	Gly	Phe	Thr	Lys	Lys	Leu	Gln	Leu	Val	Gly	Val	Gly	Tyr	Arg	Ala	
				85				90						95		

gcg	ggt	aaa	ggc	aat	gtg	att	aac	ctg	tct	ctg	ggg	ttc	tct	cat	cct	336
Ala	Val	Lys	Gly	Asn	Val	Ile	Asn	Leu	Ser	Leu	Gly	Phe	Ser	His	Pro	
		100					105						110			

ggt	gac	cat	cag	ctg	cct	gcg	ggg	atc	act	gct	gaa	tgt	ccg	act	cag	384
Val	Asp	His	Gln	Leu	Pro	Ala	Gly	Ile	Thr	Ala	Glu	Cys	Pro	Thr	Gln	
		115					120					125				

act	gaa	atc	gtg	ctg	aaa	ggc	gct	gat	aag	cag	gtg	atc	ggc	cag	ggt	432
Thr	Glu	Ile	Val	Leu	Lys	Gly	Ala	Asp	Lys	Gln	Val	Ile	Gly	Gln	Val	
	130					135					140					

gca	gcg	gat	ctg	cgc	gcc	tac	cgt	cgt	cct	gag	cct	tat	aaa	ggc	aag	480
Ala	Ala	Asp	Leu	Arg	Ala	Tyr	Arg	Arg	Pro	Glu	Pro	Tyr	Lys	Gly	Lys	
145					150					155					160	

ggg	ggt	cgt	tac	gcc	gac	gaa	gtc	gtg	cgt	acc	aaa	gag	gct	aag	aag	528
Gly	Val	Arg	Tyr	Ala	Asp	Glu	Val	Val	Arg	Thr	Lys	Glu	Ala	Lys	Lys	
			165					170						175		

aag	taa															534
Lys	*															

<210> 101

<211> 393

<212> DNA

<213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(393)

<400> 101

atg agc atg caa gat ccg atc gcg gat atg ctg acc cgt atc cgt aac	48
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn	
1 5 10 15	
ggt cag gcc gcg aac aaa gct gcg gtc acc atg cct tcc tcc aag ctg	96
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu	
20 25 30	
aaa gtg gca atc gcc aac gtg ctg aag gaa gaa ggt ttt att gaa gat	144
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp	
35 40 45	
ttt aaa gtt gaa ggc gac acc aag cct gaa ctg gaa ctt act ctg aag	192
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys	
50 55 60	
tat ttc cag ggc aaa gct gtt gta gaa agc att cag cgt gtc agc cgc	240
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg	
65 70 75 80	
cca ggt ctg cgc atc tat aaa cgt aaa gat gag ctg ccg aaa gtt atg	288
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met	
85 90 95	
gcg ggt ctg ggt atc gca gtt gtt tct acc tct aaa ggt gtt atg act	336
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr	
100 105 110	
gat cgt gca gcg cgc cag gct ggt ctt ggt ggc gaa att atc tgc tac	384
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr	
115 120 125	
gta gcc taa	393
Val Ala *	
130	

<210> 102
 <211> 306
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(306)

<400> 102

atg gct aag caa tca atg aaa gca cgc gaa gta aaa cgc gta gct tta	48
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu	
1 5 10 15	
gct gat aaa tac ttc gcg aaa cgc gct gaa ctg aaa gcg atc atc tct	96

Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser	
20 25 30	
gat gtg aac gct tcc gac gaa gat cgt tgg aac gct gtt ctc aag ctg	144
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu	
35 40 45	
cag act ctg ccg cgt gat tcc agc ccg tct cgt cag cgt aac cgc tgc	192
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys	
50 55 60	
cgt caa aca ggt cgt ccg cat ggt ttc ctg cgg aag ttc ggg ttg agc	240
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser	
65 70 75 80	
cgt att aag gtc cgt gaa gcc gct atg cgc ggt gaa atc ccg ggt ctg	288
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu	
85 90 95	
aaa aag gct agc tgg taa	306
Lys Lys Ala Ser Trp *	
100	
<210> 103	
<211> 540	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(540)	
<400> 103	
atg gcg aaa ctg cat gat tac tac aaa gac gaa gta gtt aaa aaa ctc	48
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu	
1 5 10 15	
atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag	96
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu	
20 25 30	
aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa	144
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys	
35 40 45	
ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa	192
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys	
50 55 60	
ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt	240
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg	
65 70 75 80	
cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg	288
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met	
85 90 95	

tgg gag ttc ttt gag cgc ctg atc act att gct gta cct cgt atc cgt	336
Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg	
100 105 110	
gac ttc cgt ggc ctg tcc gct aag tct ttc gac ggt cgt ggt aac tac	384
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr	
115 120 125	
agc atg ggt gtc cgt gag cag atc atc ttc cca gaa atc gac tac gat	432
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp	
130 135 140	
aaa gtc gac cgc gtt cgt ggt ttg gat att acc att acc act act gcg	480
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala	
145 150 155 160	
aaa tct gac gaa gaa ggc cgc gct ctg ctg gct gcc ttt gac ttc ccg	528
Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro	
165 170 175	
ttc cgc aag taa	540
Phe Arg Lys *	
<210> 104	
<211> 315	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(315)	
<400> 104	
atg gca gcg aaa atc cgt cgt gat gac gaa gtt atc gtg tta acc ggt	48
Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly	
1 5 10 15	
aaa gat aaa ggt aaa cgc ggt aaa gtt aag aat gtc ctg tct tcc ggc	96
Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly	
20 25 30	
aag gtc att gtt gaa ggt atc aac ctg gtt aag aaa cat cag aag ccg	144
Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro	
35 40 45	
gtt ccg gcc ctg aac caa ccg ggt ggc atc gtt gaa aaa gaa gcc gct	192
Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala	
50 55 60	
att cag gtt tcc aac gta gca atc ttc aat gcg gca acc ggc aag gct	240
Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala	
65 70 75 80	
gac cgt gta ggc ttt aga ttc gaa gac ggt aaa aaa gtc cgt ttc ttc	288

Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
85 90 95

aag tct aac agc gaa act atc aag taa 315
Lys Ser Asn Ser Glu Thr Ile Lys *
100

<210> 105
<211> 372
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(372)

<400> 105
atg atc caa gaa cag act atg ctg aac gtc gcc gac aac tcc ggt gca 48
Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
1 5 10 15

cgt cgc gta atg tgt atc aag gtt ctg ggt ggc tcg cac cgt cgc tac 96
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
20 25 30

gca ggc gta ggc gac atc atc aag atc acc atc aaa gaa gca att ccg 144
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
35 40 45

cgt ggt aag gtc aaa aaa ggt gat gtg ctg aag gcg gta gtg gtg cgc 192
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
50 55 60

acc aag aag ggt gtt cgt cgc ccg gac ggt tct gtc att cgc ttc gat 240
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65 70 75 80

ggt aat gct tgt gtt ctt ctg aac aac aac agc gag cag cct atc ggt 288
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
85 90 95

acg cgt att ttt ggg ccg gta act cgt gag ctt cgt agt gag aag ttc 336
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
100 105 110

atg aaa att atc tct ctg gca cca gaa gta ctc taa 372
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu *
115 120

<210> 106
<211> 1458
<212> DNA
<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1458)

<400> 106

gtg gga att tat ttt act aat tca gat gat caa att tac ttt aaa agg 48
Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg
1 5 10 15

agt gaa ggg atg tct gat ata aac cat gca ggt tct gac ctt ata ttt 96
Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe
20 25 30

gaa ctg gag gat cgc cct ccc ttt cat cag gct ctc gtt ggt gcc att 144
Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile
35 40 45

acc cat ctg ttg gca att ttc gtt ccg atg gta acc ccc gcg tta atc 192
Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile
50 55 60

gtg ggt gcg gcc tta cag ctt tcc gct gaa aca act gcc tat ctt gtt 240
Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val
65 70 75 80

tct atg gcg atg atc gcc tct ggt att ggt acc tgg tta caa gta aac 288
Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn
85 90 95

cgc tac ggc atc gtc ggt tct ggc cta ctc tca att cag tca gtc aat 336
Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn
100 105 110

ttt tca ttt gtt acg gtc atg att gcg ctg ggc agc agc atg aaa agc 384
Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser
115 120 125

gac ggt ttt cac gaa gag tta atc atg tcg tcg ctt ctc ggc gtc tcc 432
Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser
130 135 140

ttc gtt ggc gca ttt ctg gtt gtc gga tct tca ttt atc ttg ccc tat 480
Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr
145 150 155 160

tta cgt cgg gtt att acg cct acc gtc agc ggt att gtg gta ctg atg 528
Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met
165 170 175

atc ggc tta agc ctg att aaa gtc ggc att atc gat ttt ggt gga gga 576
Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly
180 185 190

ttt gca gcc aaa agc agc ggt acg ttc ggc aat tac gaa cat ctc ggc 624
Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly
195 200 205

gtt ggt tta ttg gtt tta att gtg gtg atc ggc ttt aac tgc tgt cgc 672

Val 210	Gly 210	Leu	Leu	Val	Leu	Ile 215	Val	Val	Ile	Gly	Phe 220	Asn	Cys	Cys	Arg	
agt Ser 225	ccg Pro	ttg Leu	cta Leu	cgc Arg	atg Met 230	gga Gly	ggg Gly	atc Ile	gcc Ala	att Ile 235	ggg Gly	cta Leu	tgt Cys	gtc Val	ggc Gly 240	720
tat Tyr	atc Ile	gca Ala	tcg Ser	tta Leu 245	tgc Cys	ctg Leu	ggc Gly	atg Met	gtg Val 250	gat Asp	ttc Phe	agc Ser	agt Ser	atg Met 255	cgc Arg	768
aat Asn	ttg Leu	ccg Pro	tta Leu 260	atc Ile	acc Thr	atc Ile	ccg Pro	cat His 265	ccg Pro	ttc Phe	aaa Lys	tac Tyr	ggc Gly 270	ttt Phe	agt Ser	816
ttt Phe	agc Ser	ttc Phe 275	cat His	cag Gln	ttc Phe	ctg Leu	gtg Val 280	gtt Val	ggc Gly	acg Thr	att Ile 285	tat Tyr	ctg Leu	ctt Leu	agc Ser	864
gtg Val 290	ctg Leu	gaa Glu	gca Ala	gtc Val	ggc Gly	gat Asp 295	atc Ile	acc Thr	gcc Ala	acg Thr	gca Ala 300	atg Met	gtt Val	tcc Ser	cgc Arg	912
cgc Arg 305	ccc Pro	att Ile	cag Gln	ggg Gly	gaa Glu 310	gag Glu	tat Tyr	cag Gln	tcc Ser	cgg Arg 315	ctg Leu	aaa Lys	ggc Gly	ggc Gly	gtg Val 320	960
ctg Leu	gca Ala	gat Asp	ggg Gly	ctg Leu 325	gtt Val	tct Ser	gtt Val	atc Ile	gcc Ala 330	tcc Ser	gct Ala	gtc Val	ggg Gly	tca Ser 335	tta Leu	1008
cca Pro	tta Leu	acc Thr	acg Thr 340	ttt Phe	gcg Ala	caa Gln	aat Asn	aat Asn 345	ggg Gly	gtt Val	att Ile	cag Gln 350	atg Met	act Thr	ggc Gly	1056
gtc Val	gct Ala	tca Ser 355	cgt Arg	tat Tyr	gtc Val	ggg Gly	cga Arg 360	acc Thr	atc Ile	gcg Ala	gta Val 365	atg Met	ctg Leu	gtt Val	atc Ile	1104
ctc Leu	ggc Gly 370	tta Leu	ttt Phe	ccg Pro	atg Met	att Ile 375	ggc Gly	ggc Gly	ttc Phe	ttc Phe 380	acg Thr	acc Thr	att Ile	ccc Pro	tcg Ser	1152
gca Ala 385	gtt Val	ctg Leu	gga Gly	ggc Gly	gca Ala 390	atg Met	acg Thr	ttg Leu	atg Met	ttt Phe 395	tcc Ser	atg Met	att Ile	ggc Ala	atc Ile 400	1200
gca Ala	ggg Gly	att Ile	cgc Arg	atc Ile 405	atc Ile	atc Ile	acc Thr	aac Asn	ggg Gly 410	tta Leu	aag Lys	cgc Arg	cgt Arg	gaa Glu 415	aca Thr	1248
ctt Leu	att Ile	gtc Val 420	gcc Ala	act Thr	tct Ser	tta Leu	ggg Gly 425	tta Leu	ggg Gly	ctt Leu	ggc Gly	gtc Val	tcc Ser	tac Tyr	gat Asp	1296
ccc Pro	gaa Glu	att Ile	ttt Phe	aaa Lys	ata Ile	ttg Leu	cca Pro	gcc Ala	tct Ser	att Ile	tat Tyr	gta Val	tta Leu	gtt Val	gaa Glu	1344

435	440	445	
aac cct att tgt gct ggc ggg tta act gcg att tta tta aat att atc			1392
Asn Pro Ile Cys Ala Gly Gly Leu Thr Ala Ile Leu Leu Asn Ile Ile			
450	455	460	
ctc cct ggt ggc tac cga cag gaa aac gtt ctg cct ggt att acc tca			1440
Leu Pro Gly Gly Tyr Arg Gln Glu Asn Val Leu Pro Gly Ile Thr Ser			
465	470	475	480
gcg gaa gag atg gat taa			1458
Ala Glu Glu Met Asp *			
485			
<210> 107			
<211> 1320			
<212> DNA			
<213> Escherichia coli			/
<220>			
<221> CDS			
<222> (1)...(1320)			
<400> 107			
atg atg tca gga gaa cac acg tta aaa gcg gta cga ggc agt ttt att			48
Met Met Ser Gly Glu His Thr Leu Lys Ala Val Arg Gly Ser Phe Ile			
1	5	10	15
gat gtc acc cgt acg atc gat aac ccg gaa gag att gcc tct gcg ctg			96
Asp Val Thr Arg Thr Ile Asp Asn Pro Glu Glu Ile Ala Ser Ala Leu			
	20	25	30
cgg ttt att gag gat ggt tta tta ctc att aaa cag gga aaa gtg gaa			144
Arg Phe Ile Glu Asp Gly Leu Leu Leu Ile Lys Gln Gly Lys Val Glu			
	35	40	45
tgg ttt ggc gaa tgg gaa aac gga aag cat caa att cct gac acc att			192
Trp Phe Gly Glu Trp Glu Asn Gly Lys His Gln Ile Pro Asp Thr Ile			
50	55	60	
cgc gtg cgc gac tat cgc ggc aaa ctg ata gta ccg ggc ttt gtc gat			240
Arg Val Arg Asp Tyr Arg Gly Lys Leu Ile Val Pro Gly Phe Val Asp			
65	70	75	80
aca cat atc cat tat ccg caa agt gaa atg gtg ggg gcc tat ggt gag			288
Thr His Ile His Tyr Pro Gln Ser Glu Met Val Gly Ala Tyr Gly Glu			
	85	90	95
caa ttg ctg gag tgg ttg aat aaa cac acc ttc cct act gaa cgt cgt			336
Gln Leu Leu Glu Trp Leu Asn Lys His Thr Phe Pro Thr Glu Arg Arg			
	100	105	110
tat gag gat tta gag tac gcc cgc gaa atg tcg gcg ttc ttc atc aag			384
Tyr Glu Asp Leu Glu Tyr Ala Arg Glu Met Ser Ala Phe Phe Ile Lys			
115	120	125	

cag ctt tta cgt aac gga acc acc acg gcg ctg gtg ttt ggc act gtt	432
Gln Leu Leu Arg Asn Gly Thr Thr Thr Ala Leu Val Phe Gly Thr Val	
130 135 140	
cat ccg caa tct gtt gat gcg ctg ttt gaa gcc gcc agt cat atc aat	480
His Pro Gln Ser Val Asp Ala Leu Phe Glu Ala Ala Ser His Ile Asn	
145 150 155 160	
atg cgt atg att gcc ggt aag gtg atg atg gac cgc aac gca ccg gat	528
Met Arg Met Ile Ala Gly Lys Val Met Met Asp Arg Asn Ala Pro Asp	
165 170 175	
tat ctg ctc gac act gcc gaa agc agc tat cac caa agc aaa gaa ctg	576
Tyr Leu Leu Asp Thr Ala Glu Ser Ser Tyr His Gln Ser Lys Glu Leu	
180 185 190	
atc gaa cgc tgg cac aaa aat ggt cgt ctg cta tat gcg att acg cca	624
Ile Glu Arg Trp His Lys Asn Gly Arg Leu Leu Tyr Ala Ile Thr Pro	
195 200 205	
cgc ttc gcc ccg acc tca tct cct gaa cag atg gcg atg gcg caa cgc	672
Arg Phe Ala Pro Thr Ser Ser Pro Glu Gln Met Ala Met Ala Gln Arg	
210 215 220	
ctg aaa gaa gaa tat ccg gat acg tgg gta cat acc cat ctc tgt gaa	720
Leu Lys Glu Glu Tyr Pro Asp Thr Trp Val His Thr His Leu Cys Glu	
225 230 235 240	
aac aaa gat gaa att gcc tgg gtg aaa tcg ctt tat cct gac cat gat	768
Asn Lys Asp Glu Ile Ala Trp Val Lys Ser Leu Tyr Pro Asp His Asp	
245 250 255	
ggt tat ctg gat gtt tac cat cag tac gcc ctg acc ggt aaa aac tgt	816
Gly Tyr Leu Asp Val Tyr His Gln Tyr Gly Leu Thr Gly Lys Asn Cys	
260 265 270	
gtc ttt gct cac tgc gtc cat ctc gaa gaa aaa gag tgg gat cgt ctc	864
Val Phe Ala His Cys Val His Leu Glu Glu Lys Glu Trp Asp Arg Leu	
275 280 285	
agc gaa acc aaa tcc agc att gct ttc tgt ccg acc tcc aac ctt tac	912
Ser Glu Thr Lys Ser Ser Ile Ala Phe Cys Pro Thr Ser Asn Leu Tyr	
290 295 300	
ctc gcc agc gcc tta ttc aac ttg aaa aaa gca tgg cag aag aaa gtt	960
Leu Gly Ser Gly Leu Phe Asn Leu Lys Lys Ala Trp Gln Lys Lys Val	
305 310 315 320	
aaa gtg gcc atg gga acg gat atc ggt gcc gga acc act ttc aac atg	1008
Lys Val Gly Met Gly Thr Asp Ile Gly Ala Gly Thr Thr Phe Asn Met	
325 330 335	
ctg caa acg ctg aac gaa gcc tac aaa gta ttg caa tta caa gcc tat	1056
Leu Gln Thr Leu Asn Glu Ala Tyr Lys Val Leu Gln Leu Gln Gly Tyr	
340 345 350	
cgc ctc tcg gca tat gaa gcg ttt tac ctg gcc acg ctc gcc gga gcg	1104


```

Arg Leu Ser Ala Tyr Glu Ala Phe Tyr Leu Ala Thr Leu Gly Gly Ala
   355                               360                               365

aaa tct ctg ggc ctt gac gat ttg att ggc aac ttt tta cct ggc aaa   1152
Lys Ser Leu Gly Leu Asp Asp Leu Ile Gly Asn Phe Leu Pro Gly Lys
   370                               375                               380

gag gct gat ttc gtg gtg atg gaa ccc acc gcc act ccg cta cag cag   1200
Glu Ala Asp Phe Val Val Met Glu Pro Thr Ala Thr Pro Leu Gln Gln
   385                               390                               395                               400

ctg cgc tat gac aac tct gtt tct tta gtc gac aaa ttg ttc gtg atg   1248
Leu Arg Tyr Asp Asn Ser Val Ser Leu Val Asp Lys Leu Phe Val Met
   405                               410                               415

atg acg ttg ggc gat gac cgt tcg atc tac cgc acc tac gtt gat ggt   1296
Met Thr Leu Gly Asp Asp Arg Ser Ile Tyr Arg Thr Tyr Val Asp Gly
   420                               425                               430

cgt ctg gtg tac gaa cgc aac taa   1320
Arg Leu Val Tyr Glu Arg Asn *
   435

<210> 108
<211> 570
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(570)

<400> 108
atg tct gga gac atc cta caa aca ccg gac gca cca aag cca cag ggc   48
Met Ser Gly Asp Ile Leu Gln Thr Pro Asp Ala Pro Lys Pro Gln Gly
   1                               5                               10                               15

gcg ctg gat aat tat ttt aaa att acc gct cgt ggc agt acc gtt cgt   96
Ala Leu Asp Asn Tyr Phe Lys Ile Thr Ala Arg Gly Ser Thr Val Arg
   20                               25                               30

cag gaa gta ctg gct ggc tta acg acc ttt ctg gcc atg gtt tat tcc   144
Gln Glu Val Leu Ala Gly Leu Thr Thr Phe Leu Ala Met Val Tyr Ser
   35                               40                               45

gtt atc gtc gtt ccg gga atg ctg ggc aaa gca ggt ttt cct ccc gca   192
Val Ile Val Val Pro Gly Met Leu Gly Lys Ala Gly Phe Pro Pro Ala
   50                               55                               60

gct gtg ttt gtt gcc acc tgt ctg gtc gcg ggc ttc ggc tcg ttg ctg   240
Ala Val Phe Val Ala Thr Cys Leu Val Ala Gly Phe Gly Ser Leu Leu
   65                               70                               75                               80

atg gga tta tgg gct aat ttg cca atg gcg att ggt tgc gcg att tcc   288
Met Gly Leu Trp Ala Asn Leu Pro Met Ala Ile Gly Cys Ala Ile Ser
   85                               90                               95

```

ttg acg gcg ttt acc gca ttc agt ctg gta ctc ggg caa caa att agc	336
Leu Thr Ala Phe Thr Ala Phe Ser Leu Val Leu Gly Gln Gln Ile Ser	
100 105 110	
gtt cct gtc gca ctg ggc gcg gta ttt ctg atg ggc gtc atc ttc acc	384
Val Pro Val Ala Leu Gly Ala Val Phe Leu Met Gly Val Ile Phe Thr	
115 120 125	
gcc att tcc gta acc ggt gtg cgt acc tgg atc tta cgt aat ttg ccg	432
Ala Ile Ser Val Thr Gly Val Arg Thr Trp Ile Leu Arg Asn Leu Pro	
130 135 140	
atg ggt atc gct cac ggt aca ggt atc ggt atc ggg ctg ttt ctg ctg	480
Met Gly Ile Ala His Gly Thr Gly Ile Gly Ile Gly Leu Phe Leu Leu	
145 150 155 160	
ctg att gct gct aac ggt gtg ggt atg gtt atc aaa aac ccg att gaa	528
Leu Ile Ala Ala Asn Gly Val Gly Met Val Ile Lys Asn Pro Ile Glu	
165 170 175	
ggc ttg cag tgg cgc tcg gtg cgt tta cct cct tcc ccg tga	570
Gly Leu Gln Trp Arg Ser Val Arg Leu Pro Pro Ser Arg *	
180 185	
<210> 109	
<211> 831	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(831)	
<400> 109	
gtg gcg ctc ggt gcg ttt acc tcc ttc ccg gtg atg atg agc ttg ctg	48
Met Ala Leu Gly Ala Phe Thr Ser Phe Pro Val Met Met Ser Leu Leu	
1 5 10 15	
ggg ctg gcg gtc atc ttc ggc ctg gag aag tgt cgc gta ccc ggc ggc	96
Gly Leu Ala Val Ile Phe Gly Leu Glu Lys Cys Arg Val Pro Gly Gly	
20 25 30	
atc ttg ttg gtg att att gca att tcg atc atc ggc tta atc ttt gac	144
Ile Leu Leu Val Ile Ile Ala Ile Ser Ile Ile Gly Leu Ile Phe Asp	
35 40 45	
cca gcg gtg aaa tac cac ggt ctg gtg gcg atg cca agc ctg act ggc	192
Pro Ala Val Lys Tyr His Gly Leu Val Ala Met Pro Ser Leu Thr Gly	
50 55 60	
gaa gat ggt aag tct ctg att ttc agc ctc gat att atg ggt gca ctc	240
Glu Asp Gly Lys Ser Leu Ile Phe Ser Leu Asp Ile Met Gly Ala Leu	
65 70 75 80	

cag cca act gta ctt ccg agt gta ctg gca ttg gtg atg acc gca gtg	288
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val	
85 90 95	
ttc gac gct act ggc acc atc cgt gcc gtc gcc ggt cag gcg aat ttg	336
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu	
100 105 110	
ttg gat aaa gac aac cag atc atc aac ggc ggc aaa gcc ctg acc agt	384
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser	
115 120 125	
gac tca gta agt tca ata ttc tcc ggc ctg gtg ggc gca gcg ccc gca	432
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala	
130 135 140	
gcg gtt tat atc gaa tca gcg gca gga acc gcc gcc ggg ggt aaa aca	480
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr	
145 150 155 160	
ggg tta acc gca acc gta gtg ggg gcg tta ttc ctg tta att ctg ttt	528
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe	
165 170 175	
tta tca ccg ctg tca ttt ttg atc cct ggt tac gcc act gca ccc gct	576
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala	
180 185 190	
ctg atg tac gta ggt ttg ctg atg tta agt aac gtc tgc aag ctg gat	624
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp	
195 200 205	
ttc aat gat ttt att gac gct atg gct ggc ctg gtg tgt gcc gtg ttc	672
Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe	
210 215 220	
atc gtt ctg act tgt aat atc gtt acc ggt att atg ctg ggc ttt gtg	720
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val	
225 230 235 240	
aca ctg gtc gta ggc cgc gtc ttt gca cgc gaa tgg caa aag ctg aat	768
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn	
245 250 255	
att ggt acg gtg atc att act gcc gca ctg gtc gca ttt tac gcg ggt	816
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly	
260 265 270	
ggg tgg gca atc taa	831
Gly Trp Ala Ile *	
275	

<210> 110

<211> 1401

<212> DNA

<213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1401)

<400> 110

atg aat agc gaa ggg ggg aaa ccg ggg aat gta ctg acc gtt aac ggc	48
Met Asn Ser Glu Gly Lys Pro Gly Asn Val Leu Thr Val Asn Gly	
1 5 10 15	
aac tat acc gga aac aat ggc ctg atg acg ttc aac gcg acg ctg ggc	96
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly	
20 25 30	
ggc gat aat tcg ccc acc gat aag atg aac gtg aaa ggc gat acc caa	144
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln	
35 40 45	
ggg aac act cgc gtt cgg gtt gat aac att ggc ggc gtc ggt gca caa	192
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln	
50 55 60	
acg gtc aac ggt att gaa ctc att gag gtt ggc ggt aat tct gca ggt	240
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly	
65 70 75 80	
aac ttc gcg ctg acc acc gga act gtc gaa gct ggg gct tac gtc tac	288
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr	
85 90 95	
acg ctg gct aaa ggg aag ggg aat gac gag aaa aac tgg tat ctg acc	336
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr	
100 105 110	
agt aaa tgg gac ggc gta acg cca gcg gat aca ccc gat ccc atc aat	384
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn	
115 120 125	
aat ccc cct gtt gtg gat ccg gaa ggc cca tca gtt tat cgc ccg gag	432
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu	
130 135 140	
gcc gga agc tat atc agc aac att gcc gca gcc aac tcg ctg ttt agc	480
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Asn Ser Leu Phe Ser	
145 150 155 160	
cat cgt tta cac gac cgt ctg ggt gag ccg cag tat aca gat tca ctg	528
His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu	
165 170 175	
cat tct cag ggg tcg gca agc agt atg tgg atg cgt cat gtc gga ggg	576
His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly	
180 185 190	
cac gaa cgt tca agg gcc ggt gac ggt cag cta aat act cag gct aac	624
His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn	
195 200 205	

cg	cg	t	g	t	c	g	g	g	g	t	t	g	c	g	t	g	a	g	a	c		672
Arg	Tyr	Val	Leu	Gln	Leu	Gly	Gly	Asp	Leu	Ala	Gln	Trp	Ser	Ser	Asn							
	210					215					220											
gc	gc	g	gc	tg	ca	ct	gc	gt	at	gc	gc	ta	gc	aa	ca							720
Ala	Gln	Asp	Arg	Trp	His	Leu	Gly	Val	Met	Ala	Gly	Tyr	Ala	Asn	Gln							
	225				230					235					240							
ca	ag	aa	ac	ca	ag	aa	cg	gt	gg	ta	aa	tc	ga	gg	cg							768
His	Ser	Asn	Thr	Gln	Ser	Asn	Arg	Val	Gly	Tyr	Lys	Ser	Asp	Gly	Arg							
			245						250					255								
at	ag	gg	ta	ag	gc	gg	ct	ta	gc	ac	tg	ta	ca	aa	ga							816
Ile	Ser	Gly	Tyr	Ser	Ala	Gly	Leu	Tyr	Ala	Thr	Trp	Tyr	Gln	Asn	Asp							
			260					265					270									
gc	aa	aa	ac	gc	gc	ta	gt	ga	ag	tg	gc	ct	ta	aa	tg							864
Ala	Asn	Lys	Thr	Gly	Ala	Tyr	Val	Asp	Ser	Trp	Ala	Leu	Tyr	Asn	Trp							
		275					280					285										
tt	ga	aa	ag	gc	ag	tc	ga	aa	cg	tc	gc	ga	ga	ta	ga							912
Phe	Asp	Asn	Ser	Val	Ser	Ser	Asp	Asn	Arg	Ser	Ala	Asp	Asp	Tyr	Asp							
	290					295					300											
tc	gc	gg	gt	ac	gc	tc	gt	ga	gg	gg	ta	ac	tt	ga	gc							960
Ser	Arg	Gly	Val	Thr	Ala	Ser	Val	Glu	Gly	Gly	Tyr	Thr	Phe	Glu	Ala							
	305				310				315					320								
gg	aa	tt	ag	gc	ag	ga	gg	ac	ct	aa	ac	tg	ta	gc	ca							1008
Gly	Thr	Phe	Ser	Gly	Ser	Glu	Gly	Thr	Leu	Asn	Thr	Trp	Tyr	Val	Gln							
			325					330						335								
cc	ca	gc	ca	at	ac	tg	at	gg	gt	aa	ga	tc	ga	ca	ac							1056
Pro	Gln	Ala	Gln	Ile	Thr	Trp	Met	Gly	Val	Lys	Asp	Ser	Asp	His	Thr							
			340				345						350									
cg	aa	ga	ga	ac	cg	at	ga	ac	ga	gg	ga	ga	aa	gt	ca							1104
Arg	Lys	Asp	Gly	Thr	Arg	Ile	Glu	Thr	Glu	Gly	Asp	Gly	Asn	Val	Gln							
		355				360					365											
ac	cg	ct	gg	gt	aa	ac	ta	ct	aa	ag	ca	ca	ca	cg	ga							1152
Thr	Arg	Leu	Gly	Val	Lys	Thr	Tyr	Leu	Asn	Ser	His	His	Gln	Arg	Asp							
	370				375						380											
ga	gg	aa	ca	cg	ga	tc	ca	cc	ta	at	ga	gc	aa	tg	at							1200
Asp	Gly	Lys	Gln	Arg	Glu	Phe	Gln	Pro	Tyr	Ile	Glu	Ala	Asn	Trp	Ile							
	385				390				395					400								
aa	aa	ag	aa	gc	ta	gc	gt	aa	at	aa	gg	ca	ac	ga	gc							1248
Asn	Asn	Ser	Lys	Val	Tyr	Ala	Val	Lys	Met	Asn	Gly	Gln	Thr	Val	Gly							
			405					410					415									
cg	ga	gg	gc	cg	aa	ct	gg	ga	ga	cg	ac	gg	gt	ga	gc							1296
Arg	Glu	Gly	Ala	Arg	Asn	Leu	Gly	Glu	Val	Arg	Thr	Gly	Val	Glu	Ala							
			420				425						430									

```

aaa gta aat aac aac ctt agc ctg tgg ggg aat gtc ggt gtg caa cta 1344
Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
      435                      440                      445

ggt gat aaa ggc tat agc gat act cag ggc atg ctg gga gtg aaa tat 1392
Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
      450                      455                      460

agc tgg taa
Ser Trp *
465

<210> 111
<211> 3978
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(3978)

<400> 111
atg aat aga atc tat cgc gtg ata tgg aat tgc act cta cag gta ttt 48
Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
  1                      5                      10                      15

cag gcc tgc tcg gaa tta act cgc agg gca ggt aaa aca tcg acg gtt 96
Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
      20                      25                      30

aat ttg cgt aaa tcc tct gga ctg aca acg aaa ttc agt aga ttg acg 144
Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
      35                      40                      45

ctg ggt gtt ttg ctg gca cta agc ggt tca gcg tct ggt gca agt ctg 192
Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
      50                      55                      60

gaa gtt gat aat gat cag att acc aat att gat act gat gtt gct tat 240
Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
      65                      70                      75                      80

gat gcc tac ctg gtt ggc tgg tat ggc act gga gtg ctt aat att ttg 288
Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
      85                      90                      95

gct ggc ggt aat gcc tcc tta acc act att act acc agc gtc att ggc 336
Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly
      100                      105                      110

gct aat gag gac tca gag ggc acc gtt aat gtt ttg ggt ggc acc tgg 384
Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp
      115                      120                      125

cga ttg tat gat agc gga aat aat gca agg cct tta aat gtg ggt caa 432
Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln

```

130	135	140	
tcc gga acg ggg acg ctg aat att aaa cag aag ggt cac gtc gat gga			480
Ser Gly Thr Gly Thr Leu Asn Ile Lys Gln Lys Gly His Val Asp Gly			
145	150	155	160
ggc tat tta aga tta ggt tct tcg aca gga ggc gtc ggg acg gtc aat			528
Gly Tyr Leu Arg Leu Gly Ser Ser Thr Gly Gly Val Gly Thr Val Asn			
	165	170	175
gtt gag gga gag gac tct gtt ctg acg acc gaa tta ttc gaa ata ggt			576
Val Glu Gly Glu Asp Ser Val Leu Thr Thr Glu Leu Phe Glu Ile Gly			
	180	185	190
agc tat ggc aca ggt tca tta aat att acg gat aag ggt tac gtc acg			624
Ser Tyr Gly Thr Gly Ser Leu Asn Ile Thr Asp Lys Gly Tyr Val Thr			
	195	200	205
agt tca atc gtc gcc att tta ggc tat cag gcg ggc agt aat ggc cag			672
Ser Ser Ile Val Ala Ile Leu Gly Tyr Gln Ala Gly Ser Asn Gly Gln			
	210	215	220
gtt gtc gtt gaa aag ggt ggc gag tgg cta ata aaa aat aat gat tcc			720
Val Val Val Glu Lys Gly Gly Glu Trp Leu Ile Lys Asn Asn Asp Ser			
	225	230	235
tca att gaa ttt caa att ggt aat caa gga act ggc gag gcg act att			768
Ser Ile Glu Phe Gln Ile Gly Asn Gln Gly Thr Gly Glu Ala Thr Ile			
	245	250	255
cgc gag ggc ggc ttg gtt acg gct gaa aat acg att atc ggt ggc aat			816
Arg Glu Gly Gly Leu Val Thr Ala Glu Asn Thr Ile Ile Gly Gly Asn			
	260	265	270
gcc acc ggt atc gga acc ctg aat gtg cag gat caa gac tct gtc atc			864
Ala Thr Gly Ile Gly Thr Leu Asn Val Gln Asp Gln Asp Ser Val Ile			
	275	280	285
acg gta cgc aga ctc tat aat gga tat ttc ggt aat ggc aca gtc aat			912
Thr Val Arg Arg Leu Tyr Asn Gly Tyr Phe Gly Asn Gly Thr Val Asn			
	290	295	300
att tcc aat aat gga ctg att aat aac aaa gaa tat tca ttg gtg ggc			960
Ile Ser Asn Asn Gly Leu Ile Asn Asn Lys Glu Tyr Ser Leu Val Gly			
	305	310	315
gtt cag gac ggt tcc cac ggt gtc gtc aac gtg acc gat aaa ggc cat			1008
Val Gln Asp Gly Ser His Gly Val Val Asn Val Thr Asp Lys Gly His			
	325	330	335
tgg aat ttc ctc gga acg ggc gaa gct ttc cgc tat atc tat atc ggt			1056
Trp Asn Phe Leu Gly Thr Gly Glu Ala Phe Arg Tyr Ile Tyr Ile Gly			
	340	345	350
gat gct ggc gac ggt gaa ctt aat gtc tcg agt gaa ggc aaa gta gat			1104
Asp Ala Gly Asp Gly Glu Leu Asn Val Ser Ser Glu Gly Lys Val Asp			
	355	360	365

gtg gat ggg cag aac tct ctt ctt gaa aca ttc aat atg tac gta ggg Val Asp Gly Gln Asn Ser Leu Leu Glu Thr Phe Asn Met Tyr Val Gly 595 600 605	1824
aca tct ggt acg ggt acg tta acc ctg acg aat aac ggt acg ctg aat Thr Ser Gly Thr Gly Thr Leu Thr Leu Thr Asn Asn Gly Thr Leu Asn 610 615 620	1872
gtc gaa ggt gga gaa gtt tac tta ggt gtt ttt gag cct gct gta gga Val Glu Gly Gly Glu Val Tyr Leu Gly Val Phe Glu Pro Ala Val Gly 625 630 635 640	1920
acg cta aac att ggt gct gct cac ggt gag gcg gcg gca gat gcc gga Thr Leu Asn Ile Gly Ala Ala His Gly Glu Ala Ala Ala Asp Ala Gly 645 650 655	1968
ttt atc acc aat gcg acg aaa gtg gag ttt ggt ctt ggc gaa ggc gtt Phe Ile Thr Asn Ala Thr Lys Val Glu Phe Gly Leu Gly Glu Gly Val 660 665 670	2016
ttt gtc ttt aat cat acc aat aac agt gat gcc ggc tac cag gtc gat Phe Val Phe Asn His Thr Asn Asn Ser Asp Ala Gly Tyr Gln Val Asp 675 680 685	2064
atg ctg att aca ggt gac gat aaa gac gga aaa gtg atc cat gat gca Met Leu Ile Thr Gly Asp Asp Lys Asp Gly Lys Val Ile His Asp Ala 690 695 700	2112
ggc cat acg gtg ttc aat gca ggg aat act tat agc ggt aaa acg ctg Gly His Thr Val Phe Asn Ala Gly Asn Thr Tyr Ser Gly Lys Thr Leu 705 710 715 720	2160
gtc aat gac ggc ctc ctg acc att gcg tct cat acg gca gat ggg gta Val Asn Asp Gly Leu Leu Thr Ile Ala Ser His Thr Ala Asp Gly Val 725 730 735	2208
acg ggc atg ggg tcg agt gaa gta acc att gca aac ccc ggt acg ctc Thr Gly Met Gly Ser Ser Glu Val Thr Ile Ala Asn Pro Gly Thr Leu 740 745 750	2256
gac att ctc gca tca acg aac agt gca gga gat tac acg ctg acc aat Asp Ile Leu Ala Ser Thr Asn Ser Ala Gly Asp Tyr Thr Leu Thr Asn 755 760 765	2304
gcg ctc aaa ggc gat ggc ttg atg cga gtg cag ctg tca tcc tcc gac Ala Leu Lys Gly Asp Gly Leu Met Arg Val Gln Leu Ser Ser Ser Asp 770 775 780	2352
aag atg ttt ggc ttt acc cat gca aca ggg act gaa ttc gcc ggt gtt Lys Met Phe Gly Phe Thr His Ala Thr Gly Thr Glu Phe Ala Gly Val 785 790 795 800	2400
gcc caa ctg aaa gac agt acc ttc act ctg gaa cgc gac aac acc gct Ala Gln Leu Lys Asp Ser Thr Phe Thr Leu Glu Arg Asp Asn Thr Ala 805 810 815	2448
gcg ctt act cac gcg atg ttg cag tct gac agt gaa aat acc aca tcg	2496

Ala	Leu	Thr	His	Ala	Met	Leu	Gln	Ser	Asp	Ser	Glu	Asn	Thr	Thr	Ser	
			820					825					830			
gta	aaa	gtt	gga	gag	caa	tcc	att	ggt	gga	ctg	gcc	atg	aat	gga	ggt	2544
Val	Lys	Val	Gly	Glu	Gln	Ser	Ile	Gly	Gly	Leu	Ala	Met	Asn	Gly	Gly	
		835					840					845				
acc	atc	att	ttc	gat	acg	gat	att	cct	gct	gcg	acg	ctc	gcg	gag	gga	2592
Thr	Ile	Ile	Phe	Asp	Thr	Asp	Ile	Pro	Ala	Ala	Thr	Leu	Ala	Glu	Gly	
	850					855					860					
tat	atc	agc	gtc	gat	acg	ctg	gtt	gtc	ggc	gcg	ggt	gac	tac	acc	tg	2640
Tyr	Ile	Ser	Val	Asp	Thr	Leu	Val	Val	Gly	Ala	Gly	Asp	Tyr	Thr	Trp	
865					870				875						880	
aaa	ggc	cgt	aac	tat	cag	gta	aac	ggg	acg	ggc	gac	gtg	ctt	atc	gac	2688
Lys	Gly	Arg	Asn	Tyr	Gln	Val	Asn	Gly	Thr	Gly	Asp	Val	Leu	Ile	Asp	
			885					890						895		
gtg	cct	aaa	ccg	tgg	aat	gat	ccc	atg	gcg	aat	aac	cct	ctg	acg	acg	2736
Val	Pro	Lys	Pro	Trp	Asn	Asp	Pro	Met	Ala	Asn	Asn	Pro	Leu	Thr	Thr	
			900				905						910			
ctc	aat	ttg	ctg	gaa	cac	gac	gat	agc	cat	gtc	ggc	gtt	caa	ctg	gtg	2784
Leu	Asn	Leu	Leu	Glu	His	Asp	Asp	Ser	His	Val	Gly	Val	Gln	Leu	Val	
		915					920					925				
aag	gcg	caa	acg	gtt	att	ggg	tcg	ggt	ggc	tca	tta	acg	tta	cgt	gat	2832
Lys	Ala	Gln	Thr	Val	Ile	Gly	Ser	Gly	Gly	Ser	Leu	Thr	Leu	Arg	Asp	
	930					935					940					
tta	cag	ggc	gac	gag	gtg	gaa	gcg	gac	aaa	acg	tta	cac	att	gcg	caa	2880
Leu	Gln	Gly	Asp	Glu	Val	Glu	Ala	Asp	Lys	Thr	Leu	His	Ile	Ala	Gln	
945					950				955						960	
aac	gga	acg	gtg	gtc	gcc	gag	ggt	gat	tat	gga	ttc	cgc	ctc	acg	acc	2928
Asn	Gly	Thr	Val	Val	Ala	Glu	Gly	Asp	Tyr	Gly	Phe	Arg	Leu	Thr	Thr	
			965					970					975			
gca	cca	ggt	aat	ggt	ttg	tac	gtt	aac	tat	ggg	ctg	aaa	gcg	ctg	aac	2976
Ala	Pro	Gly	Asn	Gly	Leu	Tyr	Val	Asn	Tyr	Gly	Leu	Lys	Ala	Leu	Asn	
			980				985					990				
atc	cat	ggt	ggg	caa	aag	ctg	acg	tta	gcc	gaa	cat	ggc	gga	gcc	tat	3024
Ile	His	Gly	Gly	Gln	Lys	Leu	Thr	Leu	Ala	Glu	His	Gly	Gly	Ala	Tyr	
		995				1000						1005				
ggc	gca	acg	gcc	gat	atg	tcg	gca	aaa	atc	ggt	ggt	gaa	ggg	gat	ctg	3072
Gly	Ala	Thr	Ala	Asp	Met	Ser	Ala	Lys	Ile	Gly	Gly	Glu	Gly	Asp	Leu	
	1010					1015					1020					
gca	atc	aat	acg	gtg	cga	cag	gtt	tcg	ctt	tcc	aac	ggt	cag	aac	gac	3120
Ala	Ile	Asn	Thr	Val	Arg	Gln	Val	Ser	Leu	Ser	Asn	Gly	Gln	Asn	Asp	
1025					1030				1035						1040	
tat	cag	ggg	gca	acc	tac	gtt	cag	atg	ggg	aca	tta	cgt	acc	gat	gcg	3168
Tyr	Gln	Gly	Ala	Thr	Tyr	Val	Gln	Met	Gly	Thr	Leu	Arg	Thr	Asp	Ala	

				1045				1050				1055					
gat	ggt	gca	ctt	ggc	aac	acc	cgg	gaa	ctg	aac	atc	agc	aac	gcg	gcc	3216	
Asp	Gly	Ala	Leu	Gly	Asn	Thr	Arg	Glu	Leu	Asn	Ile	Ser	Asn	Ala	Ala		
1060				1065				1070									
atc	gtc	gat	ctt	aat	gga	tcg	acg	cag	acg	gta	gag	aca	ttc	acc	ggg	3264	
Ile	Val	Asp	Leu	Asn	Gly	Ser	Thr	Gln	Thr	Val	Glu	Thr	Phe	Thr	Gly		
1075				1080				1085									
cag	atg	ggt	tcg	act	gtt	ttg	ttc	aaa	gag	ggg	gcg	ctg	acg	gta	aat	3312	
Gln	Met	Gly	Ser	Thr	Val	Leu	Phe	Lys	Glu	Gly	Ala	Leu	Thr	Val	Asn		
1090				1095				1100									
aaa	ggt	ggg	atc	agt	cag	ggt	gaa	ctg	aca	ggt	ggc	gga	aac	ctg	aat	3360	
Lys	Gly	Gly	Ile	Ser	Gln	Gly	Glu	Leu	Thr	Gly	Gly	Gly	Asn	Leu	Asn		
1105				1110				1115				1120					
gtt	aca	ggg	gga	acg	ctg	gct	atc	gag	ggg	ctt	aat	gca	cgc	tac	aat	3408	
Val	Thr	Gly	Gly	Thr	Leu	Ala	Ile	Glu	Gly	Leu	Asn	Ala	Arg	Tyr	Asn		
1125				1130				1135									
gcg	tta	acc	agc	att	agc	cca	aat	gcg	gaa	gtc	agc	ctc	gat	aat	act	3456	
Ala	Leu	Thr	Ser	Ile	Ser	Pro	Asn	Ala	Glu	Val	Ser	Leu	Asp	Asn	Thr		
1140				1145				1150									
cag	ggg	tta	ggc	aga	gga	aat	att	gcc	aat	gac	ggt	ctg	tta	acg	cta	3504	
Gln	Gly	Leu	Gly	Arg	Gly	Asn	Ile	Ala	Asn	Asp	Gly	Leu	Leu	Thr	Leu		
1155				1160				1165									
aaa	aac	gtg	act	ggc	gaa	ctg	cgt	aat	agc	ata	agc	ggg	aag	ggt	atc	3552	
Lys	Asn	Val	Thr	Gly	Glu	Leu	Arg	Asn	Ser	Ile	Ser	Gly	Lys	Gly	Ile		
1170				1175				1180									
gtg	agc	gca	acc	gcc	agg	aca	gat	gta	gag	ttg	gat	ggc	gat	aat	agc	3600	
Val	Ser	Ala	Thr	Ala	Arg	Thr	Asp	Val	Glu	Leu	Asp	Gly	Asp	Asn	Ser		
1185				1190				1195				1200					
cgc	ttt	gtg	ggg	caa	ttc	aac	att	gat	aca	ggc	agc	gcg	ctc	agc	gtc	3648	
Arg	Phe	Val	Gly	Gln	Phe	Asn	Ile	Asp	Thr	Gly	Ser	Ala	Leu	Ser	Val		
1205				1210				1215									
aac	gag	cag	aaa	aac	ctg	ggt	gat	gct	tcc	gtt	atc	aat	aat	ggc	ctg	3696	
Asn	Glu	Gln	Lys	Asn	Leu	Gly	Asp	Ala	Ser	Val	Ile	Asn	Asn	Gly	Leu		
1220				1225				1230									
ctc	acc	atc	tcc	act	gag	cgt	agc	tgg	gcg	atg	acg	cac	agt	atc	agc	3744	
Leu	Thr	Ile	Ser	Thr	Glu	Arg	Ser	Trp	Ala	Met	Thr	His	Ser	Ile	Ser		
1235				1240				1245									
ggt	agc	ggt	gat	gtg	aca	aaa	ctg	ggt	acc	ggg	atc	ctg	act	ctt	aac	3792	
Gly	Ser	Gly	Asp	Val	Thr	Lys	Leu	Gly	Thr	Gly	Ile	Leu	Thr	Leu	Asn		
1250				1255				1260									
aac	gat	tcc	gcg	gcg	tat	cag	ggt	acg	acg	gat	atc	gtg	ggg	ggg	gaa	3840	
Asn	Asp	Ser	Ala	Ala	Tyr	Gln	Gly	Thr	Thr	Asp	Ile	Val	Gly	Gly	Glu		
1265																	

att gct ttc ggt tcc gac tct gcc att aat atg gca agt caa cac att 3888
 Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile
 1285 1290 1295

aat atc cat aac agc ggt gtg atg tcg gga aat gtc acc act gca ggt 3936
 Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly
 1300 1305 1310

gat atg aac gtt atg cct ggg ggg ggc act gcg tgt cgc taa 3978
 Asp Met Asn Val Met Pro Gly Gly Gly Thr Ala Cys Arg *
 1315 1320 1325

<210> 112

<211> 756

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(756)

<400> 112

atg act gaa gca caa aga cat caa atc ctc ctg gaa atg ctc gca caa 48
 Met Thr Glu Ala Gln Arg His Gln Ile Leu Leu Glu Met Leu Ala Gln
 1 5 10 15

ttg ggc ttt gtg acc gtt gag aaa gtc gtt gag cgt ctg gga att tcg 96
 Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser
 20 25 30

cct gcc act gcg cga cgc gat atc aat aaa ctt gac gaa agc ggc aaa 144
 Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys
 35 40 45

ctg aaa aaa gtg cgc aat ggc gca gaa gct att acc caa cag cgc ccg 192
 Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro
 50 55 60

cgc tgg acg ccg atg aat ctg cat cag gcg cag aat cac gat gaa aaa 240
 Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys
 65 70 75 80

gta cgt atc gct aaa gcg gcc tcg cag ctg gtt aat ccg ggc gaa agc 288
 Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser
 85 90 95

gta gtc atc aac tgc ggc tcc acc gcg ttt ctg ctt ggg cgg gaa atg 336
 Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met
 100 105 110

tgt ggc aag cca gtg caa atc atc act aat tat cta ccg ctg gca aat 384
 Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn
 115 120 125

tac ctg atc gat caa gaa cat gac agc gtg atc att atg ggc gga cag	432
Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln	
130 135 140	
tac aac aaa agt cag tcc atc act tta agc ccg cag ggc agc gaa aac	480
Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn	
145 150 155 160	
agt ctc tat gcc ggg cac tgg atg ttt acc agc gga aaa ggg ctg acc	528
Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr	
165 170 175	
gca gaa ggg ttg tat aaa acc gat atg ctg aca gca atg gca gag cag	576
Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln	
180 185 190	
aag atg ctg agc gtg gta ggg aaa ctg gtg gta ctg gtt gat agc agt	624
Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser	
195 200 205	
aag att ggc gaa cgc gcg gga atg ctt ttt agc cgt gcc gat caa atc	672
Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile	
210 215 220	
gat atg ctt atc acc ggc aaa aat gct aac ccg gaa atc ctg caa caa	720
Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln	
225 230 235 240	
ctg gaa gcg caa ggg gtc agc att ctg cgt gtt taa	756
Leu Glu Ala Gln Gly Val Ser Ile Leu Arg Val *	
245 250	
<210> 113	
<211> 825	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(825)	
<400> 113	
atg acc gaa ttt aca act ctt ctt cag caa gga aac gcc tgg ttc ttc	48
Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe	
1 5 10 15	
atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg	96
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly	
20 25 30	
cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc	144
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr	
35 40 45	
att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc	192
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr	

50	55	60	
gca gtg gtc tgg tta att gcc ttt ggc ggg atg gtg atc agc aag cgc	240		
Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg			
65 70 75 80			
ttt act gct caa tca gca gaa ccg tgg ctc cag ctg att tcc gca gtg	288		
Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val			
85 90 95			
atc att att agc acc gcg ttc tgg atg ttc tgg cgt acc tgg cgc ggc	336		
Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly			
100 105 110			
gaa cgc aac tgg ctg gag aat atg cac ggg cat gat tat gag cat cat	384		
Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His			
115 120 125			
cat cac gat cac gaa cat cac cac gac cat gga cat cat cac cat cac	432		
His His Asp His Glu His His His His Asp His Gly His His His His His			
130 135 140			
gaa cat ggc gag tat cag gat gcc cat gca cga gcc cat gcc aat gac	480		
Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp			
145 150 155 160			
att aaa cga cgc ttt gat ggt aga gag gtc acc aac tgg caa att ttg	528		
Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu			
165 170 175			
tta ttt ggc tta acc ggt ggc ctt atc ccc tgc ccg gca gca att acc	576		
Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr			
180 185 190			
gtg ctg ttg ata tgc att cag ttg aaa gcc ctg aca ctg ggc gca aca	624		
Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr			
195 200 205			
ctg gtc gtc agt ttc agc att ggc ctg gcg tta acg ctt gtc acc gta	672		
Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val			
210 215 220			
ggc gtt ggc gca gca atc agc gtt cag cag gtc gca aaa cgc tgg agc	720		
Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser			
225 230 235 240			
gga ttt aac act ctc gct aaa cgc gcc ccc tat ttt tcc agt ctg ttg	768		
Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu			
245 250 255			
att ggc tta gtc ggt gtg tat atg ggc gta cat ggc ttc atg ggc ata	816		
Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile			
260 265 270			
atg cga taa	825		
Met Arg *			

<210> 114
 <211> 519
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(519)

<400> 114
 atg att ctt aaa tca gct att tcc gct gac tct ctg ctc gct aag gat 48
 Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc 96
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 act aac aaa ata tcg ctt gtc agt tat att gta tgg cag gaa aga tat 144
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 gcg act gat att aca gat ccc caa agt gga gag ttt atg acc att aaa 192
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
 50 55 60
 aat aag atg ttg ctg ggt gcg ctt ttg ctg gtt acc agt gcc gcc tgg 240
 Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
 65 70 75 80
 gcc gca cca gcc acc gcg ggt tcg acc aat acc tcg gga att tct aag 288
 Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
 85 90 95
 tat gag tta agt agt ttc att gct gac ttt aag cat ttc aaa cca ggg 336
 Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
 100 105 110
 gac acc gta cca gaa atg tac cgt acc gat gag tac aac att aag cag 384
 Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
 115 120 125
 tgg cag ttg cgt aac ctg ccc gcg cct gat gcc ggg acg cac tgg acc 432
 Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
 130 135 140
 tat atg ggt ggc gcg tac gtg ttg atc agc gac acc gac ggt aaa atc 480
 Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
 145 150 155 160
 att aaa gcc tac gac ggt gag att ttt tat cat cgc taa 519
 Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg *
 165 170

<210> 115
 <211> 1035
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1035)

<400> 115

atg gaa att cgc ata atg cta ttt ata tta atg atg atg gtt atg cct	48
Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro	
1 5 10 15	
gtg agc tat gcg gca tgt tat agt gag tta tct gtt cag cac aac ttg	96
Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu	
20 25 30	
gtt gtt cag ggg gat ttt gca ctt act caa aca caa atg gcg aca tat	144
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr	
35 40 45	
gag cat aat ttt aat gat tcg tca tgc gta agt aca aat act atc acc	192
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr	
50 55 60	
cct atg agc ccg tcg gat att att gtt gga ctt tat aac gat acc ata	240
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile	
65 70 75 80	
aaa tta aat tta cat ttt gaa tgg acc aat aaa aac aac atc acg ttg	288
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu	
85 90 95	
tca aat aat cag acc agt ttc acc agt ggt tat tca gtt acg gtg aca	336
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr	
100 105 110	
cct gcg gcc agt aat gca aaa gtg aat gtt tct gcg ggg ggc ggc ggt	384
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly	
115 120 125	
tca gtg atg att aat ggt gtt gcg aca tta tcc agt gct tca tca tcg	432
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser	
130 135 140	
aca cgc ggg agt gcc gca gta caa ttt cta ctg tgt tta tta ggt ggc	480
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly	
145 150 155 160	
aag tca tgg gat gca tgt gta aat agc tac aga aat gca ttg gca caa	528
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln	
165 170 175	
aat gca ggt gtc tat tcc ttt aat ctg aca ttg tca tac aac ccg ata	576
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile	
180 185 190	


```

acc aca acc tgc aaa ccg gac gat tta tta att act tta gac agt att 624
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
      195                      200                      205

ccc gtt tca caa tta cca gcc aca ggt aac aaa gca aca ata aat agt 672
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
      210                      215                      220

aaa caa ggg gat att att ctg cgt tgt aaa aat tta tta ggt caa caa 720
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
      225                      230                      235                      240

aat caa aca tca cgg aaa atg cag gtg tat tta tca agt tct gac ttg 768
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
      245                      250                      255

tta acc aac agc aac aca ata ctg aaa ggt gcg gaa gat aat ggc gta 816
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
      260                      265                      270

gga ttt att ctt gaa agt aat ggt tcg cca gtc aca ctt tta aat atc 864
Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
      275                      280                      285

act aac agc agt aaa gga tat aca aat tta aag gaa gtt gcg gcg aag 912
Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
      290                      295                      300

tca aaa ctt aca gat aca acg gtt tca att ccg ata aca gcc agt tac 960
Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
      305                      310                      315                      320

tac gtc tac gat aca aac aaa gtt aaa tct ggc gca ctg gag gca acc 1008
Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
      325                      330                      335

gca tta atc aac gtg aaa tac gac taa 1035
Ala Leu Ile Asn Val Lys Tyr Asp *
      340

```

```

<210> 116
<211> 2481
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> CDS
<222> (1)...(2481)

```

```

<400> 116
atg ttg aga atg acc cca ctt gca tca gca atc gta gcg tta ttg ctc 48
Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
  1                      5                      10                      15

```

```

ggc att gaa gct tat gca gct gaa gaa acc ttt gat acc cat ttt atg 96

```

Gly	Ile	Glu	Ala	Tyr	Ala	Ala	Glu	Glu	Thr	Phe	Asp	Thr	His	Phe	Met		
			20						25					30			
ata	ggt	gga	atg	aaa	gac	cag	cag	ggt	gca	aat	att	cgt	ctt	gat	gat	144	
Ile	Gly	Gly	Met	Lys	Asp	Gln	Gln	Val	Ala	Asn	Ile	Arg	Leu	Asp	Asp		
		35					40				45						
aat	caa	ccc	tta	ccg	ggg	cag	tat	gac	atc	gat	att	tat	gtc	aat	aag	192	
Asn	Gln	Pro	Leu	Pro	Gly	Gln	Tyr	Asp	Ile	Asp	Ile	Tyr	Val	Asn	Lys		
		50				55					60						
caa	tgg	cgc	ggg	aaa	tat	gag	att	att	ggt	aaa	gac	aac	ccg	caa	gaa	240	
Gln	Trp	Arg	Gly	Lys	Tyr	Glu	Ile	Ile	Val	Lys	Asp	Asn	Pro	Gln	Glu		
	65				70				75						80		
aca	tgt	tta	tca	aga	gaa	ggt	atc	aag	cgg	tta	ggc	att	aat	agc	gat	288	
Thr	Cys	Leu	Ser	Arg	Glu	Val	Ile	Lys	Arg	Leu	Gly	Ile	Asn	Ser	Asp		
			85					90					95				
aac	ttc	gcc	agc	ggt	aag	caa	tgt	tta	aca	ttt	gag	caa	ctt	ggt	cag	336	
Asn	Phe	Ala	Ser	Gly	Lys	Gln	Cys	Leu	Thr	Phe	Glu	Gln	Leu	Val	Gln		
		100					105					110					
ggt	ggg	agc	tat	acc	tgg	gat	atc	ggg	ggt	ttt	cgt	ctc	gat	ttc	agt	384	
Gly	Gly	Ser	Tyr	Thr	Trp	Asp	Ile	Gly	Val	Phe	Arg	Leu	Asp	Phe	Ser		
		115				120					125						
gtc	ccg	cag	gcc	tgg	gtg	gaa	gaa	ctg	gaa	agt	ggc	tat	ggt	cca	ccg	432	
Val	Pro	Gln	Ala	Trp	Val	Glu	Glu	Leu	Glu	Ser	Gly	Tyr	Val	Pro	Pro		
	130				135					140							
gaa	aac	tgg	gag	cgg	ggt	att	aat	gcg	ttt	tat	acc	tct	tat	tat	ctg	480	
Glu	Asn	Trp	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Tyr	Thr	Ser	Tyr	Tyr	Leu		
	145				150				155						160		
agt	cag	tat	tac	agc	gac	tat	aaa	gcg	tcg	ggt	aat	aac	aag	agt	aca	528	
Ser	Gln	Tyr	Tyr	Ser	Asp	Tyr	Lys	Ala	Ser	Gly	Asn	Asn	Lys	Ser	Thr		
			165				170						175				
tat	gta	cgt	ttt	aac	agc	ggg	tta	aat	tta	ctg	ggg	tgg	caa	ctg	cat	576	
Tyr	Val	Arg	Phe	Asn	Ser	Gly	Leu	Asn	Leu	Leu	Gly	Trp	Gln	Leu	His		
		180					185					190					
tct	gat	gcc	agt	ttc	agt	aaa	aca	aat	aac	aat	cca	ggg	gtg	tgg	aaa	624	
Ser	Asp	Ala	Ser	Phe	Ser	Lys	Thr	Asn	Asn	Asn	Pro	Gly	Val	Trp	Lys		
		195					200				205						
agc	aat	acc	ctg	tat	ctg	gaa	cgt	gga	ttt	gcc	caa	ctt	ctc	ggc	acg	672	
Ser	Asn	Thr	Leu	Tyr	Leu	Glu	Arg	Gly	Phe	Ala	Gln	Leu	Leu	Gly	Thr		
	210				215					220							
ctt	cgc	gtg	ggt	gat	atg	tac	aca	tca	agc	gat	att	ttt	gat	tct	ggt	720	
Leu	Arg	Val	Gly	Asp	Met	Tyr	Thr	Ser	Ser	Asp	Ile	Phe	Asp	Ser	Val		
	225				230					235					240		
cgc	ttc	aga	ggt	gtg	cgg	ttg	ttt	cgt	gat	atg	cag	atg	ttg	cct	aac	768	
Arg	Phe	Arg	Gly	Val	Arg	Leu	Phe	Arg	Asp	Met	Gln	Met	Leu	Pro	Asn		

	245	250	255	
tcg aaa caa aat ttt acg cca cgg gtg cag ggg att gct cag agt aac	816			
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn				
260 265 270				
gcg ctg gta act att gaa cag aat ggt ttt gtg gtt tat cag aaa gag	864			
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu				
275 280 285				
gtt cct cct ggc ccg ttc gcg att aca gat ttg cag ttg gcc ggt ggt	912			
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly				
290 295 300				
gga gca gat ctt gat gtc agc gtg aaa gag gcg gac ggc tcg gta acc	960			
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr				
305 310 315 320				
acc tat ctg gtg cct tat gca gcg gtg cca aat atg ctg caa ccc ggc	1008			
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly				
325 330 335				
gtg tcg aaa tat gat tta gcg gcg ggt cgt agc cat att gaa ggg gcg	1056			
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala				
340 345 350				
agc aaa caa agt gat ttt gtc cag gcg ggt tat cag tat ggt ttt aat	1104			
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn				
355 360 365				
aat tta ttg acg ctg tat ggt ggc tcg atg gtc gcg aat aat tat tac	1152			
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr				
370 375 380				
gcg ttt act ttg ggg gct ggc tgg aat aca cgc att ggt gcc att tcc	1200			
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser				
385 390 395 400				
gtc gat gcc act aag tcg cat agt aaa caa gac aac ggc gat gtg ttt	1248			
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe				
405 410 415				
gac ggg caa agt tat caa att gcc tac aac aaa ttt gtg agc caa acg	1296			
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr				
420 425 430				
tcg acg cgt ttt ggt ctg gcg gcc tgg cgt tat tcg tcg cgt gat tac	1344			
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr				
435 440 445				
cgg aca ttt aac gat cac gtt tgg gca aac aat aaa gat aat tat cgc	1392			
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg				
450 455 460				
cgt gat gaa aac gat gtc tat gac att gcc gat tat tac cag aac gat	1440			
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp				
465 470 475 480				

ttt ggc cgc aaa aat agc ttt tcc gcc aat atg agc cag tca ttg cca	1488
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro	
485 490 495	
gaa ggt tgg ggg tct gtg tca tta agt acg tta tgg cga gat tac tgg	1536
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp	
500 505 510	
ggg cgt agc ggc agt agt aag gat tat cag ttg agt tat tcc aac aac	1584
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn	
515 520 525	
ctg cga cgg ata agc tat acc ctc gcg gca agc cag gct tat gac gag	1632
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu	
530 535 540	
aat cat cat gaa gag aaa cgt ttt aat att ttt ata tcg att ccc ttt	1680
Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe	
545 550 555 560	
gat tgg ggt gat gac gtt tcg acg cct cgt cgg caa ata tat atg tct	1728
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser	
565 570 575	
aac tca acg acg ttt gat gat cag ggg ttt gcc tca aat aat acg gga	1776
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly	
580 585 590	
tta tca gga aca gta ggg agt cgg gat cag ttc aat tat ggt gtc aac	1824
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn	
595 600 605	
ctg agt cat caa cat cag gga aat gaa acg aca gct ggg gcg aat ttg	1872
Leu Ser His Gln His Gln Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu	
610 615 620	
acc tgg aac gcg ccg gtt gcg aca gtg aat ggc agt tat agt cag tcg	1920
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser	
625 630 635 640	
agt act tat cga cag gct gga gcc agt gtt tca ggg ggc att gtc gcc	1968
Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala	
645 650 655	
tgg tcg ggt ggc gtt aat ctg gcg aac cgt ctt tcc gaa acg ttt gct	2016
Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala	
660 665 670	
gtg atg aat gcg cca gga att aaa gat gct tat gtc aat ggg caa aaa	2064
Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys	
675 680 685	
tat cgc aca aca aac cgt aat gga gtg gtg ata tac gac gga atg aca	2112
Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr	
690 695 700	

cct tat cgg gaa aat cac ctg atg ctg gat gtg tcg caa agc gat agc	2160
Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser	
705 710 715 720	
 gaa gca gaa tta cgt ggc aac cgg aaa att gcc gcc cct tat cgc ggc	2208
Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly	
725 730 735	
 gcg gtt gta ctg gtt aat ttt gat acc gat cag cgc aag cca tgg ttt	2256
Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe	
740 745 750	
 ata aaa gcg tta aga gca gat ggg caa tca tta acg ttt ggt tat gaa	2304
Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu	
755 760 765	
 gtc aat gat atc cat ggt cat aat att ggc gtt gtc ggc cag gga agt	2352
Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser	
770 775 780	
 cag tta ttt att cgc acc aat gaa gta ccg cca tcg gtt aat gtg gca	2400
Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala	
785 790 795 800	
 att gat aag caa caa gga ctt tca tgc aca atc acc ttc ggt aaa gag	2448
Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu	
805 810 815	
 att gat gaa agt aga aat tat att tgc cag taa	2481
Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln *	
820 825	
 <210> 117	
<211> 720	
<212> DNA	
<213> Escherichia coli	
 <220>	
<221> CDS	
<222> (1)...(720)	
 <400> 117	
atg gcc gct atc cca tgg cgg cct ttt aat tta aga ggc att aaa atg	48
Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met	
1 5 10 15	
 aaa gga tta tta tct tta ctc att ttt tct atg gtc ctt cct gca cat	96
Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His	
20 25 30	
 gcc gga att gtt atc tac ggg acg cgc att att tac ccg gca gaa aat	144
Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn	
35 40 45	
 aaa gaa gtg atg gtg cag ttg atg aac cag gga aac cgt tct tcg ctg	192
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu	

50	55	60	
ctg cag gcg tgg att gat gat ggc gat acg tca tta cca cca gaa aaa			240
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys			
65	70	75	80
att cag gtt cct ttc atg tta acg cca cca gtg gca aaa ata ggg gca			288
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala			
	85	90	95
aat tcc ggg cag caa gta aaa atc aaa att atg ccg aat aaa ctg ccc			336
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro			
	100	105	110
act aat aaa gaa agc att ttt tat ctg aat gtt ctg gat att cca cca			384
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro			
	115	120	125
aat agt cca gag caa gaa ggt aag aat gca ctg aag ttt gcg atg caa			432
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln			
	130	135	140
aac aga att aag ttg ttt tac cgg cca gcg ggt att gct ccg gta aat			480
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn			
	145	150	155
aaa gcg aca ttt aaa aaa ttg ctg gta aat cgc agt ggc aat ggt ttg			528
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu			
	165	170	175
gtg ata aaa aat gac tca gct aat tgg gtg acg att tcg gat gtc aaa			576
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys			
	180	185	190
gct aat aat gtc aaa gtc aat tat gaa act att atg att gcc ccc tta			624
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu			
	195	200	205
gaa agt cag agt gtt aat gtc aaa agt aat aat gca aat aac tgg cat			672
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His			
	210	215	220
ctg acc att atc gat gac cat ggc aac tat att agt gac aaa att taa			720
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile *			
	225	230	235

<210> 118
 <211> 543
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(543)

```

<400> 118
atg aaa cgt tca att att gct gcc gct gtc ttt tct tct ttt ttt atg 48
Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
1 5 10 15

agc gct gga gta ttt gct gca gac gtt gat acc gga aca tta act att 96
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
20 25 30

aag ggg aat att gca gaa tct ccg tgt aaa ttc gaa gcg ggt ggt gat 144
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
35 40 45

tca gta agt att aat atg ccg act gta cca acc agt gtc ttt gaa ggt 192
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
50 55 60

aaa gct aaa tat tct acc tat gat gat gca gtc ggt gta acc agc agc 240
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
65 70 75 80

atg tta aaa att agc tgc ccg aaa gaa gtt gct ggt gta aaa ctc tcg 288
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
85 90 95

ttg att acc aac gat aaa ata acc ggt aac gat aag gcg ata gcc agt 336
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
100 105 110

agc aac gat acc gtg ggt tac tat ctc tat tta ggt gat aac agc gat 384
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
115 120 125

gtc ctg gat gtt tct gca cct ttt aac att gag agt tat aaa aca gcg 432
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
130 135 140

gaa ggt caa tat gct att ccg ttt aaa gca aaa tac ctg aaa ctg aca 480
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
145 150 155 160

gat aac tca gtg caa tca ggt gat gtg tta tct tct ctg gtt atg cgt 528
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
165 170 175

gtg gcg cag gat taa 543
Val Ala Gln Asp *
180

```

```

<210> 119
<211> 288
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> CDS

```

<222> (1)...(288)

<400> 119

atg ctg cac aca tta cat cgc tca ccc tgg ctg acg gat ttt gct gcg	48
Met Leu His Thr Leu His Arg Ser Pro Trp Leu Thr Asp Phe Ala Ala	
1 5 10 15	
ctg ctg cgt ctg ctc agt gaa gga gac gaa ctg cta tta ttg caa gat	96
Leu Leu Arg Leu Leu Ser Glu Gly Asp Glu Leu Leu Leu Leu Gln Asp	
20 25 30	
ggc gta act gcc gca gtt gac ggt aac cgc tac ctt gaa agt ctg cgt	144
Gly Val Thr Ala Ala Val Asp Gly Asn Arg Tyr Leu Glu Ser Leu Arg	
35 40 45	
aat gcc ccc att aag gtc tat gcc ctg aac gaa gac ctt att gcc cgc	192
Asn Ala Pro Ile Lys Val Tyr Ala Leu Asn Glu Asp Leu Ile Ala Arg	
50 55 60	
ggt ttg act ggt caa att tcg aac gac atc att ctc att gac tat act	240
Gly Leu Thr Gly Gln Ile Ser Asn Asp Ile Ile Leu Ile Asp Tyr Thr	
65 70 75 80	
gat ttc gtc aga ctt acg gtt aag cac ccc agc cag atg gcc tgg tga	288
Asp Phe Val Arg Leu Thr Val Lys His Pro Ser Gln Met Ala Trp *	
85 90 95	

<210> 120

<211> 360

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(360)

<400> 120

atg aaa cga att gcg ttt gtt ttt tct act gca cct cat ggt aca gcc	48
Met Lys Arg Ile Ala Phe Val Phe Ser Thr Ala Pro His Gly Thr Ala	
1 5 10 15	
gca ggc cgg gaa ggt tta gat gct tta ctg gca act tcc gca tta act	96
Ala Gly Arg Glu Gly Leu Asp Ala Leu Leu Ala Thr Ser Ala Leu Thr	
20 25 30	
gac gat ctg gct gtc ttc ttt ata gct gat ggc gtt ttt cag ctg ctg	144
Asp Asp Leu Ala Val Phe Phe Ile Ala Asp Gly Val Phe Gln Leu Leu	
35 40 45	
cca gga caa aag ccc gat gca gtg ctg gcg cgt gat tac att gcc act	192
Pro Gly Gln Lys Pro Asp Ala Val Leu Ala Arg Asp Tyr Ile Ala Thr	
50 55 60	
ttt aaa ttg ttg ggt ctg tac gac att gaa cag tgc tgg gtt tgt gcg	240
Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala	

65	70	75	80	
gct tca ctg cgc gaa cgc ggg tta gat ccg cag aca ccc ttt gtt gtc				288
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val				
	85	90	95	
gaa gcc acg ccg ctc gaa gca gat gcc tta cgc cgc gaa ctc gcc aac				336
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn				
	100	105	110	
tac gat gtt att ttg agg ttt tga				360
Tyr Asp Val Ile Leu Arg Phe *				
	115			
<210> 121				
<211> 387				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(387)				
<400> 121				
atg cgt ttt gcc atc gtg gtg acc ggg cca gca tac ggt acg caa cag				48
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln				
1	5	10	15	
gcg agt agt gct ttt cag ttt gcg cag gcg ctg ata gca gat ggc cat				96
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His				
	20	25	30	
gag tta agc agc gtc ttt ttc tat cgg gaa ggg gtc tat aac gct aac				144
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn				
	35	40	45	
caa ttg acc tct ccg gca agt gac gaa ttt gac ctc gta cgg gcc tgg				192
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp				
	50	55	60	
caa caa ctg aat gcg caa cat ggt gtg gcg ctg aat atc tgc gta gcg				240
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala				
	65	70	75	80
gca gca tta cgc cgt ggc gtt gtt gat gaa acg gag gcc gga aga ctg				288
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu				
	85	90	95	
ggg ctg gct tcg tca aac ctt cag cag gga ttt acc tta agc gga ctt				336
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu				
	100	105	110	
ggg gcg ctg gcg gaa gcc tcg ctg acc tgt gac agg gtg gta cag ttc				384
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe				
	115	120	125	

tga
*

387

<210> 122
<211> 735
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(735)

<400> 122

gtg ttt ttt ttc atg tcc agg tcg ctt tta acc aac gaa acc agt gag	48
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu	
1 5 10 15	
ttg gat tta ctg gat caa cgt cct ttc gac cag acc gat ttt gat att	96
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile	
20 25 30	
ctg aaa tcc tac gaa gcg gtg gtg gac ggg tta gcg atg ctt att ggc	144
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly	
35 40 45	
tcc cac tgt gaa atc gtt ttg cac tct ttg cag gat cta aaa tgt tca	192
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser	
50 55 60	
gcc att cgc att gct aac ggt gaa cat aca ggc cgg aag att ggt tcg	240
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser	
65 70 75 80	
cca att act gac ctg gcg cta cgt atg ctg cac gat atg acg gga gcg	288
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala	
85 90 95	
gat agc agc gtt tct aaa tgc tac ttt act cgc gcc aaa agc ggc gta	336
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val	
100 105 110	
tta atg aag tcc ctg act atc gcg att cgt aac cgc gaa cag cgt gta	384
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val	
115 120 125	
att ggt ctg ctg tgc atc aat atg aat ctt gat gtt ccc ttc tcg cag	432
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln	
130 135 140	
att atg agc acc ttt gtg ccg cca gaa acc ccg gat gtc ggt tca agc	480
Ile Met Ser Thr Phe Val Pro Pro Glu Thr Pro Asp Val Gly Ser Ser	
145 150 155 160	
gtc aac ttt gcc tct tct gtt gaa gat ctg gtt acc caa acg ctg gag	528
Val Asn Phe Ala Ser Ser Val Glu Asp Leu Val Thr Gln Thr Leu Glu	

	165	170	175	
ttc acc atc gaa gaa gtg aat gcc gat cgc aat gtt tct aat aac gcc				576
Phe Thr Ile Glu Glu Val Asn Ala Asp Arg Asn Val Ser Asn Asn Ala				
	180	185	190	
aaa aat cgt cag atc gtg ctg aat ctc tac gag aaa ggg atc ttc gat				624
Lys Asn Arg Gln Ile Val Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp				
	195	200	205	
att aaa gat gcg atc aac cag gtt gct gac cgc ctg aac atc tcc aaa				672
Ile Lys Asp Ala Ile Asn Gln Val Ala Asp Arg Leu Asn Ile Ser Lys				
	210	215	220	
cac act gtc tat ctc tac atc cgc cag ttc aag agc ggt gat ttc cag				720
His Thr Val Tyr Leu Tyr Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln				
	225	230	235	240
ggg caa gat aag taa				735
Gly Gln Asp Lys *				
<210>	123			
<211>	255			
<212>	DNA			
<213>	Escherichia coli			
<220>				
<221>	CDS			
<222>	(1)...(255)			
<400>	123			
atg acc gat aaa atc cgt act ctg caa ggt cgc gtt gtt agc gac aaa				48
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys				
	1	5	10	15
atg gag aaa tcc att gtt gtt gct atc gaa cgt ttt gtg aaa cac ccg				96
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro				
	20	25	30	
atc tac ggt aaa ttc atc aag cgt acg acc aaa ctg cac gta cat gac				144
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp				
	35	40	45	
gag aac aac gaa tgc ggt atc ggt gac gtg gtt gaa atc cgc gaa tgc				192
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys				
	50	55	60	
cgt ccg ctg tcc aag act aaa tcc tgg acg ctg gtt cgc gtt gta gag				240
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu				
	65	70	75	80
aaa gcg gtt ctg taa				255
Lys Ala Val Leu *				

<210> 124
 <211> 192
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(192)

<400> 124
 atg aaa gca aaa gag ctg cgt gag aag agc gtt gaa gag ctg aac acc 48
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 gag ctg ctg aac ctg ctg cgt gag cag ttc aac ctg cgt atg cag gct 96
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 gca agt ggc cag ctg caa cag tct cac ctg ttg aag caa gtg cgt cgc 144
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 gat gtc gca cgc gtt aag act tta ctg aac gag aag gcg ggt gcg taa 192
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala *
 50 55 60

<210> 125
 <211> 411
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(411)

<400> 125
 atg tta caa cca aag cgt aca aaa ttc cgt aaa atg cac aaa ggc cgt 48
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 aac cgc ggt ctg gcg cag ggt acg gat gtt agc ttc ggc agc ttc ggt 96
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 ctg aaa gct gtt ggc cgt ggt cgt ctg act gcc cgt cag atc gaa gca 144
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 gca cgt cgt gct atg acc cgt gca gtt aag cgt caa ggt aag atc tgg 192
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 atc cgt gtg ttc ccg gac aaa ccg atc act gaa aag ccg ctg gca gtg 240
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val

65	70	75	80	
cgt atg ggt aaa ggt aaa ggt aac gtg gag tat tgg gtt gcc ttg att				288
Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile	85	90	95	
cag ccg ggt aaa gtc ctg tat gaa atg gac ggt gtt ccg gaa gag ctg				336
Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu	100	105	110	
gcc cgt gaa gca ttc aag ctg gca gca gcg aaa ctg ccg att aaa acc				384
Ala Arg Glu Ala Phe Lys Leu Ala Ala Ala Lys Leu Pro Ile Lys Thr	115	120	125	
acc ttt gta act aag acg gtg atg taa				411
Thr Phe Val Thr Lys Thr Val Met *	130	135		

<210> 126
 <211> 702
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(702)

<400> 126	
atg ggt cag aaa gta cat cct aat ggt att cgc ctg ggt att gta aaa	48
Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys	
1 5 10 15	
cca tgg aac tct acc tgg ttt gcg aac acc aaa gaa ttc gct gac aac	96
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn	
20 25 30	
ctg gac agc gat ttt aaa gta cgt cag tac ctg act aag gaa ctg gct	144
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala	
35 40 45	
aaa gcg tcc gta tct cgt atc gtt atc gag cgt ccg gct aag agc atc	192
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile	
50 55 60	
cgt gta acc att cac act gct cgc ccg ggt atc gtt atc ggt aaa aaa	240
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys	
65 70 75 80	
ggt gaa gac gta gaa aaa ctg cgt aag gtc gta gcg gac atc gct ggc	288
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly	
85 90 95	
gtt cct gca cag atc aac atc gcc gaa gtt cgt aag cct gaa ctg gac	336
Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp	
100 105 110	

```

gca aaa ctg gtt gct gac agc atc act tct cag ctg gaa cgt cgc gtt 384
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
      115                      120                      125

atg ttc cgt cgt gct atg aag cgt gct gta cag aac gca atg cgt ctg 432
Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
      130                      135                      140

ggc gct aaa ggt att aaa gtt gaa gtt agc ggc cgt ctg ggc ggc gcg 480
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
      145                      150                      155                      160

gaa atc gca cgt acc gaa tgg tac cgc gaa ggt cgc gta ccg ctg cac 528
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
      165                      170                      175

act ctg cgt gct gac atc gac tac aac acc tct gaa gcg cac acc act 576
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
      180                      185                      190

tac ggt gta atc ggc gtt aaa gtg tgg atc ttc aaa ggc gag atc ctg 624
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
      195                      200                      205

ggt ggt atg gct gct gtt gaa caa ccg gaa aaa ccg gct gct cag cct 672
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
      210                      215                      220

aaa aag cag cag cgt aaa ggc cgt aaa taa 702
Lys Lys Gln Gln Arg Lys Gly Arg Lys *
      225                      230

<210> 127
<211> 333
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(333)

<400> 127
atg gaa act atc gct aaa cat cgc cat gct cgt tct tct gct cag aag 48
Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
      1                      5                      10                      15

gtt cgc ctt gtt gct gac ctg att cgc ggt aag aaa gtg tcg cag gct 96
Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
      20                      25                      30

ctg gat att ttg acc tac acc aac aag aaa gcg gct gta ctg gtc aag 144
Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
      35                      40                      45

aaa gtt ctg gaa tct gcc att gct aac gct gaa cac aac gat ggc gct 192
Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala

```

50	55	60	
gac att gac gat ctg aaa gtt acg aaa att ttc gta gac gaa ggc ccg			240
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro			
65	70	75	80
agc atg aag cgc att atg ccg cgt gca aaa ggt cgt gca gat cgc atc			288
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile			
	85	90	95
ctg aag cgc acc agc cac atc act gtg gtt gtg tcc gat cgc tga			333
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg *			
	100	105	110

<210> 128
 <211> 279
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(279)

<400> 128	
atg cca cgt tct ctc aag aaa ggt cct ttt att gac ctg cac ttg ctg	48
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu	
1	15
aag aag gta gag aaa gcg gtg gaa agc gga gac aag aag ccc ctg cgc	96
Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg	
	20 25 30
act tgg tcc cgt cgt tca acg atc ttt cct aac atg atc ggt ttg acc	144
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr	
	35 40 45
atc gct gtc cat aat ggt cgt cag cac gtt ccg gta ttt gta acc gac	192
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp	
	50 55 60
gaa atg gtt ggt cac aaa ctg ggt gaa ttc gca ccg act cgt act tat	240
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr	
	65 70 75 80
cgc ggc cac gct gct gat aaa aaa gcg aag aag aaa taa	279
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys *	
	85 90

<210> 129
 <211> 822
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS
 <222> (1)...(822)

<400> 129

atg gca gtt gtt aaa tgt aaa ccg aca tct ccg ggt cgt cgc cac gta	48
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val	
1 5 10 15	
gtt aaa gtg gtt aac cct gag ctg cac aag ggc aaa cct ttt gct ccg	96
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro	
20 25 30	
ttg ctg gaa aaa aac agc aaa tcc ggt ggt cgt aac aac aat ggc cgt	144
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg	
35 40 45	
atc acc act cgt cat atc ggt ggt ggc cac aag cag gct tac cgt att	192
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile	
50 55 60	
gtt gac ttc aaa cgc aac aaa gac ggt atc ccg gca gtt gtt gaa cgt	240
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg	
65 70 75 80	
ctt gag tac gat ccg aac cgt tcc gcg aac atc gcg ctg gtt ctg tac	288
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr	
85 90 95	
aaa gac ggt gaa cgc cgt tac atc ctg gcc cct aaa ggc ctg aaa gct	336
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala	
100 105 110	
ggc gac cag att cag tct ggc gtt gat gct gca atc aaa cca ggt aac	384
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn	
115 120 125	
acc ctg ccg atg cgc aac atc ccg gtt ggt tct act gtt cat aac gta	432
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val	
130 135 140	
gaa atg aaa cca ggt aaa ggc ggt cag ctg gca cgt tcc gct ggt act	480
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr	
145 150 155 160	
tac gtt cag atc gtt gct cgt gat ggt gct tat gtc acc ctg cgt ctg	528
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu	
165 170 175	
cgt tct ggt gaa atg cgt aaa gta gaa gca gac tgc cgt gca act ctg	576
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu	
180 185 190	
ggc gaa gtt ggc aat gct gag cat atg ctg cgc gtt ctg ggt aaa gca	624
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala	
195 200 205	
ggg gct gca cgc tgg cgt ggt gtt cgt ccg acc gtt cgc ggt acc gcg	672

Gly	Ala	Ala	Arg	Trp	Arg	Gly	Val	Arg	Pro	Thr	Val	Arg	Gly	Thr	Ala		
210						215					220						
atg	aac	ccg	gta	gac	cac	cca	cat	ggt	ggt	ggt	gaa	ggt	cgt	aac	ttt	720	
Met	Asn	Pro	Val	Asp	His	Pro	His	Gly	Gly	Gly	Glu	Gly	Arg	Asn	Phe		
225					230					235					240		
ggt	aag	cac	ccg	gta	act	ccg	tgg	ggc	gtt	cag	acc	aaa	ggt	aag	aag	768	
Gly	Lys	His	Pro	Val	Thr	Pro	Trp	Gly	Val	Gln	Thr	Lys	Gly	Lys	Lys		
				245					250					255			
acc	cgc	agc	aac	aag	cgt	act	gat	aaa	ttc	atc	gta	cgt	cgc	cgt	agc	816	
Thr	Arg	Ser	Asn	Lys	Arg	Thr	Asp	Lys	Phe	Ile	Val	Arg	Arg	Arg	Ser		
			260					265					270				
aaa	taa															822	
Lys	*																

<210> 130
 <211> 303
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(303)

<400> 130																	
atg	att	cgt	gaa	gaa	cgt	ctg	ctg	aag	gtg	ctg	cgt	gca	ccg	cac	gtt	48	
Met	Ile	Arg	Glu	Glu	Arg	Leu	Leu	Lys	Val	Leu	Arg	Ala	Pro	His	Val		
1				5					10					15			
tct	gaa	aaa	gcg	tct	act	gcg	atg	gaa	aaa	tcc	aac	acc	atc	gta	ctc	96	
Ser	Glu	Lys	Ala	Ser	Thr	Ala	Met	Glu	Lys	Ser	Asn	Thr	Ile	Val	Leu		
			20					25					30				
aaa	gtt	gct	aaa	gac	gcg	acc	aaa	gca	gaa	atc	aaa	gct	gct	gtg	cag	144	
Lys	Val	Ala	Lys	Asp	Ala	Thr	Lys	Ala	Glu	Ile	Lys	Ala	Ala	Val	Gln		
			35				40					45					
aaa	ctg	ttt	gaa	gtc	gaa	gtc	gaa	gtc	gtt	aac	acc	ctg	gta	gtt	aaa	192	
Lys	Leu	Phe	Glu	Val	Glu	Val	Glu	Val	Val	Asn	Thr	Leu	Val	Val	Lys		
			50			55					60						
ggg	aaa	gtt	aaa	cgt	cac	gga	cag	cgt	atc	ggt	cgt	cgt	agc	gac	tgg	240	
Gly	Lys	Val	Lys	Arg	His	Gly	Gln	Arg	Ile	Gly	Arg	Arg	Ser	Asp	Trp		
65					70					75					80		
aaa	aaa	gct	tac	gtc	acc	ctg	aaa	gaa	ggc	cag	aat	ctg	gac	ttc	gtt	288	
Lys	Lys	Ala	Tyr	Val	Thr	Leu	Lys	Glu	Gly	Gln	Asn	Leu	Asp	Phe	Val		
				85					90					95			
ggc	ggc	gct	gag	taa												303	
Gly	Gly	Ala	Glu	*													
				100													

<210> 131
 <211> 606
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(606)

<400> 131

atg gaa tta gta ttg aaa gac gcg cag agc gcg ctg act gtt tcc gaa	48
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu	
1 5 10 15	
act acc ttc ggt cgt gat ttc aac gaa gcg ctg gtt cac cag gtt gtt	96
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val	
20 25 30	
gtt gct tat gca gct ggt gct cgt cag ggt act cgt gct cag aag act	144
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr	
35 40 45	
cgt gct gaa gta act ggt tcc ggt aaa aaa ccg tgg cgc cag aaa ggc	192
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly	
50 55 60	
acc ggc cgt gcg cgt tct ggt tct atc aag agc ccg atc tgg cgt tct	240
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser	
65 70 75 80	
ggt ggc gtg acc ttt gct gct cgt ccg cag gac cac agt caa aaa gtt	288
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val	
85 90 95	
aac aag aag atg tac cgc ggc gcg ctg aaa agc atc ctg tcc gaa ctg	336
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu	
100 105 110	
gta cgt cag gat cgt ctg atc gtt gtc gag aag ttc tct gta gaa gcg	384
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala	
115 120 125	
ccg aaa act aag ctg ctg gca cag aaa ctg aaa gac atg gct ctg gaa	432
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu	
130 135 140	
gat gtg ctg atc atc acc ggt gag ctg gac gaa aac ctg ttc ctg gct	480
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala	
145 150 155 160	
gcg cgc aac ctg cac aag gtt gac gta cgc gat gca act ggt atc gac	528
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp	
165 170 175	
ccg gtt agc ctg atc gcc ttc gac aaa gtc gta atg act gct gat gct	576

Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190

gtt aag caa gtt gag gag atg ctg gca tga 606
 Val Lys Gln Val Glu Glu Met Leu Ala *
 195 200

<210> 132
 <211> 630
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(630)

<400> 132
 atg att ggt tta gtc ggt aaa aaa gtg ggt atg acc cgt atc ttc aca 48
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15

gaa gac ggc gtt tct atc cca gta acc gta atc gaa gtt gaa gca aac 96
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30

cgc gtt act cag gtt aaa gac ctg gct aac gat ggc tac cgt gct att 144
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45

cag gtg acc acc ggt gct aaa aaa gct aac cgt gtg acc aag cct gaa 192
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60

gct ggc cac ttc gct aaa gct ggc gta gaa gct ggc cgt ggt ctg tgg 240
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80

gaa ttc cgc ctg gct gaa ggc gaa gag ttc act gta ggt cag agc att 288
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95

agc gtt gaa ctg ttt gct gac gtt aaa aaa gtt gac gta act ggc acc 336
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110

tct aaa ggt aaa ggt ttc gca ggt acc gtt aag cgc tgg aac ttc cgt 384
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125

acc cag gac gct act cac ggt aac tcc ttg tct cac cgc gtt ccg ggt 432
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140

tct atc ggt cag aac cag act ccg ggc aaa gtg ttc aaa ggc aag aaa 480
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160

```

atg gca ggt cag atg ggt aac gaa cgt gta acc gtt cag agc ctt gac 528
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
      165                      170                      175

gta gta cgc gtt gac gct gag cgc aac ctg ctg ctg gtt aaa ggt gct 576
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
      180                      185                      190

gtc ccg ggt gca acc ggt agc gac ctg atc gtt aaa cca gct gtg aag 624
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
      195                      200                      205

gcg taa
Ala * 630

```

```

<210> 133
<211> 312
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> CDS
<222> (1)...(312)

```

```

<400> 133
atg cag aac caa aga atc cgt atc cgc ctg aaa gcg ttt gat cat cgt 48
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
      1              5              10              15

ctg atc gat caa gca acc gcg gaa atc gtc gag act gcc aag cgc act 96
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
      20              25              30

ggt gcg cag gtc cgt ggt ccg atc ccg ctg ccg aca cgc aaa gag cgc 144
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
      35              40              45

ttc act gtt ctg atc tcc ccg cac gtc aac aaa gac gcg cgc gat cag 192
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
      50              55              60

tac gaa atc cgt act cac ttg cgt ctg gtt gac atc gtt gag cca acc 240
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
      65              70              75              80

gag aaa acc gtt gat gct ctg atg cgt ctg gat ctg gct gcc ggt gta 288
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
      85              90              95

gac gtg cag atc agc ctg ggt taa
Asp Val Gln Ile Ser Leu Gly * 312
      100

```

<210> 134
 <211> 315
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(315)

<400> 134
 atg atc cgc aaa gcc ttt gtc atg cag gta aac ccc gac gcc cac gaa 48
 Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
 1 5 10 15
 gag tat cag cgt cgg cat aat ccc atc tgg cca gaa ctg gaa gca gtg 96
 Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
 20 25 30
 ctg aaa tct cac ggt gcg cat aac tac gcc atc tat ctc gac aaa gcg 144
 Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
 35 40 45
 cgt aat ctg ctg ttt gcc atg gta gag att gaa tct gaa gaa cgc tgg 192
 Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
 50 55 60
 aat gcg gtt gcc agc act gat gtt tgc caa cgt tgg tgg aaa tat atg 240
 Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
 65 70 75 80
 acc gat gtt atg ccc gct aac ccg gat aac agc ccg gtg agt agc gag 288
 Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
 85 90 95
 ctg caa gaa gtg ttt tac ctg ccg taa 315
 Leu Gln Glu Val Phe Tyr Leu Pro *

<210> 135
 <211> 864
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(864)

<400> 135
 atg atc cgc agt atg acc gcc tac gcc cgg cgt gaa atc aag ggt gaa 48
 Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
 1 5 10 15
 tgg ggg agc gca acc tgg gaa atg cgc tcg gta aac cag cgt tat ctg 96
 Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
 20 25 30

gaa act tac ttt cgt ctg ccg gag cag ttc cgt agc ctt gaa cct gtc	144
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val	
35 40 45	
ggt cgc gag cgt att cgt tct cgc ctg acg cgc ggt aaa gtg gaa tgt	192
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys	
50 55 60	
acc ctg cgc tat gag cca gat gtt agc gcg caa ggt gag ctg atc ctc	240
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu	
65 70 75 80	
aac gaa aaa ctg gct aaa cag ctg gta act gcc gcg aac tgg gta aaa	288
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys	
85 90 95	
atg cag agt gac gaa ggg gaa atc aac ccg gtt gat att cta cgc tgg	336
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp	
100 105 110	
ccg ggc gtg atg gca gcc cag gag cag gat ctt gac gcc att gcc gct	384
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala	
115 120 125	
gaa att ctc gcg gcg ctg gat ggt acg ctg gac gac ttt att gtc gcg	432
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala	
130 135 140	
cgc gaa acc gaa ggt cag gca ctg aaa gca ttg atc gag cag cgt ctg	480
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu	
145 150 155 160	
gaa ggc gtc acc gcc gaa gtg gtc aaa gtc cgc tcc cat atg ccg gaa	528
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu	
165 170 175	
atc ctg caa tgg cag cgt gag cgt ctg gtc gcg aag ctg gaa gat gct	576
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala	
180 185 190	
cag gtg caa ctg gaa aac aac cgt ctg gag cag gaa ctg gtt ctg ctg	624
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Val Leu Leu	
195 200 205	
gca caa cga att gac gtt gcc gaa gaa ctg gat cgc ctc gaa gcg cat	672
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His	
210 215 220	
gtc aaa gag acc tac aac att ctg aag aaa aaa gaa gcg gtt ggt cgt	720
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg	
225 230 235 240	
cgt ctg gat ttt atg atg cag gag ttc aac cgc gag tcg aac act ctt	768
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu	
245 250 255	
gcg tcg aag tct atc aat gcc gaa gtg aca aac tcc gcc atc gag ctg	816

Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
 260 265 270

aaa gtg ttg att gag cag atg cgc gag cag att cag aac atc gaa taa 864
 Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu *
 275 280 285

<210> 136
 <211> 492
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(492)

<400> 136
 atg agc aca gaa aca att gaa ata ttc aat aat agt gat gaa tgg gca 48
 Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
 1 5 10 15
 aat caa cta aaa cac gca tta tcg aaa gga gaa aat ctg gca tta cta 96
 Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
 20 25 30
 cat ggt tta act cct gat atc ctt gat aga ata tat gca tat gca ttc 144
 His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
 35 40 45
 gac tac cat gaa aag ggt aat ata acg gac gca gaa att tat tat aaa 192
 Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
 50 55 60
 ttc ttg tgc att tat gcg ttc gaa aat cat gag tat cta aaa gat ttt 240
 Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
 65 70 75 80
 gca tca gta tgt cag ccc aaa aag aaa tat caa caa gca tat gac ctt 288
 Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
 85 90 95
 tac aaa cta agt tac aat tac ttc ccg tat gat gac tat tca gtt att 336
 Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
 100 105 110
 tat cgt atg ggt caa tgt cag att ggg gct aaa aat atc gat aac gca 384
 Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
 115 120 125
 atg caa tgt ttc tat cac att att aac aat tgt gag gat gat agt gtt 432
 Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
 130 135 140
 aag agt aaa gcg cag gca tat att gaa ctc tta aac gat aat tca gaa 480
 Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu

145	150	155	160	
gat aat ggc taa				492
Asp Asn Gly *				
<210> 137				
<211> 1947				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(1947)				
<400> 137				
atg aat att tta ggt ttt ttc cag cga ctc ggt agg gcg tta cag ctc				48
Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu				
1 5 10 15				
cct atc gcg gtg ctg ccg gtg gcg gca ctg ttg ctg cga ttc ggt cag				96
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln				
20 25 30				
cca gat tta ctt aac gtt gcg ttt att gcc cag gcg ggc ggt gcg att				144
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile				
35 40 45				
ttt gat aac ctc gca tta atc ttc gcc atc ggt gtg gca tcc agc tgg				192
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp				
50 55 60				
tcg aaa gac agc gct ggt gcg gcg gcg ctg gcg ggt gcg gta ggt tac				240
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr				
65 70 75 80				
ttt gtg tta acc aaa gcg atg gtg acc atc aac cca gaa att aac atg				288
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met				
85 90 95				
ggt gta ctg gcg ggt atc att acc ggt ctg gtt ggt ggc gca gcc tat				336
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr				
100 105 110				
aac cgt tgg tcc gat att aaa ctg ccg gac ttc ctg agc ttc ttc ggc				384
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly				
115 120 125				
ggc aaa cgc ttt gtg ccg att gcc acc gga ttc ttc tgc ctg gtg ctg				432
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu				
130 135 140				
gcg gcc att ttt ggt tac gtc tgg ccg ccg gta cag cac gct atc cat				480
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His				
145 150 155 160				

gca ggc ggc gag tgg atc gtt tct gcg ggc gcg ctg ggt tcc ggt atc Ala Gly Gly Glu Trp Ile Val Ser Ala Gly Ala Leu Gly Ser Gly Ile 165 170 175	528
ttt ggt ttc atc aac cgt ctg ctg atc cca acc ggt ctg cat cag gta Phe Gly Phe Ile Asn Arg Leu Leu Ile Pro Thr Gly Leu His Gln Val 180 185 190	576
ctg aac acc atc gcc tgg ttc cag att ggt gaa ttc acc aac gcg gcg Leu Asn Thr Ile Ala Trp Phe Gln Ile Gly Glu Phe Thr Asn Ala Ala 195 200 205	624
ggt acg gtt ttc cac ggt gac att aac cgc ttc tat gcc ggt gac gcg Gly Thr Val Phe His Gly Asp Ile Asn Arg Phe Tyr Ala Gly Asp Gly 210 215 220	672
acc gcg ggg atg ttc atg tcc ggc ttc ttc ccg atc atg atg ttc ggt Thr Ala Gly Met Phe Met Ser Gly Phe Phe Pro Ile Met Met Phe Gly 225 230 235 240	720
ctg ccg ggt gcg gcg ctg gcg atg tac ttc gca gca ccg aaa gag cgt Leu Pro Gly Ala Ala Leu Ala Met Tyr Phe Ala Ala Pro Lys Glu Arg 245 250 255	768
cgt ccg atg gtt ggc ggt atg ctg ctt tct gtt gct gtt act gcg ttc Arg Pro Met Val Gly Gly Met Leu Leu Ser Val Ala Val Thr Ala Phe 260 265 270	816
ctg acc ggt gtg act gag ccg ctg gaa ttc ctg ttc atg ttc ctt gct Leu Thr Gly Val Thr Glu Pro Leu Glu Phe Leu Phe Met Phe Leu Ala 275 280 285	864
ccg ctg ctg tac ctc ctg cac gca ctg ctg acc ggt atc agc ctg ttt Pro Leu Leu Tyr Leu Leu His Ala Leu Leu Thr Gly Ile Ser Leu Phe 290 295 300	912
gtg gca acg ctg ctg ggt atc cac gcg ggc ttc tct ttc tct gcg ggg Val Ala Thr Leu Leu Gly Ile His Ala Gly Phe Ser Phe Ser Ala Gly 305 310 315 320	960
gct atc gac tac gcg ttg atg tat aac ctg ccg gcc gcc agc cag aac Ala Ile Asp Tyr Ala Leu Met Tyr Asn Leu Pro Ala Ala Ser Gln Asn 325 330 335	1008
gtc tgg atg ctg ctg gtg atg ggc gtt atc ttc ttc gct atc tac ttc Val Trp Met Leu Leu Val Met Gly Val Ile Phe Phe Ala Ile Tyr Phe 340 345 350	1056
gtg gtg ttc agt ttg gtt atc cgc atg ttc aac ctg aaa acg ccg ggt Val Val Phe Ser Leu Val Ile Arg Met Phe Asn Leu Lys Thr Pro Gly 355 360 365	1104
cgt gaa gat aaa gaa gac gag atc gtt act gaa gaa gcc aac agc aac Arg Glu Asp Lys Glu Asp Glu Ile Val Thr Glu Glu Ala Asn Ser Asn 370 375 380	1152
act gaa gaa ggt ctg act caa ctg gca acc aac tat att gct gcg gtt	1200

610 615 620

ttc agt ggc ttg atc att aaa gct cag ggc cat att gtg gcg ggt caa 1920
Phe Ser Gly Leu Ile Ile Lys Ala Gln Gly His Ile Val Ala Gly Gln
625 630 635 640

aca ccg ctg tat gaa atc aaa aag taa 1947
Thr Pro Leu Tyr Glu Ile Lys Lys *
645

<210> 138
<211> 1239
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1239)

<400> 138

atg aag act atc ttc agg tac att ctt ttt tta gca ctg tat tct tgt 48
Met Lys Thr Ile Phe Arg Tyr Ile Leu Phe Leu Ala Leu Tyr Ser Cys
1 5 10 15

tgt aat aca gtc agt gca tat aca agt ttt att gtg gga aat aat gca 96
Cys Asn Thr Val Ser Ala Tyr Thr Ser Phe Ile Val Gly Asn Asn Ala
20 25 30

gga gtt gat aac tat cga ggc ccc tcc act gcc gca cag atg acc ttt 144
Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
35 40 45

aat tac aca tca aca gca agc aac ttg gtt ttt tat aaa ccc acg cag 192
Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
50 55 60

ctc ggc ccg act ggg gta aaa atg tac tgg tca tac ctg gat aca ggt 240
Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
65 70 75 80

acc ggt ggt ggt att ctt tac tgc aat aca tct ggc aga gcg aat cct 288
Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
85 90 95

ggt cca ata act att gaa aat gcc atg gtc tat tca ggt aaa gat tat 336
Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
100 105 110

ggc gga cat aaa cta ttt aat aca tct gtt cct ggt ctg tat tac acc 384
Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
115 120 125

atg tta ata tca agg gtc tgg tct gca tac gat aca ata act gac att 432
Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
130 135 140

caa tcg cca gga atc tat atc gga gat cct tcc aac caa gaa ttt ttc	480
Gln Ser Pro Gly Ile Tyr Ile Gly Asp Pro Ser Asn Gln Glu Phe Phe	
145 150 155 160	
ttt tcc gtc aca gac agc gat cta caa act aag ggt tgc aac aaa gca	528
Phe Ser Val Thr Asp Ser Asp Leu Gln Thr Lys Gly Cys Asn Lys Ala	
165 170 175	
gac gac tac gat aag ttt tgg gct att ggt ggt ata gta cac aac ata	576
Asp Asp Tyr Asp Lys Phe Trp Ala Ile Gly Gly Ile Val His Asn Ile	
180 185 190	
act gtt gaa ttt tat aca gat act aat ttc gat cct aca ctt aat cag	624
Thr Val Glu Phe Tyr Thr Asp Thr Asn Phe Asp Pro Thr Leu Asn Gln	
195 200 205	
caa gtc cag tta tcc agt tca tca aat tac ctt tat tcg ttt aag gcc	672
Gln Val Gln Leu Ser Ser Ser Ser Asn Tyr Leu Tyr Ser Phe Lys Ala	
210 215 220	
tac agt cct ggt aca aaa gtt gta gat cac agc aac cac att tat gtc	720
Tyr Ser Pro Gly Thr Lys Val Val Asp His Ser Asn His Ile Tyr Val	
225 230 235 240	
aat ttc aca ctg aat aat gtc aaa tta acc tta cca aca tgt ttt acc	768
Asn Phe Thr Leu Asn Asn Val Lys Leu Thr Leu Pro Thr Cys Phe Thr	
245 250 255	
tcc ata ctt acc ggg cca tca gtc aat ggt tca acg gtt aga atg gga	816
Ser Ile Leu Thr Gly Pro Ser Val Asn Gly Ser Thr Val Arg Met Gly	
260 265 270	
gaa tat agc tct ggg aca att aaa aat ggc gct tca cct gtt ccc ttt	864
Glu Tyr Ser Ser Gly Thr Ile Lys Asn Gly Ala Ser Pro Val Pro Phe	
275 280 285	
gat atc tcg ctt cag aat tgt att cgt gtg cgt aat att gaa aca aaa	912
Asp Ile Ser Leu Gln Asn Cys Ile Arg Val Arg Asn Ile Glu Thr Lys	
290 295 300	
ctc gtc act gga aaa gta ggt act caa aac aca caa ctg ctt ggt aat	960
Leu Val Thr Gly Lys Val Gly Thr Gln Asn Thr Gln Leu Leu Gly Asn	
305 310 315 320	
acg ctt act gga agc act gcc gcc aaa ggc gtt ggc gta ctc att gaa	1008
Thr Leu Thr Gly Ser Thr Ala Ala Lys Gly Val Gly Val Leu Ile Glu	
325 330 335	
ggg tta gca acc agt aaa aat ccg cta atg aca tta aaa cct aat gat	1056
Gly Leu Ala Thr Ser Lys Asn Pro Leu Met Thr Leu Lys Pro Asn Asp	
340 345 350	
acg aat tct gtt tat ata gat tat gaa acc gaa gat gac acc tcc gat	1104
Thr Asn Ser Val Tyr Ile Asp Tyr Glu Thr Glu Asp Asp Thr Ser Asp	
355 360 365	
ggg gtt tac cct aat caa ggt aac ggc aca tca cag cct ctt cat ttc	1152


```

ctt aat gct tca ggc gga tct cgt tcc gtt tat cca gta atg tcg gat 480
Leu Asn Ala Ser Gly Gly Ser Arg Ser Val Tyr Pro Val Met Ser Asp
145          150          155          160

gac atg aat ggt tca tcc tgg aaa ttt agc acc cga atg caa aaa atc 528
Asp Met Asn Gly Ser Ser Trp Lys Phe Ser Thr Arg Met Gln Lys Ile
          165          170          175

gat cct gca ttg agt gtt aca tct ggt caa ctt atg agc cat gtg tta 576
Asp Pro Ala Leu Ser Val Thr Ser Gly Gln Leu Met Ser His Val Leu
          180          185          190

gtg gat att tac tac gaa taa 597
Val Asp Ile Tyr Tyr Glu *
          195

<210> 140
<211> 606
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(606)

<400> 140
atg atg aca ttt aaa aat tta cgt tat gga tta tcc agc agt gtc gtt 48
Met Met Thr Phe Lys Asn Leu Arg Tyr Gly Leu Ser Ser Ser Val Val
  1          5          10          15

ttg gct gcc tca ttg ttc agc gta ctc tct tat gcg gca aca gac agt 96
Leu Ala Ala Ser Leu Phe Ser Val Leu Ser Tyr Ala Ala Thr Asp Ser
          20          25          30

att gga ctg acc gtt att act act gta gaa atg ggt act tgt acc gct 144
Ile Gly Leu Thr Val Ile Thr Thr Val Glu Met Gly Thr Cys Thr Ala
          35          40          45

aca tta gta aat gac tct gat cag gac att tct gtt gtt gat ttt ggt 192
Thr Leu Val Asn Asp Ser Asp Gln Asp Ile Ser Val Val Asp Phe Gly
          50          55          60

gat gta tat att tct gaa atc aat gcc aag acc aaa gta aaa aca ttc 240
Asp Val Tyr Ile Ser Glu Ile Asn Ala Lys Thr Lys Val Lys Thr Phe
          65          70          75          80

aaa ctc aaa ttc aaa gac tgt gcg ggt atc ccc aat aaa aaa gcg caa 288
Lys Leu Lys Phe Lys Asp Cys Ala Gly Ile Pro Asn Lys Lys Ala Gln
          85          90          95

ata aaa tta acc aag cga gcc aca tgc gag gga act gct aat gac ggt 336
Ile Lys Leu Thr Lys Arg Ala Thr Cys Glu Gly Thr Ala Asn Asp Gly
          100          105          110

gcg ggg ttt gca aat ggt tcc aca gcc gca gat aaa gca agt gct gtc 384

```

Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val	
115 120 125	
gcc gtt gaa gtc tgg agc act gta act ccg gca aca ggg agt gca aca	432
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr	
130 135 140	
caa ttt agc tgt gta aca cca gca tca caa gag gta aca atc tcc act	480
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr	
145 150 155 160	
gca gcc aat gcg gtc gtt tat tat ccg atg agt gca cgc ctg gtc gtg	528
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val	
165 170 175	
gaa aaa aat aaa acc gta aac aat gtc act gcg ggt aag ttt tct gca	576
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala	
180 185 190	
cca gcc aca ttt aca gta acc tat aac taa	606
Pro Ala Thr Phe Thr Val Thr Tyr Asn *	
195 200	
<210> 141	
<211> 612	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(612)	
<400> 141	
atg gaa ttc ggt gtc aga ttc agt aac tac aag gga cgt caa atg ata	48
Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile	
1 5 10 15	
aaa aca acg cca cat aaa ata gtg ata ctg atg gga ata tta tta tca	96
Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser	
20 25 30	
ccc tca gta ttt gca acg gat att aat gta gag ttt aca gcc act gtc	144
Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val	
35 40 45	
aaa gcg aca acc tgt aac atc aca ctt act ggt aat aac gtc acg aat	192
Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn	
50 55 60	
gat ggc aat aat aac tac aca ttg aga atc cct aag atg ggt ctg gat	240
Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp	
65 70 75 80	
aag atc gcg aat aaa acg aca gaa tct cag gct gat ttt aaa ctg gtt	288
Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val	
85 90 95	

```

gcc agt ggg tgc agc agt ggc atc agt tgg att gat acc act ctg acc 336
Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
      100                      105                      110

gga aat gca tca tca agc tca cct aag ctt att ata ccg cag tct ggt 384
Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
      115                      120                      125

gat tca tct tcg acg aca agt aat atc ggt atg ggt ttc aaa aaa cgg 432
Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
      130                      135                      140

act act gat gat gcc act ttc ctt aaa cct aac agt gcg gaa aag ata 480
Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
      145                      150                      155                      160

cgc tgg agc aca gac gag atg cag ccc gat aag ggt ctt gaa atg acc 528
Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
      165                      170                      175

gtt gcg cta cgt gaa aca gat gca ggg caa ggc gta ccg ggg aat ttt 576
Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
      180                      185                      190

cgt gca ctg gcg acg ttt aat ttc atc tat caa taa 612
Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln *
      195                      200

<210> 142
<211> 420
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(420)

<400> 142
atg gca atg act tac cac ctg gac gtc gtc agc gca gag caa caa atg 48
Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
      1                      5                      10                      15

ttc tct ggt ctg gtc gag aaa atc cag gta acg ggt agc gaa ggt gaa 96
Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
      20                      25                      30

ctg ggg atc tac cct ggc cac gca ccg ctg ctc acc gcc att aag cct 144
Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
      35                      40                      45

ggt atg att cgc atc gtg aaa cag cac ggt cac gaa gag ttt atc tat 192
Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
      50                      55                      60

ctg tct ggc ggc att ctt gaa gtg cag cct ggc aac gtg acc gtt ctg 240

```


Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
 65 70 75 80
 gcc gac acc gca att cgc ggc cag gat ctc gac gaa gcg cga gcc atg 288
 Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
 85 90 95
 gaa gcg aaa cgt aag gct gaa gag cac att agc agc tct cac ggc gac 336
 Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp
 100 105 110
 gta gat tac gct cag gcg tct gcg gaa ctg gcc aaa gcg atc gcg cag 384
 Val Asp Tyr Ala Gln Ala Ser Ala Glu Leu Ala Lys Ala Ile Ala Gln
 115 120 125
 ctg cgc gtt atc gag ttg acc aaa aaa gcg atg taa 420
 Leu Arg Val Ile Glu Leu Thr Lys Lys Ala Met *
 130 135

<210> 143
 <211> 1383
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1383)

<400> 143
 atg gct act gga aag att gtc cag gta atc ggc gcc gta gtt gac gtc 48
 Met Ala Thr Gly Lys Ile Val Gln Val Ile Gly Ala Val Val Asp Val
 1 5 10 15
 gaa ttc cct cag gat gcc gta ccg cgc gtg tac gat gct ctt gag gtg 96
 Glu Phe Pro Gln Asp Ala Val Pro Arg Val Tyr Asp Ala Leu Glu Val
 20 25 30
 caa aat ggt aat gag cgt ctg gtg ctg gaa gtt cag cag cag ctc ggc 144
 Gln Asn Gly Asn Glu Arg Leu Val Leu Glu Val Gln Gln Gln Leu Gly
 35 40 45
 ggc ggt atc gta cgt acc atc gca atg ggt tcc tcc gac ggt ctg cgt 192
 Gly Gly Ile Val Arg Thr Ile Ala Met Gly Ser Ser Asp Gly Leu Arg
 50 55 60
 cgc ggt ctg gat gta aaa gac ctc gaa cac ccg att gaa gtc ccg gta 240
 Arg Gly Leu Asp Val Lys Asp Leu Glu His Pro Ile Glu Val Pro Val
 65 70 75 80
 ggt aaa gcg act ctg ggc cgt atc atg aac gta ctg ggt gaa ccg gtc 288
 Gly Lys Ala Thr Leu Gly Arg Ile Met Asn Val Leu Gly Glu Pro Val
 85 90 95
 gac atg aaa ggc gag atc ggt gaa gaa gag cgt tgg gcg att cac cgc 336
 Asp Met Lys Gly Glu Ile Gly Glu Glu Glu Arg Trp Ala Ile His Arg
 100 105 110

gca gca cct tcc tac gaa gag ctg tca aac tct cag gaa ctg ctg gaa	384
Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu	
115 120 125	
acc ggt atc aaa gtt atc gac ctg atg tgt ccg ttc gct aag ggc ggt	432
Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly	
130 135 140	
aaa gtt ggt ctg ttc ggt ggt gcg ggt gta ggt aaa acc gta aac atg	480
Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met	
145 150 155 160	
atg gag ctc att cgt aac atc gcg atc gag cac tcc ggt tac tct gtg	528
Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val	
165 170 175	
ttt gcg ggc gta ggt gaa cgt act cgt gag ggt aac gac ttc tac cac	576
Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His	
180 185 190	
gaa atg acc gac tcc aac gtt atc gac aaa gta tcc ctg gtg tat ggc	624
Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly	
195 200 205	
cag atg aac gag ccg ccg gga aac cgt ctg cgc gtt gct ctg acc ggt	672
Gln Met Asn Glu Pro Pro Gln Asn Arg Leu Arg Val Ala Leu Thr Gly	
210 215 220	
ctg acc atg gct gag aaa ttc cgt gac gaa ggt cgt gac gtt ctg ctg	720
Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu	
225 230 235 240	
ttc gtt gac aac atc tat cgt tac acc ctg gcc ggt acg gaa gta tcc	768
Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser	
245 250 255	
gca ctg ctg ggc cgt atg cct tca gcg gta ggt tat cag ccg acc ctg	816
Ala Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu	
260 265 270	
gcg gaa gag atg ggc gtt ctg cag gaa cgt atc acc tcc acc aaa act	864
Ala Glu Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Thr	
275 280 285	
ggt tct atc acc tcc gta cag gca gta tac gta cct gcg gat gac ttg	912
Gly Ser Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu	
290 295 300	
act gac ccg tct ccg gca acc acc ttt gcg cac ctt gac gca acc gtg	960
Thr Asp Pro Ser Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Val	
305 310 315 320	
gta ctg agc cgt cag atc gcg tct ctg ggt atc tac ccg gcc gtt gac	1008
Val Leu Ser Arg Gln Ile Ala Ser Leu Gly Ile Tyr Pro Ala Val Asp	
325 330 335	

ccg ctg gac tcc acc agc cgt cag ctg gac ccg ctg gtg gtt ggt cag	1056
Pro Leu Asp Ser Thr Ser Arg Gln Leu Asp Pro Leu Val Val Gly Gln	
340 345 350	
gaa cac tac gac acc gcg cgt ggc gtt cag tcc atc ctg caa cgt tat	1104
Glu His Tyr Asp Thr Ala Arg Gly Val Gln Ser Ile Leu Gln Arg Tyr	
355 360 365	
cag gaa ctg aaa gac atc atc gcc atc ctg ggt atg gat gaa ctg tct	1152
Gln Glu Leu Lys Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser	
370 375 380	
gaa gaa gac aaa ctg gtg gta gcg cgt gct cgt aag atc cag cgc ttc	1200
Glu Glu Asp Lys Leu Val Val Ala Arg Ala Arg Lys Ile Gln Arg Phe	
385 390 395 400	
ctg tcc cag ccg ttc ttc gtg gca gaa gta ttc acc ggt tct ccg ggt	1248
Leu Ser Gln Pro Phe Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly	
405 410 415	
aaa tac gtc tcc ctg aaa gac acc atc cgt ggc ttt aaa ggc atc atg	1296
Lys Tyr Val Ser Leu Lys Asp Thr Ile Arg Gly Phe Lys Gly Ile Met	
420 425 430	
gaa ggc gaa tac gat cac ctg ccg gag cag gcg ttc tac atg gtc ggt	1344
Glu Gly Glu Tyr Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly	
435 440 445	
tcc atc gaa gaa gct gtg gaa aaa gcc aaa aaa ctt taa	1383
Ser Ile Glu Glu Ala Val Glu Lys Ala Lys Lys Leu *	
450 455 460	
<210> 144	
<211> 864	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(864)	
<400> 144	
atg gcc ggc gca aaa gag ata cgt agt aag atc gca agc gtc cag aac	48
Met Ala Gly Ala Lys Glu Ile Arg Ser Lys Ile Ala Ser Val Gln Asn	
1 5 10 15	
acg caa aag atc act aaa gcg atg gag atg gtc gcc gct tcc aaa atg	96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met	
20 25 30	
cgt aaa tcg cag gat cgc atg gcg gcc agc cgt cct tat gca gaa acc	144
Arg Lys Ser Gln Asp Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Thr	
35 40 45	
atg cgc aaa gtg att ggt cac ctt gca cac ggt aat ctg gaa tat aag	192
Met Arg Lys Val Ile Gly His Leu Ala His Gly Asn Leu Glu Tyr Lys	

50	55	60	
cac cct tac ctg gaa gac cgc gac gtt aaa cgc gtg ggc tac ctg gtg	240		
His Pro Tyr Leu Glu Asp Arg Asp Val Lys Arg Val Gly Tyr Leu Val			
65 70 75 80			
gtg tcg acc gac cgt ggt ttg tgc ggt ggt ttg aac att aac ctg ttc	288		
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe			
85 90 95			
aaa aaa ctg ctg gcg gaa atg aag acc tgg acc gac aaa ggc gtt caa	336		
Lys Lys Leu Leu Ala Glu Met Lys Thr Trp Thr Asp Lys Gly Val Gln			
100 105 110			
tgc gac ctc gca atg atc ggc tcg aaa ggc gtg tcg ttc ttc aac tcc	384		
Cys Asp Leu Ala Met Ile Gly Ser Lys Gly Val Ser Phe Phe Asn Ser			
115 120 125			
gtg ggc ggc aat gtt gtt gcc cag gtc acc ggc atg ggg gat aac cct	432		
Val Gly Gly Asn Val Val Ala Gln Val Thr Gly Met Gly Asp Asn Pro			
130 135 140			
tcc ctg tcc gaa ctg atc ggt ccg gta aaa gtg atg ttg cag gcc tac	480		
Ser Leu Ser Glu Leu Ile Gly Pro Val Lys Val Met Leu Gln Ala Tyr			
145 150 155 160			
gac gaa ggc cgt ctg gac aag ctt tac att gtc agc aac aaa ttt att	528		
Asp Glu Gly Arg Leu Asp Lys Leu Tyr Ile Val Ser Asn Lys Phe Ile			
165 170 175			
aac acc atg tct cag gtt ccg acc atc agc cag ctg ctg ccg tta ccg	576		
Asn Thr Met Ser Gln Val Pro Thr Ile Ser Gln Leu Leu Pro Leu Pro			
180 185 190			
gca tca gat gat gat gat ctg aaa cat aaa tcc tgg gat tac ctg tac	624		
Ala Ser Asp Asp Asp Asp Leu Lys His Lys Ser Trp Asp Tyr Leu Tyr			
195 200 205			
gaa ccc gat ccg aag gcg ttg ctg gat acc ctg ctg cgt cgt tat gtc	672		
Glu Pro Asp Pro Lys Ala Leu Leu Asp Thr Leu Leu Arg Arg Tyr Val			
210 215 220			
gaa tct cag gtt tat cag ggc gtg gtt gaa aac ctg gcc agc gag cag	720		
Glu Ser Gln Val Tyr Gln Gly Val Val Glu Asn Leu Ala Ser Glu Gln			
225 230 235 240			
gcc gcc cgt atg gtg gcg atg aaa gcc gcg acc gac aat ggc ggc agc	768		
Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Gly Gly Ser			
245 250 255			
ctg att aaa gag ctg cag ttg gta tac aac aaa gct cgt cag gcc agc	816		
Leu Ile Lys Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala Ser			
260 265 270			
att act cag gaa ctc acc gag atc gtc tcg ggg gcc gcc gcg gtt taa	864		
Ile Thr Gln Glu Leu Thr Glu Ile Val Ser Gly Ala Ala Val *			
275 280 285			

<210> 145
 <211> 1542
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1542)

<400> 145
 atg caa ctg aat tcc acc gaa atc agc gaa ctg atc aag cag cgc att 48
 Met Gln Leu Asn Ser Thr Glu Ile Ser Glu Leu Ile Lys Gln Arg Ile
 1 5 10 15
 gct cag ttc aat gtt gtg agt gaa gct cac aac gaa ggt act att gtt 96
 Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
 20 25 30
 tct gta agt gac ggt gtt atc cgc att cac ggc ctg gcc gat tgt atg 144
 Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
 35 40 45
 cag ggt gaa atg atc tcc ctg ccg ggt aac cgt tac gct atc gca ctg 192
 Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
 50 55 60
 aac ctc gag cgc gac tct gta ggt gcg gtt gtt atg ggt ccg tac gct 240
 Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
 65 70 75 80
 gac ctt gcc gaa ggc atg aaa gtt aag tgt act ggc cgt atc ctg gaa 288
 Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
 85 90 95
 gtt ccg gtt ggc cgt ggc ctg ctg ggc cgt gtg gtt aac act ctg ggt 336
 Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
 100 105 110
 gca cca atc gac ggt aaa ggt ccg ctg gat cac gac ggc ttc tct gct 384
 Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
 115 120 125
 gta gaa gca atc gct ccg ggc gtt atc gaa cgt cag tcc gta gat cag 432
 Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln
 130 135 140
 ccg gta cag acc ggt tat aaa gcc gtt gac tcc atg atc cca atc ggt 480
 Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly
 145 150 155 160
 cgt ggt cag cgt gaa ttg atc atc ggt gac cgt cag aca ggt aaa acc 528
 Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
 165 170 175

gca ctg gct atc gat gcc atc atc aac cag cgc gat tcc ggt atc aaa	576
Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys	
180 185 190	
tgt atc tat gtc gct atc ggc cag aaa gcg tcc acc att tct aac gtg	624
Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val	
195 200 205	
gta cgt aaa ctg gaa gag cac ggc gca ctg gct aac acc atc gtt gtg	672
Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val	
210 215 220	
gta gca acc gcg tct gaa tcc gct gca ctg caa tac ctg gca ccg tat	720
Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr	
225 230 235 240	
gcc ggt tgc gca atg ggc gaa tac ttc cgt gac cgc ggt gaa gat gcg	768
Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala	
245 250 255	
ctg atc att tac gat gac ctg tct aaa cag gct gtt gct tac cgt cag	816
Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln	
260 265 270	
atc tcc ctg ctg ctc cgt cgt ccg cca gga cgt gaa gca ttc ccg ggc	864
Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly	
275 280 285	
gac gtt ttc tac ctc cac tct cgt ctg ctg gag cgt gct gca cgt gtt	912
Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val	
290 295 300	
aac gcc gaa tac gtt gaa gcc ttc acc aaa ggt gaa gtg aaa ggg aaa	960
Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys	
305 310 315 320	
acc ggt tct ctg acc gca ctg ccg att atc gaa act cag gcg ggt gac	1008
Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp	
325 330 335	
gtt tct gcg ttc gtt ccg acc aac gta atc tcc att acc gat ggt cag	1056
Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln	
340 345 350	
atc ttc ctg gaa acc aac ctg ttc aac gcc ggt att cgt cct gcg gtt	1104
Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val	
355 360 365	
aac ccg ggt att tcc gta tcc cgt gtt ggt ggt gca gca cag acc aag	1152
Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys	
370 375 380	
atc atg aaa aaa ctg tcc ggt ggt atc cgt acc gct ctg gca cag tat	1200
Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr	
385 390 395 400	
cgt gaa ctg gca gcg ttc tct cag ttt gca tcc gac ctt gac gat gca	1248

Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala	
405 410 415	
aca cgt aag cag ctt gac cac ggt cag aaa gtg acc gaa ctg ctg aaa	1296
Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys	
420 425 430	
cag aaa cag tat gcg ccg atg tcc gtt gcg cag cag tct ctg gtt ctg	1344
Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu	
435 440 445	
ttc gca gca gaa cgt ggt tac ctg gcg gat gtt gaa ctg tcg aaa att	1392
Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile	
450 455 460	
ggc agc ttc gaa gcc gct ctg ctg gct tac gtc gac cgt gat cac gct	1440
Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala	
465 470 475 480	
ccg ttg atg caa gag atc aac cag acc ggt ggc tac aac gac gaa atc	1488
Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile	
485 490 495	
gaa ggc aag ctg aaa ggc atc ctc gat tcc ttc aaa gca acc caa tcc	1536
Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser	
500 505 510	
tgg taa	1542
Trp *	
<210> 146	
<211> 534	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(534)	
<400> 146	
atg tct gaa ttt att acg gta gct cgc ccc tac gcc aaa gca gct ttt	48
Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe	
1 5 10 15	
gac ttt gcc gtc gaa cac caa agt gta gaa cgc tgg cag gac atg ctg	96
Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu	
20 25 30	
gcg ttt gcc gcc gag gta acc aaa aac gaa caa atg gca gag ctt ctc	144
Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu	
35 40 45	
tct ggc gcg ctt gcg cca gaa acg ctc gcc gag tcg ttt atc gca gtt	192
Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val	
50 55 60	

tgt ggt gag caa ctg gac gaa aac ggt cag aac ctg att cgg gtt atg	240
Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met	
65 70 75 80	
gct gaa aat ggt cgt ctt aac gcg ctc ccg gat gtt ctg gag cag ttt	288
Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe	
85 90 95	
att cac ctg cgt gcc gtg agt gag gct acc gct gag gta gac gtc att	336
Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile	
100 105 110	
tcc gct gcc gca ctg agt gaa caa cag ctc gcg aaa att tct gct gcg	384
Ser Ala Ala Ala Leu Ser Glu Gln Gln Leu Ala Lys Ile Ser Ala Ala	
115 120 125	
atg gaa aaa cgt ctg tca cgc aaa gtt aag ctg aat tgc aaa atc gat	432
Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp	
130 135 140	
aag tct gta atg gca ggc gtt atc atc cga gcg ggt gat atg gtc att	480
Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile	
145 150 155 160	
gat ggc agc gta cgc ggt cgt ctt gag cgc ctt gca gac gtc ttg cag	528
Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln	
165 170 175	
tct taa	534
Ser *	
<210> 147	
<211> 471	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(471)	
<400> 147	
gtg aat ctt aac gca aca atc ctc ggc cag gcc atc gcg ttt gtc ctg	48
Met Asn Leu Asn Ala Thr Ile Leu Gly Gln Ala Ile Ala Phe Val Leu	
1 5 10 15	
ttc gtt ctg ttc tgc atg aag tac gta tgg ccg cca tta atg gca gcc	96
Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala	
20 25 30	
atc gaa aaa cgt caa aaa gaa att gct gac ggc ctt gct tcc gca gaa	144
Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu	
35 40 45	
cga gca cat aag gac ctt gac ctt gca aag gcc agc gcg acc gac cag	192


```

Arg Ala His Lys Asp Leu Asp Leu Ala Lys Ala Ser Ala Thr Asp Gln
 50                      55                      60

ctg aaa aaa gcg aaa gcg gaa gcc cag gta atc atc gag cag gcg aac 240
Leu Lys Lys Ala Lys Ala Glu Ala Gln Val Ile Ile Glu Gln Ala Asn
 65                      70                      75                      80

aaa cgc cgc tcg cag att ctg gac gaa gcg aaa gct gag gca gaa cag 288
Lys Arg Arg Ser Gln Ile Leu Asp Glu Ala Lys Ala Glu Ala Glu Gln
                      85                      90                      95

gaa cgt act aaa atc gtg gcc cag gcg cag gcg gaa att gaa gcc gag 336
Glu Arg Thr Lys Ile Val Ala Gln Ala Gln Ala Glu Ile Glu Ala Glu
                      100                      105                      110

cgt aaa cgt gcc cgt gaa gag ctg cgt aag caa gtt gct atc ctg gct 384
Arg Lys Arg Ala Arg Glu Glu Leu Arg Lys Gln Val Ala Ile Leu Ala
                      115                      120                      125

gtt gct ggc gcc gag aag atc atc gaa cgt tcc gtg gat gaa gct gct 432
Val Ala Gly Ala Glu Lys Ile Ile Glu Arg Ser Val Asp Glu Ala Ala
                      130                      135                      140

aac agc gac atc gtg gat aaa ctt gtc gct gaa ctg taa 471
Asn Ser Asp Ile Val Asp Lys Leu Val Ala Glu Leu *
145                      150                      155

<210> 148
<211> 240
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(240)

<400> 148
atg gaa aac ctg aat atg gat ctg ctg tac atg gct gcc gct gtg atg 48
Met Glu Asn Leu Asn Met Asp Leu Leu Tyr Met Ala Ala Ala Val Met
 1                      5                      10                      15

atg ggt ctg gcg gca atc ggt gct gcg atc ggt atc ggc atc ctc ggg 96
Met Gly Leu Ala Ala Ile Gly Ala Ala Ile Gly Ile Gly Ile Leu Gly
                      20                      25                      30

ggt aaa ttc ctg gaa ggc gca gcg cgt caa cct gat ctg att cct ctg 144
Gly Lys Phe Leu Glu Gly Ala Ala Arg Gln Pro Asp Leu Ile Pro Leu
                      35                      40                      45

ctg cgt act cag ttc ttt atc gtt atg ggt ctg gtg gat gct atc ccg 192
Leu Arg Thr Gln Phe Phe Ile Val Met Gly Leu Val Asp Ala Ile Pro
                      50                      55                      60

atg atc gct gta ggt ctg ggt ctg tac gtg atg ttc gct gtc gcg tag 240
Met Ile Ala Val Gly Leu Gly Leu Tyr Val Met Phe Ala Val Ala *
 65                      70                      75

```

<210> 149
 <211> 816
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(816)

<400> 149

atg gct tca gaa aat atg acg ccg cag gat tac ata gga cac cac ctg	48
Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu	
1 5 10 15	
aat aac ctt cag ctg gac ctg cgt aca ttc tcg ctg gtg gat cca caa	96
Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln	
20 25 30	
aac ccc cca gcc acc ttc tgg aca atc aat att gac tcc atg ttc ttc	144
Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe	
35 40 45	
tcg gtg gtg ctg ggt ctg ttg ttc ctg gtt tta ttc cgt agc gta gcc	192
Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala	
50 55 60	
aaa aag gcg acc agc ggt gtg cca ggt aag ttt cag acc gcg att gag	240
Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu	
65 70 75 80	
ctg gtg atc ggc ttt gtt aat ggt agc gtg aaa gac atg tac cat ggc	288
Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly	
85 90 95	
aaa agc aag ctg att gct ccg ctg gcc ctg acg atc ttc gtc tgg gta	336
Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val	
100 105 110	
ttc ctg atg aac ctg atg gat tta ctg cct atc gac ctg ctg ccg tac	384
Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr	
115 120 125	
att gct gaa cat gta ctg ggt ctg cct gca ctg cgt gtg gtt ccg tct	432
Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser	
130 135 140	
gcg gac gtg aac gta acg ctg tct atg gca ctg ggc gta ttt atc ctg	480
Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu	
145 150 155 160	
att ctg ttc tac agc atc aaa atg aaa ggc atc ggc ggc ttc acg aaa	528
Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys	
165 170 175	

Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn
180 185 190

tta atc ctt gaa ggg gta agc ctg ctg tcc aaa cca gtt tca ctc ggt 624
Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly
195 200 205

ttg cga ctg ttc ggt aac atg tat gcc ggt gag ctg att ttc att ctg 672
Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu
210 215 220

att gct ggt ctg ttg ccg tgg tgg tca cag tgg atc ctg aat gtg ccg 720
Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro
225 230 235 240

tgg gcc att ttc cac atc ctg atc att acg ctg caa gcc ttc atc ttc 768
Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe
245 250 255

atg gtt ctg acg atc gtc tat ctg tcg atg gcg tct gaa gaa cat taa 816
Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His *
260 265 270

<210> 150
<211> 393
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(393)

<400> 150
gtg aaa aac gtg atg tct gtg tcg ctc gtg agt cga aac gtt gct cgg 48
Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg
1 5 10 15

aag ctt ctg ctc gtt cag tta ctg gtg gtg ata gca agt gga ttg ctg 96
Lys Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu
20 25 30

ttc agc ctc aaa gac ccc ttc tgg ggc gtc tct gca ata agc ggg ggc 144
Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly
35 40 45

ctg gca gtc ttt ctg cct aac gtt ttg ttt atg ata ttt gcc tgg cgt 192
Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg
50 55 60

cac cag gcg cat aca cca gcg aaa ggc cgg gtg gcc tgg aca ttc gca 240
His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala
65 70 75 80

ttt ggc gaa gct ttc aaa gtt ctg gcg atg ttg gtg tta ctg gtg gtg 288


```

cca acc att gaa gag atg cgt gaa gct cgt cgc cag aac cgc aat acc 1104
Pro Thr Ile Glu Glu Met Arg Glu Ala Arg Arg Gln Asn Arg Asn Thr
      355                360                365

cgt ccg gcg ttg acg aaa cat acg ccg atg gcg acc cag cgt cag acg 1152
Arg Pro Ala Leu Thr Lys His Thr Pro Met Ala Thr Gln Arg Gln Thr
      370                375                380

cct gct acg gca aaa aaa gcg tcg tct acg caa tct cgt ccg gtg aat 1200
Pro Ala Thr Ala Lys Lys Ala Ser Ser Thr Gln Ser Arg Pro Val Asn
      385                390                395                400

gct ggt gcg aag aaa cgg cct aaa gcg gcg gtt gga cgt taa 1242
Ala Gly Ala Lys Lys Arg Pro Lys Ala Ala Val Gly Arg *
      405                410

<210> 152
<211> 978
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(978)

<400> 152
atg agc tct atc tcc ctg atc caa ccg gat cgc gac ctg ttc tcc tgg 48
Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp
  1                5                10                15

ccg cag tac tgg gcc gcc tgt ttt gga ccg gca ccg ttt ttg ccg atg 96
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met
      20                25                30

tct cgt gaa gag atg gat caa ctt ggc tgg gat agc tgc gac atc att 144
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile
      35                40                45

ttg gtt act ggc gac gcg tat gtc gat cac cca agc ttc ggg atg gcg 192
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala
      50                55                60

att tgc ggt cgt atg ctg gaa gcg cag ggc ttt cgc gtc ggg atc atc 240
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile
      65                70                75                80

gcc cag ccg gac tgg agc agc aaa gac gac ttt atg cgt ctg ggt aaa 288
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys
      85                90                95

ccg aat ctg ttt ttc ggt gtt act gct ggc aac atg gat tcg atg atc 336
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile
      100                105                110

aac cgt tat acc gcc gat cgc cgt tta cgt cat gac gat gcc tac acg 384

```

Asn	Arg	Tyr	Thr	Ala	Asp	Arg	Leu	Arg	His	Asp	Asp	Ala	Tyr	Thr				
115																120	125	
cgc	gat	aac	gtc	gcg	ggt	aag	cgc	cgc	gat	cgc	gcc	aca	ctg	gtt	tat	432		
Pro	Asp	Asn	Val	Ala	Gly	Lys	Arg	Pro	Asp	Arg	Ala	Thr	Leu	Val	Tyr			
130																135	140	
acc	cag	cgt	tgt	aaa	gag	gcg	tgg	aaa	gat	gta	cgc	gtg	atc	ctc	ggc	480		
Thr	Gln	Arg	Cys	Lys	Glu	Ala	Trp	Lys	Asp	Val	Pro	Val	Ile	Leu	Gly			
145																150	155	
ggt	att	gag	gct	agt	ctg	cgc	cgt	acc	gcg	cat	tat	gat	tac	tgg	tcc	528		
Gly	Ile	Glu	Ala	Ser	Leu	Arg	Arg	Thr	Ala	His	Tyr	Asp	Tyr	Trp	Ser			
165																170	175	
gat	acc	gtg	cgc	cgt	tcc	gtg	ctg	gtg	gat	tcg	aaa	gcc	gac	atg	ctg	576		
Asp	Thr	Val	Arg	Arg	Ser	Val	Leu	Val	Asp	Ser	Lys	Ala	Asp	Met	Leu			
180																185	190	
atg	ttt	ggt	aac	ggt	gag	cgt	ccg	ctg	gtg	gaa	gtg	gcg	cat	cgt	ctg	624		
Met	Phe	Gly	Asn	Gly	Glu	Arg	Pro	Leu	Val	Glu	Val	Ala	His	Arg	Leu			
195																200	205	
gcg	atg	ggc	gag	cca	att	agt	gaa	atc	cgc	gat	gtg	cgt	aat	acc	gcg	672		
Ala	Met	Gly	Glu	Pro	Ile	Ser	Glu	Ile	Arg	Asp	Val	Arg	Asn	Thr	Ala			
210																215	220	
att	atc	gtg	aaa	gag	gcg	ctg	cct	ggc	tgg	agc	ggc	gtg	gat	tcc	acc	720		
Ile	Ile	Val	Lys	Glu	Ala	Leu	Pro	Gly	Trp	Ser	Gly	Val	Asp	Ser	Thr			
225																230	235	
cgt	ctt	gat	acc	cct	gga	aaa	atc	gac	cca	atc	ccg	cat	ccg	tat	ggt	768		
Arg	Leu	Asp	Thr	Pro	Gly	Lys	Ile	Asp	Pro	Ile	Pro	His	Pro	Tyr	Gly			
245																250	255	
gaa	gat	ttg	ccg	tgc	gcg	gat	aac	aaa	ccg	gtg	gca	ccg	aaa	aag	cag	816		
Glu	Asp	Leu	Pro	Cys	Ala	Asp	Asn	Lys	Pro	Val	Ala	Pro	Lys	Lys	Gln			
260																265	270	
gaa	gcc	aaa	gcc	gta	acc	gtg	cag	cca	ccg	cgc	ccg	aaa	ccg	tgg	gaa	864		
Glu	Ala	Lys	Ala	Val	Thr	Val	Gln	Pro	Pro	Arg	Pro	Lys	Pro	Trp	Glu			
275																280	285	
aaa	acc	tac	gtg	ttg	ctg	cct	tct	ttc	gag	aaa	gtg	aag	ggc	gat	aaa	912		
Lys	Thr	Tyr	Val	Leu	Leu	Pro	Ser	Phe	Glu	Lys	Val	Lys	Gly	Asp	Lys			
290																295	300	
gtg	ctg	tac	gcc	cat	gct	tcg	cgt	att	ctg	cac	cac	gaa	acc	aac	cca	960		
Val	Leu	Tyr	Ala	His	Ala	Ser	Arg	Ile	Leu	His	His	Glu	Thr	Asn	Pro			
305																310	315	
gct	gtg	ccc	gcg	cat	tga											978		
Ala	Val	Pro	Ala	His	*													
325																		

<210> 153

<211> 681
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(681)

<400> 153

atg att cag tat ctg aac gtc ttt ttt tac gat atc tac ccg tac att	48
Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile	
1 5 10 15	
tgt gcg acg gtg ttt ttc ctc ggc agc tgg ctg cgc tac gac tac ggg	96
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly	
20 25 30	
cag tac acc tgg cgc gcc tcc tca agt caa atg ctc gat aaa cgc ggg	144
Gln Tyr Thr Trp Arg Ala Ser Ser Ser Gln Met Leu Asp Lys Arg Gly	
35 40 45	
atg gtg ata tgg tcg aat ctg ttc cat atc ggc att ttg ggg att ttc	192
Met Val Ile Trp Ser Asn Leu Phe His Ile Gly Ile Leu Gly Ile Phe	
50 55 60	
ttc ggg cac ttg ttc ggc atg tta acg ccg cac tgg atg tac gcg tgg	240
Phe Gly His Leu Phe Gly Met Leu Thr Pro His Trp Met Tyr Ala Trp	
65 70 75 80	
ttt ttg cca gtg gca gcg aaa caa ctc atg gcg atg gtg ctc ggc ggt	288
Phe Leu Pro Val Ala Ala Lys Gln Leu Met Ala Met Val Leu Gly Gly	
85 90 95	
att tgc ggt gtg ttg acg ttg att ggc ggc gca gga ctg ctg tgg cgc	336
Ile Cys Gly Val Leu Thr Leu Ile Gly Gly Ala Gly Leu Leu Trp Arg	
100 105 110	
agg ctg aca aat cag cgc gtg cgt gcc act tcc act acg ccg gat atc	384
Arg Leu Thr Asn Gln Arg Val Arg Ala Thr Ser Thr Thr Pro Asp Ile	
115 120 125	
atc atc atg agc att ttg ctg atc cag tgt ctg ttg ggg cta agt acc	432
Ile Ile Met Ser Ile Leu Leu Ile Gln Cys Leu Leu Gly Leu Ser Thr	
130 135 140	
ata ccg ttt tca gca cag tat cct gat ggt agc gaa atg atg aag ctg	480
Ile Pro Phe Ser Ala Gln Tyr Pro Asp Gly Ser Glu Met Met Lys Leu	
145 150 155 160	
gtg ggt tgg gcg caa agc att gtc act ttc cgt ggt gga tcg tca gag	528
Val Gly Trp Ala Gln Ser Ile Val Thr Phe Arg Gly Gly Ser Ser Glu	
165 170 175	
atg ctc aac ggc gta gcg ttc gtc ttc cgc ctg cat ctg gtg ttg gga	576
Met Leu Asn Gly Val Ala Phe Val Phe Arg Leu His Leu Val Leu Gly	
180 185 190	

atg acc atc ttc ctg ctc ttc ccg ttc acc cga ctg gtg cat gtg tgg	624
Met Thr Ile Phe Leu Leu Phe Pro Phe Thr Arg Leu Val His Val Trp	
195 200 205	

agc gcg ccg ttt gag tac ttt act cgt cga tat caa att gtg cgt tcg	672
Ser Ala Pro Phe Glu Tyr Phe Thr Arg Arg Tyr Gln Ile Val Arg Ser	
210 215 220	

cgg cga taa	681
Arg Arg *	
225	

<210> 154
 <211> 696
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(696)

<400> 154	
atg cag atc ctc aaa gtg atc ggc ctg ttg atg gag tat ccg gac gag	48
Met Gln Ile Leu Lys Val Ile Gly Leu Leu Met Glu Tyr Pro Asp Glu	
1 5 10 15	
ctg ttg tgg gaa tgc aag gag gac gcg ctg gcg ttg atc cgc cgc gac	96
Leu Leu Trp Glu Cys Lys Glu Asp Ala Leu Ala Leu Ile Arg Arg Asp	
20 25 30	
gcg ccg atg ctt acg gat ttc acc cac aac ctg ctt aac gcg ccg ctg	144
Ala Pro Met Leu Thr Asp Phe Thr His Asn Leu Leu Asn Ala Pro Leu	
35 40 45	
ctg gat aaa cag gcc gaa tgg tgc gaa gtg ttt gac cgc ggg cgc acc	192
Leu Asp Lys Gln Ala Glu Trp Cys Glu Val Phe Asp Arg Gly Arg Thr	
50 55 60	
acg tcg ctg ctg ctg ttc gaa cat gtt cat gcc gag tcc cgc gat cgc	240
Thr Ser Leu Leu Leu Phe Glu His Val His Ala Glu Ser Arg Asp Arg	
65 70 75 80	
ggc cag gca atg gtg gac ctg ctg gcg gag tat gaa aag gtc ggc ctg	288
Gly Gln Ala Met Val Asp Leu Leu Ala Glu Tyr Glu Lys Val Gly Leu	
85 90 95	
cag ctg gat tgt cgg gaa ctg ccc gat tat cta ccg ctg tat ctg gag	336
Gln Leu Asp Cys Arg Glu Leu Pro Asp Tyr Leu Pro Leu Tyr Leu Glu	
100 105 110	
tat tta agc gta ctg cct gac gat cag gcg aaa gaa gga ttg ctc aat	384
Tyr Leu Ser Val Leu Pro Asp Asp Gln Ala Lys Glu Gly Leu Leu Asn	
115 120 125	
gtt gcg ccg atc ctc gcc ctg ctt ggc ggt cgc tta aaa caa cgc gag	432
Val Ala Pro Ile Leu Ala Leu Leu Gly Gly Arg Leu Lys Gln Arg Glu	

130	135	140	
gca ccg tgg tac gcg ttg ttt gat gct ctg ctg caa ctg gcg gga agc			480
Ala Pro Trp Tyr Ala Leu Phe Asp Ala Leu Leu Gln Leu Ala Gly Ser			
145	150	155	160
tcc ctt tca agt gac agt gtc aca aaa caa gta aac agc gaa gag cgc			528
Ser Leu Ser Ser Asp Ser Val Thr Lys Gln Val Asn Ser Glu Glu Arg			
	165	170	175
gat gac acc cgc cag gcg ctt gat gca gtg tgg gaa gag gaa cag gtg			576
Asp Asp Thr Arg Gln Ala Leu Asp Ala Val Trp Glu Glu Glu Gln Val			
	180	185	190
aag ttt att gaa gat aac gcc acg gcg tgt gac agc tcg ccg ctt aat			624
Lys Phe Ile Glu Asp Asn Ala Thr Ala Cys Asp Ser Ser Pro Leu Asn			
	195	200	205
caa tat cag cga cgc ttt agc cag gat gtc gcg ccg caa tat gtc gac			672
Gln Tyr Gln Arg Arg Phe Ser Gln Asp Val Ala Pro Gln Tyr Val Asp			
	210	215	220
atc agt gcg gga ggt ggg aaa tga			696
Ile Ser Ala Gly Gly Gly Lys *			
225	230		
<210> 155			
<211> 1545			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(1545)			
<400> 155			
atg aaa atc cgt tca caa gtc ggc atg gtg ctt aac ctc gac aaa tgt			48
Met Lys Ile Arg Ser Gln Val Gly Met Val Leu Asn Leu Asp Lys Cys			
1	5	10	15
atc ggc tgc cat acc tgt tcg gtg acc tgt aaa aac gtc tgg acc ggg			96
Ile Gly Cys His Thr Cys Ser Val Thr Cys Lys Asn Val Trp Thr Gly			
	20	25	30
cgc gaa ggc atg gag tac gca tgg ttt aac aac gtc gaa acc aaa ccg			144
Arg Glu Gly Met Glu Tyr Ala Trp Phe Asn Asn Val Glu Thr Lys Pro			
	35	40	45
ggc att ggt tat ccg aaa aac tgg gaa gat cag gaa gag tgg caa ggc			192
Gly Ile Gly Tyr Pro Lys Asn Trp Glu Asp Gln Glu Glu Trp Gln Gly			
	50	55	60
ggc tgg gtg cgt gat gtg aat ggc aag ata cgc ccg cgt ctg ggc aac			240
Gly Trp Val Arg Asp Val Asn Gly Lys Ile Arg Pro Arg Leu Gly Asn			
65	70	75	80

aag atg ggc gta ata acc aaa atc ttc gcc aac ccg gtg gtg ccg cag	288
Lys Met Gly Val Ile Thr Lys Ile Phe Ala Asn Pro Val Val Pro Gln	
85 90 95	
att gat gat tac tac gaa cct ttc acc ttc gac tac gaa cat ttg cat	336
Ile Asp Asp Tyr Tyr Glu Pro Phe Thr Phe Asp Tyr Glu His Leu His	
100 105 110	
agc gca ccg gaa ggc aaa cat att cct act gct cgc ccg cgt tca ctg	384
Ser Ala Pro Glu Gly Lys His Ile Pro Thr Ala Arg Pro Arg Ser Leu	
115 120 125	
att gac ggc aaa cgg atg gac aaa gtg atc tgg ggg cca aac tgg gaa	432
Ile Asp Gly Lys Arg Met Asp Lys Val Ile Trp Gly Pro Asn Trp Glu	
130 135 140	
gaa ctg ctg ggc ggt gag ttc gaa aaa cgt gcc cgc gac cgc aac ttc	480
Glu Leu Leu Gly Gly Glu Phe Glu Lys Arg Ala Arg Asp Arg Asn Phe	
145 150 155 160	
gag gcc atg caa aag gag atg tac ggg cag ttt gaa aac acc ttc atg	528
Glu Ala Met Gln Lys Glu Met Tyr Gly Gln Phe Glu Asn Thr Phe Met	
165 170 175	
atg tac ctg ccg cgc ctg tgc gaa cac tgc ctc aat ccc agc tgc gtg	576
Met Tyr Leu Pro Arg Leu Cys Glu His Cys Leu Asn Pro Ser Cys Val	
180 185 190	
gcg acc tgc cca agc ggc gct atc tac aaa cgc gaa gaa gac ggc att	624
Ala Thr Cys Pro Ser Gly Ala Ile Tyr Lys Arg Glu Glu Asp Gly Ile	
195 200 205	
gtg ctg att gat cag gat aaa tgc cgt ggc tgg cgt ttg tgc ata agc	672
Val Leu Ile Asp Gln Asp Lys Cys Arg Gly Trp Arg Leu Cys Ile Ser	
210 215 220	
ggt tgt ccg tac aaa aaa atc tac ttc aac tgg aaa agc ggc aag tca	720
Gly Cys Pro Tyr Lys Lys Ile Tyr Phe Asn Trp Lys Ser Gly Lys Ser	
225 230 235 240	
gaa aaa tgc atc ttc tgt tac cca cga att gag tcc ggt caa ccg acc	768
Glu Lys Cys Ile Phe Cys Tyr Pro Arg Ile Glu Ser Gly Gln Pro Thr	
245 250 255	
gtg tgc tca gaa acc tgc gtg ggt cgc atc cgg tat ctg ggc gtg ctg	816
Val Cys Ser Glu Thr Cys Val Gly Arg Ile Arg Tyr Leu Gly Val Leu	
260 265 270	
ctt tac gac gcc gac cgc atc gag gaa gcg gcg agc acc gag cgc gaa	864
Leu Tyr Asp Ala Asp Arg Ile Glu Glu Ala Ala Ser Thr Glu Arg Glu	
275 280 285	
gtt gac ctc tat gaa cgc cag tgc gaa gtg ttc ctc gat cca cac gat	912
Val Asp Leu Tyr Glu Arg Gln Cys Glu Val Phe Leu Asp Pro His Asp	
290 295 300	
ccc tca gtg atc gag gaa gcc ctg aaa caa ggt att cca caa aat gtg	960

Pro Ser Val Ile Glu Glu Ala Leu Lys Gln Gly Ile Pro Gln Asn Val	
305 310 315 320	
att gac gct gcc cag cgt tcg cca gtc tac aaa atg gcg atg gac tgg	1008
Ile Asp Ala Ala Gln Arg Ser Pro Val Tyr Lys Met Ala Met Asp Trp	
325 330 335	
aaa ctg gca cta ccg ttg cac cct gaa tac cgc acc ctg ccg atg gtc	1056
Lys Leu Ala Leu Pro Leu His Pro Glu Tyr Arg Thr Leu Pro Met Val	
340 345 350	
tgg tac gtt cct ccg ctg tca ccg att cag tcc tac gca gat gcg ggc	1104
Trp Tyr Val Pro Pro Leu Ser Pro Ile Gln Ser Tyr Ala Asp Ala Gly	
355 360 365	
ggc ttg ccg aaa agc gaa ggc gtg ctg ccc gcc atc gaa agc ctg cgt	1152
Gly Leu Pro Lys Ser Glu Gly Val Leu Pro Ala Ile Glu Ser Leu Arg	
370 375 380	
att ccg gtg caa tat ctc gcc aat atg ttg agt gcc ggc gat acc ggt	1200
Ile Pro Val Gln Tyr Leu Ala Asn Met Leu Ser Ala Gly Asp Thr Gly	
385 390 395 400	
ccg gta ctg cgg gcg ctg aaa cgg atg atg gcg atg cgc cac tat atg	1248
Pro Val Leu Arg Ala Leu Lys Arg Met Met Ala Met Arg His Tyr Met	
405 410 415	
cgt tca caa acc gtg gaa ggc gtt act gat act cgt gcc atc gac gaa	1296
Arg Ser Gln Thr Val Glu Gly Val Thr Asp Thr Arg Ala Ile Asp Glu	
420 425 430	
gta ggc ctg agc gtc gcc cag gtc gaa gag atg tat cgc tat ctc gcc	1344
Val Gly Leu Ser Val Ala Gln Val Glu Glu Met Tyr Arg Tyr Leu Ala	
435 440 445	
att gcc aac tat gaa gat cgt ttt gtt atc ccg acc agc cat cgg gaa	1392
Ile Ala Asn Tyr Glu Asp Arg Phe Val Ile Pro Thr Ser His Arg Glu	
450 455 460	
atg gcg ggc gat gcc ttc gca gaa cgc aac ggc tgc ggt ttt acc ttt	1440
Met Ala Gly Asp Ala Phe Ala Glu Arg Asn Gly Cys Gly Phe Thr Phe	
465 470 475 480	
ggc gac ggt tgc cac ggt tcg gac agt aaa ttc aac ctg ttc aac agt	1488
Gly Asp Gly Cys His Gly Ser Asp Ser Lys Phe Asn Leu Phe Asn Ser	
485 490 495	
agc cgt atc gat gcc atc aac atc acc gaa gtg cgc gac aaa gcg gag	1536
Ser Arg Ile Asp Ala Ile Asn Ile Thr Glu Val Arg Asp Lys Ala Glu	
500 505 510	
ggc gaa taa	1545
Gly Glu *	

. <210> 156

<211> 3741
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3741)

<400> 156

atg agt aaa ctt ttg gat cgc ttt cgc tac ttc aaa caa aag ggc gaa	48
Met Ser Lys Leu Leu Asp Arg Phe Arg Tyr Phe Lys Gln Lys Gly Glu	
1 5 10 15	
acc ttt gcc gat ggt cac gga cag gtg atg cat agc aac cgc gac tgg	96
Thr Phe Ala Asp Gly His Gly Gln Val Met His Ser Asn Arg Asp Trp	
20 25 30	
gag gac agc tat cgc cag cgt tgg cag ttc gac aaa atc gtg cgt tcc	144
Glu Asp Ser Tyr Arg Gln Arg Trp Gln Phe Asp Lys Ile Val Arg Ser	
35 40 45	
acc cac ggt gtt aac tgt aca ggc tcc tgt agc tgg aaa atc tac gtt	192
Thr His Gly Val Asn Cys Thr Gly Ser Cys Ser Trp Lys Ile Tyr Val	
50 55 60	
aaa aat ggt ctg gtg acc tgg gaa atc caa cag acc gac tac ccg cgc	240
Lys Asn Gly Leu Val Thr Trp Glu Ile Gln Gln Thr Asp Tyr Pro Arg	
65 70 75 80	
act cgc cct gac ctg ccc aat cat gaa cct cgc ggc tgc ccg cgt ggc	288
Thr Arg Pro Asp Leu Pro Asn His Glu Pro Arg Gly Cys Pro Arg Gly	
85 90 95	
gca agt tac tcc tgg tat ctt tac agc gct aac cgc ctg aaa tac ccg	336
Ala Ser Tyr Ser Trp Tyr Leu Tyr Ser Ala Asn Arg Leu Lys Tyr Pro	
100 105 110	
ctc att cgt aaa cga ctg att gaa ctg tgg cgc gaa gcc ctc aag caa	384
Leu Ile Arg Lys Arg Leu Ile Glu Leu Trp Arg Glu Ala Leu Lys Gln	
115 120 125	
cac agc gat ccg gta ctg gcg tgg gca tcg att atg aac gat ccg caa	432
His Ser Asp Pro Val Leu Ala Trp Ala Ser Ile Met Asn Asp Pro Gln	
130 135 140	
aag tgc ctg agc tac aaa caa gtg cgt ggg cgc ggc ggc ttt atc cgc	480
Lys Cys Leu Ser Tyr Lys Gln Val Arg Gly Arg Gly Gly Phe Ile Arg	
145 150 155 160	
tcc aac tgg cag gaa cta aac cag ctg att gcc gcc gct aac gtc tgg	528
Ser Asn Trp Gln Glu Leu Asn Gln Leu Ile Ala Ala Ala Asn Val Trp	
165 170 175	
acc atc aaa acc tac ggc ccg gat cgc gtt gcc ggt ttc tcg ccg atc	576
Thr Ile Lys Thr Tyr Gly Pro Asp Arg Val Ala Gly Phe Ser Pro Ile	
180 185 190	

ccg gcg atg tcg atg gtt tct tac gcc gcc gga acg cgt tat ctg tcg	624
Pro Ala Met Ser Met Val Ser Tyr Ala Ala Gly Thr Arg Tyr Leu Ser	
195 200 205	
ctg ctt ggc ggc acc tgt tta agt ttc tac gac tgg tat tgc gac ctg	672
Leu Leu Gly Gly Thr Cys Leu Ser Phe Tyr Asp Trp Tyr Cys Asp Leu	
210 215 220	
ccg ccc gcc tcg ccg atg acc tgg ggc gag caa acc gac gta ccg gaa	720
Pro Pro Ala Ser Pro Met Thr Trp Gly Glu Gln Thr Asp Val Pro Glu	
225 230 235 240	
tct gcc gac tgg tat aac tcc agc tac atc atc gcc tgg ggg tct aac	768
Ser Ala Asp Trp Tyr Asn Ser Ser Tyr Ile Ile Ala Trp Gly Ser Asn	
245 250 255	
gta ccg cag aca cgt acg ccg gac gcc cac ttc ttt acc gaa gta cgc	816
Val Pro Gln Thr Arg Thr Pro Asp Ala His Phe Phe Thr Glu Val Arg	
260 265 270	
tac aaa ggc act aaa acc atc gcc att acc cct gac tac tct gaa gtg	864
Tyr Lys Gly Thr Lys Thr Ile Ala Ile Thr Pro Asp Tyr Ser Glu Val	
275 280 285	
gcc aaa ttg tgc gac cag tgg ctg gca ccg aaa caa ggc act gat agc	912
Ala Lys Leu Cys Asp Gln Trp Leu Ala Pro Lys Gln Gly Thr Asp Ser	
290 295 300	
gcc ctg gcg atg gca atg ggc cat gtg att tta aaa gag ttt cat ctc	960
Ala Leu Ala Met Ala Met Gly His Val Ile Leu Lys Glu Phe His Leu	
305 310 315 320	
gat aat ccc agc gac tac ttt atc aac tac tgc cgc cgc tac agc gac	1008
Asp Asn Pro Ser Asp Tyr Phe Ile Asn Tyr Cys Arg Arg Tyr Ser Asp	
325 330 335	
atg ccg atg ctg gta atg ctg gag cct cgc gac gat ggt agc tac gtt	1056
Met Pro Met Leu Val Met Leu Glu Pro Arg Asp Asp Gly Ser Tyr Val	
340 345 350	
ccc ggg cgc atg atc cgc gca tct gac ctg gtg gat gga ctg ggc gaa	1104
Pro Gly Arg Met Ile Arg Ala Ser Asp Leu Val Asp Gly Leu Gly Glu	
355 360 365	
agc aac aat ccg cag tgg aaa acc gta gca gtt aat acc gca ggt gaa	1152
Ser Asn Asn Pro Gln Trp Lys Thr Val Ala Val Asn Thr Ala Gly Glu	
370 375 380	
ttg gta gtg ccg aac ggt tcg att ggt ttc cgc tgg gga gaa aaa ggc	1200
Leu Val Val Pro Asn Gly Ser Ile Gly Phe Arg Trp Gly Glu Lys Gly	
385 390 395 400	
aaa tgg aat ctg gaa tcc att gcc gcc ggt acg gaa acc gaa ttg tcg	1248
Lys Trp Asn Leu Glu Ser Ile Ala Ala Gly Thr Glu Thr Glu Leu Ser	
405 410 415	
tta acc ctg ctc ggt caa cat gac gct gtt gca ggc gtg gcc ttc ccc	1296

Leu	Thr	Leu	Leu	Gly	Gln	His	Asp	Ala	Val	Ala	Gly	Val	Ala	Phe	Pro	
			420					425					430			
tac	ttt	ggc	ggc	att	gaa	aat	ccg	cat	ttt	cgc	agc	gta	aaa	cac	aat	1344
Tyr	Phe	Gly	Gly	Ile	Glu	Asn	Pro	His	Phe	Arg	Ser	Val	Lys	His	Asn	
		435					440					445				
ccg	gtg	ctg	gtg	cgc	caa	ttg	ccc	gtt	aaa	aac	ctg	acg	tta	gtc	gat	1392
Pro	Val	Leu	Val	Arg	Gln	Leu	Pro	Val	Lys	Asn	Leu	Thr	Leu	Val	Asp	
	450					455					460					
ggc	aac	acc	tgt	ccg	gtg	gtc	agc	gtt	tat	gat	ttg	gta	ctg	gcg	aat	1440
Gly	Asn	Thr	Cys	Pro	Val	Val	Ser	Val	Tyr	Asp	Leu	Val	Leu	Ala	Asn	
465					470					475					480	
tac	ggc	ctc	gat	cgc	ggg	ctg	gaa	gat	gaa	aac	agt	gcg	aaa	gat	tac	1488
Tyr	Gly	Leu	Asp	Arg	Gly	Leu	Glu	Asp	Glu	Asn	Ser	Ala	Lys	Asp	Tyr	
				485					490					495		
gct	gaa	atc	aaa	ccg	tac	acc	cca	gcc	tgg	ggt	gag	caa	att	acc	ggc	1536
Ala	Glu	Ile	Lys	Pro	Tyr	Thr	Pro	Ala	Trp	Gly	Glu	Gln	Ile	Thr	Gly	
			500					505					510			
gtg	ccg	cgc	cag	tat	att	gaa	acc	atc	gcc	cgt	gaa	ttt	gcc	gat	acc	1584
Val	Pro	Arg	Gln	Tyr	Ile	Glu	Thr	Ile	Ala	Arg	Glu	Phe	Ala	Asp	Thr	
		515					520					525				
gcc	cat	aaa	acg	cat	ggg	cgc	tcg	atg	att	atc	ctc	ggc	gca	ggt	gtt	1632
Ala	His	Lys	Thr	His	Gly	Arg	Ser	Met	Ile	Ile	Leu	Gly	Ala	Gly	Val	
	530					535					540					
aac	cac	tgg	tat	cac	atg	gac	atg	aac	tac	cgc	ggg	atg	atc	aat	atg	1680
Asn	His	Trp	Tyr	His	Met	Asp	Met	Asn	Tyr	Arg	Gly	Met	Ile	Asn	Met	
545					550					555					560	
ctg	atc	ttc	tgc	ggc	tgt	gtc	ggg	caa	agc	ggt	ggc	ggc	tgg	gca	cac	1728
Leu	Ile	Phe	Cys	Gly	Cys	Val	Gly	Gln	Ser	Gly	Gly	Gly	Trp	Ala	His	
				565					570					575		
tat	gtc	ggc	cag	gaa	aaa	ctg	cgc	cca	caa	acc	ggc	tgg	ttg	cca	ctg	1776
Tyr	Val	Gly	Gln	Glu	Lys	Leu	Arg	Pro	Gln	Thr	Gly	Trp	Leu	Pro	Leu	
			580					585					590			
gcc	ttt	gcg	ctc	gac	tgg	aac	cga	cca	ccg	cgc	caa	atg	aac	agc	acc	1824
Ala	Phe	Ala	Leu	Asp	Trp	Asn	Arg	Pro	Pro	Arg	Gln	Met	Asn	Ser	Thr	
		595					600					605				
tcg	ttt	ttc	tac	aat	cat	tcc	agc	caa	tgg	cgc	tat	gaa	aaa	gtc	tct	1872
Ser	Phe	Phe	Tyr	Asn	His	Ser	Ser	Gln	Trp	Arg	Tyr	Glu	Lys	Val	Ser	
	610					615					620					
gct	cag	gag	tta	ctt	tca	ccg	ctc	gcc	gat	gcc	agt	aag	tac	agc	ggt	1920
Ala	Gln	Glu	Leu	Leu	Ser	Pro	Leu	Ala	Asp							

645	650	655	
tct gcg ccg cag ctg ggg cgt aac ccg ctc ggg att aaa gct gaa gcc Ser Ala Pro Gln Leu Gly Arg Asn Pro Leu Gly Ile Lys Ala Glu Ala 660 665 670			2016
gac aag gcc gga tta tcc ccc aca gaa ttt acc gcc cag gcg ctg aaa Asp Lys Ala Gly Leu Ser Pro Thr Glu Phe Thr Ala Gln Ala Leu Lys 675 680 685			2064
tcg ggc gat tta cgt atg gcc tgc gaa caa cca gat agc agc agc aat Ser Gly Asp Leu Arg Met Ala Cys Glu Gln Pro Asp Ser Ser Ser Asn 690 695 700			2112
cat ccg cgt aat ttg ttt gtc tgg cgc tct aac ctg ctt ggc tcc tcc His Pro Arg Asn Leu Phe Val Trp Arg Ser Asn Leu Leu Gly Ser Ser 705 710 715 720			2160
ggc aaa ggc cac gag tat atg cag aag tat ctg ctg ggg acc gaa agc Gly Lys Gly His Glu Tyr Met Gln Lys Tyr Leu Leu Gly Thr Glu Ser 725 730 735			2208
ggg att cag ggc gag gaa ctc ggt gcc agc gac ggg atc aaa ccg gaa Gly Ile Gln Gly Glu Glu Leu Gly Ala Ser Asp Gly Ile Lys Pro Glu 740 745 750			2256
gaa gtc gag tgg caa act gca gcg att gaa ggc aag ctc gac ctg ctg Glu Val Glu Trp Gln Thr Ala Ala Ile Glu Gly Lys Leu Asp Leu Leu 755 760 765			2304
gtg acg ctc gac ttc cgc atg tcc agt acc tgc ctg ttc tcc gat atc Val Thr Leu Asp Phe Arg Met Ser Ser Thr Cys Leu Phe Ser Asp Ile 770 775 780			2352
gtt ctg ccc acc gcc acc tgg tac gaa aaa gac gat atg aac acc tcg Val Leu Pro Thr Ala Thr Trp Tyr Glu Lys Asp Asp Met Asn Thr Ser 785 790 795 800			2400
gat atg cat ccg ttt att cat ccg ctt tct gcg gcg gtc gat ccg gcg Asp Met His Pro Phe Ile His Pro Leu Ser Ala Ala Val Asp Pro Ala 805 810 815			2448
tgg gaa tca cgc agc gac tgg gaa atc tac aaa ggt atc gcc aaa gca Trp Glu Ser Arg Ser Asp Trp Glu Ile Tyr Lys Gly Ile Ala Lys Ala 820 825 830			2496
ttt tcg caa gtg tgc gtg ggt cat ctt ggc aaa gaa acc gac gtg gta Phe Ser Gln Val Cys Val Gly His Leu Gly Lys Glu Thr Asp Val Val 835 840 845			2544
tta caa ccc cta ctg cat gac tct ccg gca gag ctc tca cag ccg tgt Leu Gln Pro Leu Leu His Asp Ser Pro Ala Glu Leu Ser Gln Pro Cys 850 855 860			2592
gaa gtg ctc gac tgg cgc aaa ggc gaa tgc gat ctg att cca ggc aaa Glu Val Leu Asp Trp Arg Lys Gly Glu Cys Asp Leu Ile Pro Gly Lys 865 870 875 880			2640

acc gcg ccg aat att gtg gcg gtg gag cgc gac tac cct gct acg tat	2688
Thr Ala Pro Asn Ile Val Ala Val Glu Arg Asp Tyr Pro Ala Thr Tyr	
885 890 895	
gaa cgc ttt acc tcg ctc ggg cca ttg atg gac aaa ctt ggc aat ggc	2736
Glu Arg Phe Thr Ser Leu Gly Pro Leu Met Asp Lys Leu Gly Asn Gly	
900 905 910	
ggt aaa ggg att tcg tgg aat acc cag gat gaa atc gat ttc ctc ggc	2784
Gly Lys Gly Ile Ser Trp Asn Thr Gln Asp Glu Ile Asp Phe Leu Gly	
915 920 925	
aaa ctc aat tac acc aag cgt gat ggc ccg gca cag ggg cgt ccg ctg	2832
Lys Leu Asn Tyr Thr Lys Arg Asp Gly Pro Ala Gln Gly Arg Pro Leu	
930 935 940	
att gac acc gcc att gac gct tca gaa gtg att ctg gca ctg gca ccg	2880
Ile Asp Thr Ala Ile Asp Ala Ser Glu Val Ile Leu Ala Leu Ala Pro	
945 950 955 960	
gaa acc aac ggt cat gtt gca gtc aaa gcg tgg cag gcg ctg ggc gag	2928
Glu Thr Asn Gly His Val Ala Val Lys Ala Trp Gln Ala Leu Gly Glu	
965 970 975	
atc acc ggg cgc gaa cat acc cat ctg gcg ctg cac aaa gag gac gag	2976
Ile Thr Gly Arg Glu His Thr His Leu Ala Leu His Lys Glu Asp Glu	
980 985 990	
aag att cgc ttt cgc gat att cag gcg cag ccg cgt aaa att atc tcc	3024
Lys Ile Arg Phe Arg Asp Ile Gln Ala Gln Pro Arg Lys Ile Ile Ser	
995 1000 1005	
agc ccc acc tgg tcc ggt ctg gaa agc gat cac gtc tcc tat aac gcg	3072
Ser Pro Thr Trp Ser Gly Leu Glu Ser Asp His Val Ser Tyr Asn Ala	
1010 1015 1020	
gga tac acc aac gtt cat gag tta att ccg tgg gcg acg ctg tcg gga	3120
Gly Tyr Thr Asn Val His Glu Leu Ile Pro Trp Arg Thr Leu Ser Gly	
1025 1030 1035 1040	
cgc cag cag ctc tat cag gat cat ccg tgg atg cgt gct ttt ggt gaa	3168
Arg Gln Gln Leu Tyr Gln Asp His Pro Trp Met Arg Ala Phe Gly Glu	
1045 1050 1055	
agc ctg gtg gct tat cgc ccg cct atc gac acc cgt agc gtc agt gag	3216
Ser Leu Val Ala Tyr Arg Pro Pro Ile Asp Thr Arg Ser Val Ser Glu	
1060 1065 1070	
atg cgc cag ata ccg cca aac ggc ttc ccg gaa aaa gca ctt aac ttc	3264
Met Arg Gln Ile Pro Pro Asn Gly Phe Pro Glu Lys Ala Leu Asn Phe	
1075 1080 1085	
ctg acg ccg cac cag aaa tgg ggc att cac tca acc tac agt gaa aac	3312
Leu Thr Pro His Gln Lys Trp Gly Ile His Ser Thr Tyr Ser Glu Asn	
1090 1095 1100	

```

ctg cta atg ctg acg ctc tct cgc ggt gga ccg att gtc tgg atc agc 3360
Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser
1105          1110          1115          1120

gaa aca gat gcc cga gaa ctg acc att gtc gat aac gac tgg gtg gaa 3408
Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu
          1125          1130          1135

gta ttc aac gcc aac ggc gcg ctg act gcc cgc gcg gtg gtc agc caa 3456
Val Phe Asn Ala Asn Gly Ala Leu Thr Ala Arg Ala Val Val Ser Gln
          1140          1145          1150

cgt gta ccg ccg ggc atg acc atg atg tat cac gcc cag gaa cgc att 3504
Arg Val Pro Pro Gly Met Thr Met Met Tyr His Ala Gln Glu Arg Ile
          1155          1160          1165

atg aat att cct ggt tcg gaa gta act ggc atg cgc ggc ggc att cat 3552
Met Asn Ile Pro Gly Ser Glu Val Thr Gly Met Arg Gly Gly Ile His
          1170          1175          1180

aac tcg gtt acc cgc gtt tgc ccg aaa cca acg cat atg att ggc ggt 3600
Asn Ser Val Thr Arg Val Cys Pro Lys Pro Thr His Met Ile Gly Gly
1185          1190          1195          1200

tac gcg cag ctg gcc tgg ggc ttt aac tac tac ggc acc gtc gga tcg 3648
Tyr Ala Gln Leu Ala Trp Gly Phe Asn Tyr Tyr Gly Thr Val Gly Ser
          1205          1210          1215

aac cgc gat gag ttc atc atg atc cgc aag atg aag aac gtt aac tgg 3696
Asn Arg Asp Glu Phe Ile Met Ile Arg Lys Met Lys Asn Val Asn Trp
          1220          1225          1230

ctg gat gat gaa ggt cgc gat cag gta cag gag gcg aaa aaa tga 3741
Leu Asp Asp Glu Gly Arg Asp Gln Val Gln Glu Ala Lys Lys *
          1235          1240          1245

```

<210> 157
 <211> 498
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(498)

```

<400> 157
atg gat ttg tca cag cta aca cca cgt cgt ccc tat ctg ctg cgt gca 48
Met Asp Leu Ser Gln Leu Thr Pro Arg Arg Pro Tyr Leu Leu Arg Ala
1          5          10          15

ttc tat gag tgg ttg ctg gat aac cag ctc acg ccg cac ctg gtg gtg 96
Phe Tyr Glu Trp Leu Leu Asp Asn Gln Leu Thr Pro His Leu Val Val
          20          25          30

gat gtg acg ctc cct ggc gtg cag gtt cct atg gaa tat gcg cgt gac 144

```

```

Asp Val Thr Leu Pro Gly Val Gln Val Pro Met Glu Tyr Ala Arg Asp
    35                                40                                45

ggg caa atc gta ctc aac att gcg ccg cgt gct gtc ggc aat ctg gaa   192
Gly Gln Ile Val Leu Asn Ile Ala Pro Arg Ala Val Gly Asn Leu Glu
    50                                55                                60

ctg gcg aat gat gag gtg cgc ttt aac gcg cgc ttt ggt ggc att ccg   240
Leu Ala Asn Asp Glu Val Arg Phe Asn Ala Arg Phe Gly Gly Ile Pro
    65                                70                                75                                80

cgt cag gtt tct gtg ccg ctg gct gcc gtg ctg gct atc tac gcc cgt   288
Arg Gln Val Ser Val Pro Leu Ala Ala Val Leu Ala Ile Tyr Ala Arg
                        85                                90                                95

gaa aat ggc gca ggc acg atg ttt gag cct gaa gct gcc tac gat gaa   336
Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu
                        100                                105                                110

gat acc agc atc atg aat gat gaa gag gca tcg gca gac aac gaa acc   384
Asp Thr Ser Ile Met Asn Asp Glu Glu Ala Ser Ala Asp Asn Glu Thr
                        115                                120                                125

gtt atg tcg gtt att gat ggc gac aag cca gat cac gat gat gac act   432
Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr
                        130                                135                                140

cat cct gac gat gaa cct ccg cag cca cca cgc ggt ggt cga ccg gca   480
His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala
                        145                                150                                155                                160

tta cgc gtt gtg aag taa
Leu Arg Val Val Lys *
                        165

```

<210> 158
 <211> 639
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(639)

```

<400> 158
atg gct gtc gct gcc aac aaa cgt tcg gta atg acg ctg ttt tcc ggt   48
Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly
    1                                5                                10                                15

cct act gac atc tat agc cat cag gtc cgc att gtg ctg gct gag aaa   96
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys
                        20                                25                                30

ggt gta agt ttc gag atc gaa cac gtg gaa aag gac aat ccg cct cag   144
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln
                        35                                40                                45

```

gat ctg att gac ctc aac ccg aat cag agc gtt ccg acc ctg gtg gat	192
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp	
50 55 60	
cg t gag ctg acc ctg tgg gaa tct cgc atc att atg gaa tat ctg gat	240
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp	
65 70 75 80	
gag cgt ttc ccg cat ccg cca ctg atg cct gtt tac ccg gta gct cgc	288
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg	
85 90 95	
ggt gaa agc cgt ctg tac atg cat cgc atc gaa aaa gac tgg tac acg	336
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr	
100 105 110	
ctg atg aac acc atc atc aac ggt tca gct tct gaa gca gat gcc gca	384
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala	
115 120 125	
cg t aag caa ctg cgc gaa gaa ctg ctg gcg att gcg ccg gtc ttc ggt	432
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly	
130 135 140	
cag aag ccg tac ttc ctg agc gat gag ttc agc ctg gtc gat tgc tat	480
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr	
145 150 155 160	
ctt gct ccg ctg ctg tgg cgt ctg ccg caa ctg ggc atc gag ttc agc	528
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser	
165 170 175	
ggc ccg ggt gcg aaa gag ctg aaa ggc tat atg acc cgc gtc ttt gag	576
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu	
180 185 190	
cg t gac tct ttc ctt gct tct tta act gaa gca gaa cgt gaa atg cgt	624
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg	
195 200 205	
ctg ggc cgg agt taa	639
Leu Gly Arg Ser *	
210	

<210> 159

<211> 1518

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1518)

<400> 159

atg tct gaa caa cac gca cag ggc gct gac gcg gta gtc gat ctt aac	48
---	----

Met	Ser	Glu	Gln	His	Ala	Gln	Gly	Ala	Asp	Ala	Val	Val	Asp	Leu	Asn	
1				5					10					15		
aat	gaa	ctg	aaa	acg	cgt	cgt	gag	aag	ctg	gcg	aac	ctg	cgc	gag	cag	96
Asn	Glu	Leu	Lys	Thr	Arg	Arg	Glu	Lys	Leu	Ala	Asn	Leu	Arg	Glu	Gln	
			20					25					30			
ggg	att	gcc	ttc	ccg	aac	gat	ttc	cgt	cgc	gat	cat	acc	tct	gac	caa	144
Gly	Ile	Ala	Phe	Pro	Asn	Asp	Phe	Arg	Arg	Asp	His	Thr	Ser	Asp	Gln	
		35					40					45				
ttg	cac	gca	gaa	ttc	gac	ggc	aaa	gag	aac	gaa	gaa	ctg	gaa	gcg	ctg	192
Leu	His	Ala	Glu	Phe	Asp	Gly	Lys	Glu	Asn	Glu		Leu	Glu	Ala	Leu	
	50					55				60						
aac	atc	gaa	gtc	gcc	gtt	gct	ggc	cgc	atg	atg	acc	cgt	cgt	att	atg	240
Asn	Ile	Glu	Val	Ala	Val	Ala	Gly	Arg	Met	Met	Thr	Arg	Arg	Ile	Met	
	65				70					75					80	
ggg	aaa	gcg	tct	ttc	gtt	acc	ctg	cag	gac	gtt	ggc	ggg	cgc	att	cag	288
Gly	Lys	Ala	Ser	Phe	Val	Thr	Leu	Gln	Asp	Val	Gly	Gly	Arg	Ile	Gln	
				85					90					95		
ctg	tac	gtt	gcc	cgt	gac	gat	ctc	ccg	gaa	ggc	gtt	tat	aac	gag	cag	336
Leu	Tyr	Val	Ala	Arg	Asp	Asp	Leu	Pro	Glu	Gly	Val	Tyr	Asn	Glu	Gln	
			100					105					110			
ttc	aaa	aaa	tgg	gac	ctc	ggc	gac	atc	ctc	ggc	gcg	aaa	ggg	aag	ctg	384
Phe	Lys	Lys	Trp	Asp	Leu	Gly	Asp	Ile	Leu	Gly	Ala	Lys	Gly	Lys	Leu	
		115					120					125				
ttc	aaa	acc	aaa	acc	ggc	gaa	ctg	tct	atc	cac	tgc	acc	gag	ttg	cgt	432
Phe	Lys	Thr	Lys	Thr	Gly	Glu	Leu	Ser	Ile	His	Cys	Thr	Glu	Leu	Arg	
		130				135					140					
ctg	ctg	acc	aaa	gca	ctg	cgt	ccg	ctg	ccg	gat	aaa	ttc	cac	ggc	ttg	480
Leu	Leu	Thr	Lys	Ala	Leu	Arg	Pro	Leu	Pro	Asp	Lys	Phe	His	Gly	Leu	
	145				150					155					160	
cag	gat	cag	gaa	gcg	cgc	tat	cgt	cag	cgt	tat	ctc	gat	ctc	atc	tcc	528
Gln	Asp	Gln	Glu	Ala	Arg	Tyr	Arg	Gln	Arg	Tyr	Leu	Asp	Leu	Ile	Ser	
				165				170						175		
aac	gat	gaa	tcc	cgc	aac	acc	ttt	aaa	gtg	cgc	tcg	cag	atc	ctc	tct	576
Asn	Asp	Glu	Ser	Arg	Asn	Thr	Phe	Lys	Val	Arg	Ser	Gln	Ile	Leu	Ser	
			180					185					190			
ggg	att	cgc	cag	ttc	atg	gtg	aac	cgc	ggc	ttt	atg	gaa	gtt	gaa	acg	624
Gly	Ile	Arg	Gln	Phe	Met	Val	Asn	Arg	Gly	Phe	Met	Glu	Val	Glu	Thr	
		195					200				205					
ccg	atg	atg	cag	gtg	atc	cct	ggc	ggg	gcc	gct	gcg	cgt	ccg	ttt	atc	672
Pro	Met	Met	Gln	Val	Ile	Pro	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Ile	
		210				215					220					
acc	cac	cat	aac	gcg	ctg	gat	ctc	gac	atg	tac	ctg	cgt	atc	gcg	ccg	720
Thr	His	His	Asn	Ala	Leu	Asp	Leu	Asp	Met	Tyr	Leu	Arg	Ile	Ala	Pro	

225											230											235											240	
gaa ctg tac ctc aag cgt ctg gtg gtt ggt ggc ttc gag cgt gta ttc																				768														
Glu Leu Tyr Leu Lys Arg Leu Val Val Gly Gly Phe Glu Arg Val Phe																																		
										245											250											255		
gaa atc aac cgt aac ttc cgt aac gaa ggt att tcc gta cgt cat aac																				816														
Glu Ile Asn Arg Asn Phe Arg Asn Glu Gly Ile Ser Val Arg His Asn																																		
										260											265											270		
cca gag ttc acc atg atg gaa ctc tac atg gct tac gca gat tac aaa																				864														
Pro Glu Phe Thr Met Met Glu Leu Tyr Met Ala Tyr Ala Asp Tyr Lys																																		
										275											280											285		
gat ctg atc gag ctg acc gaa tcg ctg ttc cgt act ctg gca cag gat																				912														
Asp Leu Ile Glu Leu Thr Glu Ser Leu Phe Arg Thr Leu Ala Gln Asp																																		
										290											295											300		
att ctc ggt aag acg gaa gtg acc tac ggc gac gtg acg ctg gac ttc																				960														
Ile Leu Gly Lys Thr Glu Val Thr Tyr Gly Asp Val Thr Leu Asp Phe																																		
										305											310											315		
ggt aaa ccg ttc gaa aaa ctg acc atg cgt gaa gcg atc aag aaa tat																				1008														
Gly Lys Pro Phe Glu Lys Leu Thr Met Arg Glu Ala Ile Lys Lys Tyr																																		
										325											330											335		
cgc ccg gaa acc gac atg gcg gat ctg gac aac ttc gac tct gcg aaa																				1056														
Arg Pro Glu Thr Asp Met Ala Asp Leu Asp Asn Phe Asp Ser Ala Lys																																		
										340											345											350		
gca att gct gaa tct atc ggc atc cac gtt gag aag agc tgg ggt ctg																				1104														
Ala Ile Ala Glu Ser Ile Gly Ile His Val Glu Lys Ser Trp Gly Leu																																		
										355											360											365		
ggc cgt atc gtt acc gag atc ttc gaa gaa gtg gca gaa gca cat ctg																				1152														
Gly Arg Ile Val Thr Glu Ile Phe Glu Glu Val Ala Glu Ala His Leu																																		
										370											375											380		
att cag ccg acc ttc att act gaa tat ccg gca gaa gtt tct ccg ctg																				1200														
Ile Gln Pro Thr Phe Ile Thr Glu Tyr Pro Ala Glu Val Ser Pro Leu																																		
										385											390											395		
gcg cgt cgt aac gac gtt aac ccg gaa atc aca gac cgc ttt gag ttc																				1248														
Ala Arg Arg Asn Asp Val Asn Pro Glu Ile Thr Asp Arg Phe Glu Phe																																		
										405											410											415		
ttc att ggt ggt cgt gaa atc ggt aac ggc ttt agc gag ctg aat gac																				1296														
Phe Ile Gly Gly Arg Glu Ile Gly Asn Gly Phe Ser Glu Leu Asn Asp																																		
										420											425											430		
gcg gaa gat cag gcg caa cgc ttc ctg gat cag gtt gcc gcg aaa gac																				1344														
Ala Glu Asp Gln Ala Gln Arg Phe Leu Asp Gln Val Ala Ala Lys Asp																																		
										435											440											445		
gca ggt gac gac gaa gcg atg ttc tac gat gaa gat tac gtc acc gca																				1392														
Ala Gly Asp Asp Glu Ala Met Phe Tyr Asp Glu Asp Tyr Val Thr Ala																																		
										450											455											460		

ctg gaa cat ggc tta ccg ccg aca gca ggt ctg gga att ggt atc gac 1440
 Leu Glu His Gly Leu Pro Pro Thr Ala Gly Leu Gly Ile Gly Ile Asp
 465 470 475 480

cgt atg gta atg ctg ttc acc aac agc cat acc atc cgc gac gtt att 1488
 Arg Met Val Met Leu Phe Thr Asn Ser His Thr Ile Arg Asp Val Ile
 485 490 495

ctg ttc ccg gcg atg cgt ccg gta aaa taa 1518
 Leu Phe Pro Ala Met Arg Pro Val Lys *
 500 505

<210> 160
 <211> 1098
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 160
 atg ttt gaa att aat ccg gta aat aat cgc att cag gac ctc acg gaa 48
 Met Phe Glu Ile Asn Pro Val Asn Asn Arg Ile Gln Asp Leu Thr Glu
 1 5 10 15

cgc tcc gac gtt ctt agg ggg tat ctt gac tac gac gcc aag aaa gag 96
 Arg Ser Asp Val Leu Arg Gly Tyr Leu Asp Tyr Asp Ala Lys Lys Glu
 20 25 30

cgt ctg gaa gaa gta aac gcc gag ctg gaa cag ccg gat gtc tgg aac 144
 Arg Leu Glu Glu Val Asn Ala Glu Leu Glu Gln Pro Asp Val Trp Asn
 35 40 45

gaa ccc gaa cgc gca cag gcg ctg ggt aaa gag cgt tcc tcc ctc gaa 192
 Glu Pro Glu Arg Ala Gln Ala Leu Gly Lys Glu Arg Ser Ser Leu Glu
 50 55 60

gcc gtt gtc gac acc ctc gac caa atg aaa cag ggg ctg gaa gat gtt 240
 Ala Val Val Asp Thr Leu Asp Gln Met Lys Gln Gly Leu Glu Asp Val
 65 70 75 80

tct ggt ctg ctg gaa ctg gct gta gaa gct gac gac gaa gaa acc ttt 288
 Ser Gly Leu Leu Glu Leu Ala Val Glu Ala Asp Asp Glu Glu Thr Phe
 85 90 95

aac gaa gcc gtt gct gaa ctc gac gcc ctg gaa gaa aaa ctg gcg cag 336
 Asn Glu Ala Val Ala Glu Leu Asp Ala Leu Glu Glu Lys Leu Ala Gln
 100 105 110

ctt gag ttc cgc cgt atg ttc tct ggc gaa tat gac agc gcc gac tgc 384
 Leu Glu Phe Arg Arg Met Phe Ser Gly Glu Tyr Asp Ser Ala Asp Cys
 115 120 125

tac ctc gat att cag gcg ggg tct ggc ggt acg gaa gca cag gac tgg 432

Tyr	Leu	Asp	Ile	Gln	Ala	Gly	Ser	Gly	Gly	Thr	Glu	Ala	Gln	Asp	Trp	
130						135					140					
gcg	agc	atg	ctt	gag	cgt	atg	tat	ctg	cgc	tgg	gca	gaa	tcg	cgt	ggc	480
Ala	Ser	Met	Leu	Glu	Arg	Met	Tyr	Leu	Arg	Trp	Ala	Glu	Ser	Arg	Gly	
145					150				155						160	
ttc	aaa	act	gaa	atc	atc	gaa	gag	tcg	gaa	ggc	gaa	gtg	gcg	ggc	att	528
Phe	Lys	Thr	Glu	Ile	Ile	Glu	Glu	Ser	Glu	Gly	Glu	Val	Ala	Gly	Ile	
			165						170					175		
aaa	tcc	gtg	acg	atc	aaa	atc	tcc	ggc	gat	tac	gct	tac	ggc	tgg	ctg	576
Lys	Ser	Val	Thr	Ile	Lys	Ile	Ser	Gly	Asp	Tyr	Ala	Tyr	Gly	Trp	Leu	
			180					185						190		
cgt	aca	gaa	acc	ggc	gtt	cac	cgc	ctg	gtg	cgt	aaa	agc	ccg	ttt	gac	624
Arg	Thr	Glu	Thr	Gly	Val	His	Arg	Leu	Val	Arg	Lys	Ser	Pro	Phe	Asp	
		195					200					205				
tcc	ggc	ggc	cgt	cgc	cac	acg	tcg	tcc	agc	tcc	gcg	ttt	gtt	tat	ccg	672
Ser	Gly	Gly	Arg	Arg	His	Thr	Ser	Phe	Ser	Ser	Ala	Phe	Val	Tyr	Pro	
		210				215					220					
gaa	gtt	gat	gat	gat	att	gat	atc	gaa	atc	aac	ccg	gcg	gat	ctg	cgc	720
Glu	Val	Asp	Asp	Asp	Ile	Asp	Ile	Glu	Ile	Asn	Pro	Ala	Asp	Leu	Arg	
225					230					235					240	
att	gac	gtt	tat	cgc	acg	tcc	ggc	gcg	ggc	ggc	cag	cac	gtt	aac	cgt	768
Ile	Asp	Val	Tyr	Arg	Thr	Ser	Gly	Ala	Gly	Gly	Gln	His	Val	Asn	Arg	
				245					250					255		
acc	gaa	tct	gcg	gtg	cgt	att	acc	cac	atc	ccg	acc	ggg	atc	gtg	acc	816
Thr	Glu	Ser	Ala	Val	Arg	Ile	Thr	His	Ile	Pro	Thr	Gly	Ile	Val	Thr	
			260					265					270			
cag	tgc	cag	aac	gac	cgt	tcc	cag	cac	aag	aac	aaa	gat	cag	gcc	atg	864
Gln	Cys	Gln	Asn	Asp	Arg	Ser	Gln	His	Lys	Asn	Lys	Asp	Gln	Ala	Met	
		275					280					285				
aag	cag	atg	aaa	gcg	aag	ctt	tat	gaa	ctg	gag	atg	cag	aag	aaa	aat	912
Lys	Gln	Met	Lys	Ala	Lys	Leu	Tyr	Glu	Leu	Glu	Met	Gln	Lys	Lys	Asn	
		290				295					300					
gcc	gag	aaa	cag	gcg	atg	gaa	gat	aac	aaa	tcc	gac	atc	ggc	tgg	ggc	960
Ala	Glu	Lys	Gln	Ala	Met	Glu	Asp	Asn	Lys	Ser	Asp	Ile	Gly	Trp	Gly	
305					310					315					320	
agc	cag	att	cgt	tct	tat	gtc	ctt	gat	gac	tcc	cgc	att	aaa	gat	ctg	1008
Ser	Gln	Ile	Arg	Ser	Tyr	Val	Leu	Asp	Asp	Ser	Arg	Ile	Lys	Asp	Leu	
				325					330					335		
cgc	acc	ggg	gta	gaa	acc	cgc	aac	acg	cag	gcc	gtg	ctg	gac	ggc	agc	1056
Arg	Thr	Gly	Val	Glu	Thr	Arg	Asn	Thr	Gln	Ala	Val	Leu	Asp	Gly	Ser	
			340					345					350			
ctg	gat	caa	ttt	atc	gaa	gca	agt	ttg	aaa	gca	ggg	tta	tga			1098
Leu	Asp	Gln	Phe	Ile	Glu	Ala	Ser	Leu	Lys	Ala	Gly	Leu	*			

355

360

365

<210> 161

<211> 1734

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1734)

<400> 161

gtg aaa caa cag ata caa ctt cgt cgc cgt gaa gtc gat gaa acg gca	48
Met Lys Gln Gln Ile Gln Leu Arg Arg Arg Glu Val Asp Glu Thr Ala	
1 5 10 15	
gac ttg ccc gct gaa ttg cct ccc ttg ctg cgc cgt tta tac gcc agc	96
Asp Leu Pro Ala Glu Leu Pro Pro Leu Leu Arg Arg Leu Tyr Ala Ser	
20 25 30	
cgg gga gta cgc agt gcg caa gaa ctg gaa cgc agt gtt aaa ggt atg	144
Arg Gly Val Arg Ser Ala Gln Glu Leu Glu Arg Ser Val Lys Gly Met	
35 40 45	
ctg ccc tgg cag caa ctg agc ggc gtc gaa aag gcc gtt gag atc ctt	192
Leu Pro Trp Gln Gln Leu Ser Gly Val Glu Lys Ala Val Glu Ile Leu	
50 55 60	
tac aac gct ttt cgc gaa gga acg cgg att att gtg gtc ggt gat ttc	240
Tyr Asn Ala Phe Arg Glu Gly Thr Arg Ile Ile Val Val Gly Asp Phe	
65 70 75 80	
gac gcc gac ggc gcg acc agc acg gct cta agc gtg ctg gcg atg cgc	288
Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg	
85 90 95	
tcg ctt ggt tgc agc aat atc gac tac ctg gta cca aac cgt ttc gaa	336
Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu	
100 105 110	
gac ggt tac ggc tta agc ccg gaa gtg gtc gat cag gcc cat gcc cgt	384
Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg	
115 120 125	
ggc gcg cag tta att gtc acg gtg gat aac ggt att tcc tcc cat gcg	432
Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala	
130 135 140	
ggg gtt gag cac gct cgc tcg ttg ggc atc ccg gtt att gtt acc gat	480
Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp	
145 150 155 160	
cac cat ttg cca ggc gac aca tta ccc gca gcg gaa gcg atc att aac	528
His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn	
165 170 175	

cct aac ttg cgc gac tgt aat ttc ccg tcg aaa tca ctg gca ggc gtg	576
Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val	
180 185 190	
ggt gtg gcg ttt tat ctg atg ctg gcg ctg cgc acc ttt ttg cgc gat	624
Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp	
195 200 205	
cag ggc tgg ttt gat gag cgt aac atc gca att cct aac ctg gca gaa	672
Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu	
210 215 220	
ctg ctg gat ctg gtc gcg ctg ggg aca gtg gcg gac gtc gtg ccg ctg	720
Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu	
225 230 235 240	
gac gct aat aat cgc att ctg acc tgg cag ggg atg agt cgc atc cga	768
Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg	
245 250 255	
gcc gga aag tgc cgt ccg ggg att aaa gcg ctg ctt gaa gtg gca aac	816
Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn	
260 265 270	
cgt gat gca caa aaa ctc gcc gcc agc gat tta ggt ttt gcg ctg ggg	864
Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly	
275 280 285	
cca cgt ctc aat gct gcc gga cga ctg gac gat atg tcc gtc ggt gtg	912
Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val	
290 295 300	
gcg ctg ttg ttg tgc gac aac atc ggc gaa gcg cgc gtg ctg gca aat	960
Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn	
305 310 315 320	
gaa ctc gat gcg cta aac cag acg cga aaa gag atc gaa caa gga atg	1008
Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met	
325 330 335	
caa att gaa gcc ctg acc ctg tgc gag aaa ctg gag cgc agc cgt gac	1056
Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp	
340 345 350	
acg cta ccc gcc ggg ctg gca atg tat cac ccc gaa tgg cat cag ggc	1104
Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly	
355 360 365	
gtt gtc ggt att ctg gct tcg cgc atc aaa gag cgt ttt cac cgt ccg	1152
Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro	
370 375 380	
gtt atc gcg ttt gcg cca gca ggt gac ggt acg ctg aaa ggt tcc ggt	1200
Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly	
385 390 395 400	

cgc tcc att cag ggg ctg cat atg cgt gat gcg ctg gag cga tta gac	1248
Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp	
405 410 415	
aca ctc tac cct ggc atg atg ctg aag ttt ggc ggt cat gcg atg gcg	1296
Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala	
420 425 430	
gcg ggt ttg tcg ctg gaa gag gat aaa ttc aaa ctc ttt caa caa cgg	1344
Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg	
435 440 445	
ttt ggc gaa ctg gtt act gag tgg ctg gac cct tcg cta ttg caa ggc	1392
Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly	
450 455 460	
gaa gtg gta tca gac ggt ccg tta agc ccg gcc gaa atg acc atg gaa	1440
Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu	
465 470 475 480	
gtg gcg cag ctg ctg cgc gat gct ggc ccg tgg ggg cag atg ttc ccg	1488
Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro	
485 490 495	
gag ccg ctg ttt gac ggt cat ttc cgt ctg ctg caa cag ccg ctg gtg	1536
Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val	
500 505 510	
ggc gaa cgt cat ttg aag gtg atg gtc gaa ccg gtc ggc ggc ggt cca	1584
Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro	
515 520 525	
ctg ctg gat ggt att gct ttt aat gtc gat acc gcc ctc tgg ccg gat	1632
Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp	
530 535 540	
aac ggc gtg cgc gaa gtg caa ctg gct tat aag ctc gat atc aac gag	1680
Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu	
545 550 555 560	
ttt cgc ggc aac cgc agc ctg caa att atc atc gac aat atc tgg cca	1728
Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro	
565 570 575	
att tag	1734
Ile *	

<210> 162
 <211> 711
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(711)

```

<400> 162
atg aag aaa ggt ttt atg ttg ttt act ttg tta gcg gcg ttt tca ggc 48
Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
1 5 10 15

ttt gct cag gct gat gac gcg gca att caa caa acg tta gcc aaa atg 96
Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
20 25 30

ggc atc aaa agc agc gat att cag ccc gcg cct gta gct ggc atg aag 144
Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
35 40 45

aca gtt ctg act aac agc ggc gtg ttg tac atc acc gat gat ggt aaa 192
Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
50 55 60

cat atc att cag ggg cca atg tat gac gtt agt ggc acg gct ccg gtc 240
His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
65 70 75 80

aat gtc acc aat aag atg ctg tta aag cag ttg aat gcg ctt gaa aaa 288
Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
85 90 95

gag atg atc gtt tat aaa gcg ccg cag gaa aaa cac gtc atc acc gtg 336
Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
100 105 110

ttt act gat att acc tgt ggt tac tgc cac aaa ctg cat gag caa atg 384
Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
115 120 125

gca gac tac aac gcg ctg ggg atc acc gtg cgt tat ctt gct ttc ccg 432
Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
130 135 140

cgc cag ggg ctg gac agc gat gca gag aaa gaa atg aaa gct atc tgg 480
Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
145 150 155 160

tgt gcg aaa gat aaa aac aaa gcg ttt gat gat gtg atg gca ggt aaa 528
Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
165 170 175

agc gtc gca cca gcc agt tgc gac gtg gat att gcc gac cat tac gca 576
Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
180 185 190

ctt ggc gtc cag ctt ggc gtt agc ggt act ccg gca gtt gtg ctg agc 624
Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
195 200 205

aat ggc aca ctt gtt ccg ggt tac cag ccg ccg aaa gag atg aaa gaa 672
Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
210 215 220

```



```

Ser Leu Arg Gln Gly Val Val Arg Val Ile Gly Lys Gly Asn Lys Glu
      165                      170                      175

cgt ctg gtg ccg tta ggt gaa gag gcg gtt tac tgg ctg gaa acc tat   576
Arg Leu Val Pro Leu Gly Glu Glu Ala Val Tyr Trp Leu Glu Thr Tyr
      180                      185                      190

ctg gaa cat ggg cgt ccg tgg ctg ctg aat ggt gtg tca att gac gtg   624
Leu Glu His Gly Arg Pro Trp Leu Leu Asn Gly Val Ser Ile Asp Val
      195                      200                      205

ttg ttt ccc agc cag cgt gcg cag cag atg acg cga cag acc ttc tgg   672
Leu Phe Pro Ser Gln Arg Ala Gln Gln Met Thr Arg Gln Thr Phe Trp
      210                      215                      220

cac cgt att aaa cat tat gct gtg ctg gcg ggt atc gac agc gaa aag   720
His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys
      225                      230                      235                      240

ctg tca ccg cat gtg ttg cgt cac gct ttt gcc act cat tta tta aat   768
Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn
      245                      250                      255

cat ggt gcg gat tta cgc gtg gtg cag atg cta ctg ggc cac agc gat   816
His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp
      260                      265                      270

ctc tcc acc acg caa att tat acg cat gtc gct acc gag cgt ctg cgg   864
Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg
      275                      280                      285

caa ctt cat caa cag cat cac ccg cgg gcg tga   897
Gln Leu His Gln Gln His His Pro Arg Ala *
      290                      295

<210> 164
<211> 1104
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1104)

<400> 164
atg agt gac agc cag acg ctg gtg gta aaa ctc ggc acc agt gtg cta   48
Met Ser Asp Ser Gln Thr Leu Val Val Lys Leu Gly Thr Ser Val Leu
      1                      5                      10                      15

aca ggc gga tcg cgc cgt ctg aac cgt gcc cat atc gtt gaa ctt gtt   96
Thr Gly Gly Ser Arg Arg Leu Asn Arg Ala His Ile Val Glu Leu Val
      20                      25                      30

cgc cag tgc gcg cag tta cat gcc gcc ggg cat cgg att gtt att gtg   144
Arg Gln Cys Ala Gln Leu His Ala Ala Gly His Arg Ile Val Ile Val
      35                      40                      45

```

acg tcg ggc gcg atc gcc gcc gga cgt gag cac ctg ggt tac ccg gaa	192
Thr Ser Gly Ala Ile Ala Ala Gly Arg Glu His Leu Gly Tyr Pro Glu	
50 55 60	
ctg cca gcg acc atc gcc tcg aaa caa ctg ctg gcg gcg gta ggg cag	240
Leu Pro Ala Thr Ile Ala Ser Lys Gln Leu Leu Ala Ala Val Gly Gln	
65 70 75 80	
agt cga ctg att caa ctg tgg gaa cag ctg ttt tcg att tat ggc att	288
Ser Arg Leu Ile Gln Leu Trp Glu Gln Leu Phe Ser Ile Tyr Gly Ile	
85 90 95	
cac gtc ggg caa atg ctg ctg acc cgt gct gat atg gaa gac cgt gaa	336
His Val Gly Gln Met Leu Leu Thr Arg Ala Asp Met Glu Asp Arg Glu	
100 105 110	
cgc ttc ctg aac gcc cgc gac acc ctg cga gcg ttg ctc gat aac aat	384
Arg Phe Leu Asn Ala Arg Asp Thr Leu Arg Ala Leu Leu Asp Asn Asn	
115 120 125	
atc gtt ccg gta atc aat gag aac gat gct gtc gct acg gca gag att	432
Ile Val Pro Val Ile Asn Glu Asn Asp Ala Val Ala Thr Ala Glu Ile	
130 135 140	
aag gtc ggc gat aac gat aac ctt tct gcg ctg gcg gcg att ctt gcg	480
Lys Val Gly Asp Asn Asp Asn Leu Ser Ala Leu Ala Ala Ile Leu Ala	
145 150 155 160	
ggg gcc gat aaa ctg ttg ctg ctg acc gat caa aaa ggt ttg tat acc	528
Gly Ala Asp Lys Leu Leu Leu Leu Thr Asp Gln Lys Gly Leu Tyr Thr	
165 170 175	
gct gac ccg cgc agc aat ccg cag gca gaa ctg att aaa gat gtt tac	576
Ala Asp Pro Arg Ser Asn Pro Gln Ala Glu Leu Ile Lys Asp Val Tyr	
180 185 190	
ggc att gat gac gca ctg cgc gcg att gcc ggt gac agc gtt tca ggc	624
Gly Ile Asp Asp Ala Leu Arg Ala Ile Ala Gly Asp Ser Val Ser Gly	
195 200 205	
ctc gga act ggc ggc atg agt acc aaa ttg cag gcc gct gac gtg gct	672
Leu Gly Thr Gly Gly Met Ser Thr Lys Leu Gln Ala Ala Asp Val Ala	
210 215 220	
tgc cgt gcg ggt atc gac acc att att gcc gcg ggc agc aag ccg ggc	720
Cys Arg Ala Gly Ile Asp Thr Ile Ile Ala Ala Gly Ser Lys Pro Gly	
225 230 235 240	
gtt att ggt gat gtg atg gaa ggc att tcc gtc ggt acg ctg ttc cat	768
Val Ile Gly Asp Val Met Glu Gly Ile Ser Val Gly Thr Leu Phe His	
245 250 255	
gcc cag gcg act ccg ctt gaa aac cgt aaa cgc tgg att ttc ggt gcg	816
Ala Gln Ala Thr Pro Leu Glu Asn Arg Lys Arg Trp Ile Phe Gly Ala	
260 265 270	

ccg ccg gcg ggt gaa atc acg gta gat gaa ggg gca act gcc gcc att	864
Pro Pro Ala Gly Glu Ile Thr Val Asp Glu Gly Ala Thr Ala Ala Ile	
275 280 285	
ctg gaa cgc ggc agc tcc ctg ttg ccg aaa ggc att aaa agc gtg act	912
Leu Glu Arg Gly Ser Ser Leu Leu Pro Lys Gly Ile Lys Ser Val Thr	
290 295 300	
ggc aat ttc tcg cgt ggt gaa gtc atc cgc att tgc aac ctc gaa ggc	960
Gly Asn Phe Ser Arg Gly Glu Val Ile Arg Ile Cys Asn Leu Glu Gly	
305 310 315 320	
cgc gat atc gcc cac ggc gtc agt cgt tac aac agc gat gca tta cgc	1008
Arg Asp Ile Ala His Gly Val Ser Arg Tyr Asn Ser Asp Ala Leu Arg	
325 330 335	
cgt att gcc gga cac cac tcg caa gaa att gat gca ata ctg gga tat	1056
Arg Ile Ala Gly His His Ser Gln Glu Ile Asp Ala Ile Leu Gly Tyr	
340 345 350	
gaa tac ggc ccg gtt gcc gtt cac cgt gat gac atg att acc cgt taa	1104
Glu Tyr Gly Pro Val Ala Val His Arg Asp Asp Met Ile Thr Arg *	
355 360 365	
<210> 165	
<211> 1254	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(1254)	
<400> 165	
atg ctg gaa caa atg ggc att gcc gcg aag caa gcc tcg tat aaa tta	48
Met Leu Glu Gln Met Gly Ile Ala Ala Lys Gln Ala Ser Tyr Lys Leu	
1 5 10 15	
gcg caa ctc tcc agc cgc gaa aaa aat cgc gtg ctg gaa aaa atc gcc	96
Ala Gln Leu Ser Ser Arg Glu Lys Asn Arg Val Leu Glu Lys Ile Ala	
20 25 30	
gat gaa ctg gaa gca caa agc gaa atc atc ctc aac gct aac gcc cag	144
Asp Glu Leu Glu Ala Gln Ser Glu Ile Ile Leu Asn Ala Asn Ala Gln	
35 40 45	
gat gtt gct gac gcg cga gcc aat ggc ctt agc gaa gcg atg ctt gac	192
Asp Val Ala Asp Ala Arg Ala Asn Gly Leu Ser Glu Ala Met Leu Asp	
50 55 60	
cgt ctg gca ctg acg ccc gca cgg ctg aaa ggc att gcc gac gat gta	240
Arg Leu Ala Leu Thr Pro Ala Arg Leu Lys Gly Ile Ala Asp Asp Val	
65 70 75 80	
cgt cag gtg tgc aac ctc gcc gat ccg gtg ggg cag gta atc gat ggc	288

Arg	Gln	Val	Cys	Asn	Leu	Ala	Asp	Pro	Val	Gly	Gln	Val	Ile	Asp	Gly	
				85					90					95		
ggc	gta	ctg	gac	agc	ggc	ctg	cgt	ctt	gag	cgt	cgt	cgc	gta	ccg	ctg	336
Gly	Val	Leu	Asp	Ser	Gly	Leu	Arg	Leu	Glu	Arg	Arg	Arg	Val	Pro	Leu	
			100					105					110			
ggg	gtt	att	ggc	gtg	att	tat	gaa	gcg	cgc	ccg	aac	gtg	acg	gtt	gat	384
Gly	Val	Ile	Gly	Val	Ile	Tyr	Glu	Ala	Arg	Pro	Asn	Val	Thr	Val	Asp	
		115					120					125				
gtc	gct	tcg	ctg	tgc	ctg	aaa	acc	ggg	aat	gcg	gtg	atc	ctg	cgc	ggg	432
Val	Ala	Ser	Leu	Cys	Leu	Lys	Thr	Gly	Asn	Ala	Val	Ile	Leu	Arg	Gly	
	130					135					140					
ggc	aaa	gaa	acg	tgt	cgc	act	aac	gct	gca	acg	gtg	gcg	gtg	att	cag	480
Gly	Lys	Glu	Thr	Cys	Arg	Thr	Asn	Ala	Ala	Thr	Val	Ala	Val	Ile	Gln	
145				150						155					160	
gac	gcc	ctg	aaa	tcc	tgc	ggc	tta	ccg	gcg	ggg	gcc	gtg	cag	gcg	att	528
Asp	Ala	Leu	Lys	Ser	Cys	Gly	Leu	Pro	Ala	Gly	Ala	Val	Gln	Ala	Ile	
			165					170					175			
gat	aat	cct	gac	cgt	gcg	ctg	gtc	agt	gaa	atg	ctg	cgt	atg	gat	aaa	576
Asp	Asn	Pro	Asp	Arg	Ala	Leu	Val	Ser	Glu	Met	Leu	Arg	Met	Asp	Lys	
			180					185					190			
tac	atc	gac	atg	ctg	atc	ccg	cgt	ggg	ggc	gct	ggg	ttg	cat	aaa	ctg	624
Tyr	Ile	Asp	Met	Leu	Ile	Pro	Arg	Gly	Gly	Ala	Gly	Leu	His	Lys	Leu	
		195				200						205				
tgc	cgt	gaa	cag	tcg	aca	atc	ccg	gtg	atc	aca	ggg	ggg	ata	ggc	gta	672
Cys	Arg	Glu	Gln	Ser	Thr	Ile	Pro	Val	Ile	Thr	Gly	Gly	Ile	Gly	Val	
	210					215					220					
tgc	cat	att	tac	gtt	gat	gaa	agt	gta	gag	atc	gct	gaa	gca	tta	aaa	720
Cys	His	Ile	Tyr	Val	Asp	Glu	Ser	Val	Glu	Ile	Ala	Glu	Ala	Leu	Lys	
225				230					235						240	
gtg	atc	gtc	aac	gcg	aaa	act	cag	cgt	ccg	agc	aca	tgt	aat	acg	gtt	768
Val	Ile	Val	Asn	Ala	Lys	Thr	Gln	Arg	Pro	Ser	Thr	Cys	Asn	Thr	Val	
			245					250					255			
gaa	acg	ttg	ctg	gtg	aat	aaa	aac	atc	gcc	gat	agc	ttc	ctg	ccc	gca	816
Glu	Thr	Leu	Leu	Val	Asn	Lys	Asn	Ile	Ala	Asp	Ser	Phe	Leu	Pro	Ala	
		260					265					270				
tta	agc	aaa	caa	atg	gcg	gaa	agc	ggc	gtg	aca	tta	cac	gca	gat	gca	864
Leu	Ser	Lys	Gln	Met	Ala	Glu	Ser	Gly	Val	Thr	Leu	His	Ala	Asp	Ala	
		275				280					285					
gct	gca	ctg	gcg	cag	ttg	cag	gca	ggc	cct	gcg	aag	gtg	gtt	gct	gtt	912
Ala	Ala	Leu	Ala	Gln	Leu	Gln	Ala	Gly	Pro	Ala	Lys	Val	Val	Ala	Val	
	290					295			300							
aaa	gcc	gaa	gag	tat	gac	gat	gag	ttt	ctg	tca	tta	gat	ttg	aac	gtc	960
Lys	Ala	Glu	Glu	Tyr	Asp	Asp	Glu	Phe	Leu	Ser	Leu	Asp	Leu	Asn	Val	

305	310	315	320	
aaa atc gtc agc gat ctt gac gat gcc atc gcc cat att cgt gaa cac				1008
Lys Ile Val Ser Asp Leu Asp Asp Ala Ile Ala His Ile Arg Glu His	325	330	335	
ggc aca caa cac tcc gat gcg atc ctg acc cgc gat atg cgc aac gcc				1056
Gly Thr Gln His Ser Asp Ala Ile Leu Thr Arg Asp Met Arg Asn Ala	340	345	350	
cag cgt ttt gtt aac gaa gtg gat tcg tcc gct gtt tac gtt aac gcc				1104
Gln Arg Phe Val Asn Glu Val Asp Ser Ser Ala Val Tyr Val Asn Ala	355	360	365	
tct acg cgt ttt acc gac ggc ggc cag ttt ggt ctg ggt gcg gaa gtg				1152
Ser Thr Arg Phe Thr Asp Gly Gly Gln Phe Gly Leu Gly Ala Glu Val	370	375	380	
gcg gta agc aca caa aaa ctc cac gcg cgt ggc cca atg ggg ctg gaa				1200
Ala Val Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Gly Leu Glu	385	390	400	
gca ctg acc act tac aag tgg atc ggc att ggt gat tac acc att cgt				1248
Ala Leu Thr Thr Tyr Lys Trp Ile Gly Ile Gly Asp Tyr Thr Ile Arg	405	410	415	
gcg taa				1254
Ala *				
<210> 166				
<211> 561				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(561)				
<400> 166				
atg atg aca agg cag gca tca atg aaa ggc ttc cca att gcg cat att				48
Met Met Thr Arg Gln Ala Ser Met Lys Gly Phe Pro Ile Ala His Ile	1	5	10	15
ttt cac cct tca atc ccg cca atg cac gca gtg gtt aac aat cac aat				96
Phe His Pro Ser Ile Pro Pro Met His Ala Val Val Asn Asn His Asn	20	25	30	
aga aat att gat tat tgg acg gta aaa aga aag ttt gca gaa att gtc				144
Arg Asn Ile Asp Tyr Trp Thr Val Lys Arg Lys Phe Ala Glu Ile Val	35	40	45	
tcc acc aat gac gtt aat aaa att tac agt ata agt aat gaa ctg cgg				192
Ser Thr Asn Asp Val Asn Lys Ile Tyr Ser Ile Ser Asn Glu Leu Arg	50	55	60	

50	55	60	
act ggt gat ttt caa aaa gaa tta gcg tac tta caa aat gta att ctt	240		
Thr Gly Asp Phe Gln Lys Glu Leu Ala Tyr Leu Gln Asn Val Ile Leu			
65 70 75 80			
tat aat gtc tcg tct ctt cgt ctg gat ttt tta ggt tat aac gcc caa	288		
Tyr Asn Val Ser Ser Leu Arg Leu Asp Phe Leu Gly Tyr Asn Ala Gln			
85 90 95			
att att caa cga tcg gac aat act tgt gaa ctt acc att aat gaa ccg	336		
Ile Ile Gln Arg Ser Asp Asn Thr Cys Glu Leu Thr Ile Asn Glu Pro			
100 105 110			
tta aaa aac cag gaa ata tcc aca ggt aat atc aat att aat tgc cca	384		
Leu Lys Asn Gln Glu Ile Ser Thr Gly Asn Ile Asn Ile Asn Cys Pro			
115 120 125			
tta aaa gat att tac aat gaa atc agg agg tta aac gta att ttt agt	432		
Leu Lys Asp Ile Tyr Asn Glu Ile Arg Arg Leu Asn Val Ile Phe Ser			
130 135 140			
tgt ggg act gga gat atc gtt gat cta tcc tct ctg gac tta cgt aat	480		
Cys Gly Thr Gly Asp Ile Val Asp Leu Ser Ser Leu Asp Leu Arg Asn			
145 150 155 160			
gtc gat tta gat tat tat gat ttc aca gat aaa cat atg gct aat act	528		
Val Asp Leu Asp Tyr Tyr Asp Phe Thr Asp Lys His Met Ala Asn Thr			
165 170 175			
att tta aat cct ttt aaa ttg aat tca aca aat ttt act aat gcc aac	576		
Ile Leu Asn Pro Phe Lys Leu Asn Ser Thr Asn Phe Thr Asn Ala Asn			
180 185 190			
atg ttt cag gtt aat ttt gtt agt tca aca caa aac gcc aca atc tcc	624		
Met Phe Gln Val Asn Phe Val Ser Ser Thr Gln Asn Ala Thr Ile Ser			
195 200 205			
tgg gat tat tta cta aaa ata acg cct gtt tta ata agc att agc gat	672		
Trp Asp Tyr Leu Leu Lys Ile Thr Pro Val Leu Ile Ser Ile Ser Asp			
210 215 220			
atg tat tct gaa gaa aaa atc aag ttt gtc gaa agt tgt tta aat gag	720		
Met Tyr Ser Glu Glu Lys Ile Lys Phe Val Glu Ser Cys Leu Asn Glu			
225 230 235 240			
cct gga gac att acc gaa gaa caa tta aaa att atg aga ttt gca att	768		
Pro Gly Asp Ile Thr Glu Glu Gln Leu Lys Ile Met Arg Phe Ala Ile			
245 250 255			
ata aaa tct ata cca agg gca act ctt aca gat aaa tta gaa aat gaa	816		
Ile Lys Ser Ile Pro Arg Ala Thr Leu Thr Asp Lys Leu Glu Asn Glu			
260 265 270			
tta aca aaa gaa ata tat aaa agc tca tcg aaa atc atc aat tgc ttg	864		
Leu Thr Lys Glu Ile Tyr Lys Ser Ser Ser Lys Ile Ile Asn Cys Leu			
275 280 285			

```

aac aga att aaa tta aca gag atg aaa gaa ttc tca tca gaa aaa ata 912
Asn Arg Ile Lys Leu Thr Glu Met Lys Glu Phe Ser Ser Glu Lys Ile
290 295 300

tat gat tac atc gat ata atc att gaa gat tat gaa aat acc aaa gaa 960
Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu
305 310 315 320

aat gct tat ctg gtc gtc ccc caa att aat tat act atg gat tta aac 1008
Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn
325 330 335

ata gaa gac tct agc tca gaa gag tta ctt tca gat aat acc ctc gag 1056
Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu
340 345 350

aaa gac gaa aat tct ccg gac aat ggc ttt gag gtc ggg gaa tat aac 1104
Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn
355 360 365

aca tat gaa gca tat aac tca gag aag caa tat ttt acc aga gag gac 1152
Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp
370 375 380

tat acg tat gat tac gac ctt tta aat gca ata tag 1188
Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile *
385 390 395

<210> 168
<211> 948
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(948)

<400> 168
gtg tgt cat cgc gca ttt cga ctt cat ctt tgc aag gac tgg gtt ttc 48
Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe
1 5 10 15

atg ttt tct ggg ctg tta atc att ctg gtt ccc ctg att gtg ggt tac 96
Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr
20 25 30

ctc att ccg ctt cgc caa caa gct gcg tta aaa gtt att aat cag cta 144
Leu Ile Pro Leu Arg Gln Gln Ala Ala Leu Lys Val Ile Asn Gln Leu
35 40 45

tta agc tgg atg gtt tac ctt att ctc ttt ttt atg ggt atc agt ctg 192
Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu
50 55 60

gcg ttt ctc gat aac ctc gcc agt aac ctg ttg gcg att ctg cat tat 240

```

Ala Phe Leu Asp Asn Leu Ala Ser Asn Leu Leu Ala Ile Leu His Tyr	
65 70 75 80	
tct gcc gtc agt att acc gtt att tta ctg tgt aat att gcc gcc ctg	288
Ser Ala Val Ser Ile Thr Val Ile Leu Leu Cys Asn Ile Ala Ala Leu	
85 90 95	
atg tgg ctg gag cga ggc ctg ccg tgg cgc aac cac cat cag caa gaa	336
Met Trp Leu Glu Arg Gly Leu Pro Trp Arg Asn His His Gln Gln Glu	
100 105 110	
aaa ctc ccg tcg cgt att gcg atg gcg ctg gag tcg cta aaa ctg tgc	384
Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys	
115 120 125	
ggc gta gta gtg att ggt ttt gcc att ggt cta agt gga ctg gct ttc	432
Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe	
130 135 140	
tta caa cac gcg acc gaa gcc agt gaa tac acg tta att ttg cta ctt	480
Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu	
145 150 155 160	
ttc ctc gtt ggt att cag ttg cgc aat aat ggc atg acc tta aag cag	528
Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln	
165 170 175	
att gtc ctt aat cgc cgg gga atg att gtc gcc gtg gtg gtg gtt gtc	576
Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val Val	
180 185 190	
agt tca tta att ggt ggt tta att aac gcc ttt att ctt gat ctc ccc	624
Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro	
195 200 205	
atc aat acc gcg ctg gca atg gcc tcc ggt ttc gcc tgg tat tct ctt	672
Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu	
210 215 220	
tcc ggt att tta ttg acc gaa tct ttt ggt ccg gta atc ggg agc gcg	720
Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala	
225 230 235 240	
gcg ttt ttt aat gat ctg gcc cgt gaa ctg att gct att atg ttg atc	768
Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile	
245 250 255	
cct ggg ctg att cgc cgc agc cgc tct act gca ctg gcc tta tgc ggt	816
Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly	
260 265 270	
gcc aca tca atg gat ttc acc ctg ccc gtt ctt caa cgt act ggc ggg	864
Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly	
275 280 285	
ctg gat atg gtc ccg gcg gca att gtt cac ggt ttt att ctt agc ctg	912
Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu	

290

295

300

tta gtg ccg atc ctc atc gcc ttt ttc tct gcg taa 948
 Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala *
 305 310 315

<210> 169

<211> 291

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(291)

<400> 169

atg caa aac aca act cat gac aac gta att ctg gag ctc acc gtt cgc 48
 Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
 1 5 10 15

aac cat ccg ggc gta atg acc cac gtt tgt ggc ctt ttt gcc cgc cgc 96
 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
 20 25 30

gct ttt aac gtt gaa ggc att ctt tgt ctg ccg att cag gac agc gac 144
 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
 35 40 45

aaa agc cat atc tgg cta ctg gtc aat gac gac cag cgt ctg gag cag 192
 Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
 50 55 60

atg ata agc caa atc gat aag ctg gaa gat gtc gtg aaa gtg cag cgt 240
 Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
 65 70 75 80

aat cag tcc gat ccg acg atg ttt aac aag atc gcg gtg ttt ttt cag 288
 Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
 85 90 95

taa 291
 *

<210> 170

<211> 1689

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1689)

<400> 170

atg gca agt tcg ggc aca aca tcg acg cgt aag cgc ttt acc ggc gca 48

Met	Ala	Ser	Ser	Gly	Thr	Thr	Ser	Thr	Arg	Lys	Arg	Phe	Thr	Gly	Ala		
1				5					10					15			
gaa ttt atc gtt cat ttc ctg gaa cag cag ggc att aag att gtg aca 96																	
Glu	Phe	Ile	Val	His	Phe	Leu	Glu	Gln	Gln	Gly	Ile	Lys	Ile	Val	Thr		
			20					25					30				
ggc att ccg ggc ggt tct atc ctg cct gtt tac gat gcc tta agc caa 144																	
Gly	Ile	Pro	Gly	Gly	Ser	Ile	Leu	Pro	Val	Tyr	Asp	Ala	Leu	Ser	Gln		
		35				40					45						
agc acg caa atc cgc cat att ctg gcc cgt cat gaa cag ggc gcg ggc 192																	
Ser	Thr	Gln	Ile	Arg	His	Ile	Leu	Ala	Arg	His	Glu	Gln	Gly	Ala	Gly		
	50					55				60							
ttt atc gct cag gga atg gcg cgc acc gac ggt aaa ccg gcg gtc tgt 240																	
Phe	Ile	Ala	Gln	Gly	Met	Ala	Arg	Thr	Asp	Gly	Lys	Pro	Ala	Val	Cys		
65				70				75						80			
atg gcc tgt agc gga ccg ggt gcg act aac ctg gtg acc gcc att gcc 288																	
Met	Ala	Cys	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Thr	Ala	Ile	Ala		
			85					90					95				
gat gcg cgg ctg gac tcc atc ccg ctg att tgc atc act ggt cag gtt 336																	
Asp	Ala	Arg	Leu	Asp	Ser	Ile	Pro	Leu	Ile	Cys	Ile	Thr	Gly	Gln	Val		
			100					105					110				
ccc gcc tcg atg atc ggc acc gac gcc ttc cag gaa gtg gac acc tac 384																	
Pro	Ala	Ser	Met	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Val	Asp	Thr	Tyr		
		115					120					125					
ggc atc tct atc ccc atc acc aaa cac aac tat ctg gtc aga cat atc 432																	
Gly	Ile	Ser	Ile	Pro	Ile	Thr	Lys	His	Asn	Tyr	Leu	Val	Arg	His	Ile		
	130					135				140							
gaa gaa ctc ccg cag gtc atg agc gat gcc ttc cgc att gcg caa tca 480																	
Glu	Glu	Leu	Pro	Gln	Val	Met	Ser	Asp	Ala	Phe	Arg	Ile	Ala	Gln	Ser		
145				150					155					160			
ggc cgc cca ggc ccg gtg tgg ata gac att cct aag gat gtg caa acg 528																	
Gly	Arg	Pro	Gly	Pro	Val	Trp	Ile	Asp	Ile	Pro	Lys	Asp	Val	Gln	Thr		
			165					170					175				
gca gtt ttt gag att gaa aca cag ccc gct atg gca gaa aaa gcc gcc 576																	
Ala	Val	Phe	Glu	Ile	Glu	Thr	Gln	Pro	Ala	Met	Ala	Glu	Lys	Ala	Ala		
		180						185					190				
gcc ccc gcc ttt agc gaa gaa agc att cgt gac gca gcg gcg atg att 624																	
Ala	Pro	Ala	Phe	Ser	Glu	Glu	Ser	Ile	Arg	Asp	Ala	Ala	Ala	Met	Ile		
		195					200					205					
aac gct gcc aaa cgc ccg gtg ctt tat ctg ggc ggc ggt gtg atc aat 672																	
Asn	Ala	Ala	Lys	Arg	Pro	Val	Leu	Tyr	Leu	Gly	Gly	Gly	Val	Ile	Asn		
	210					215				220							
gcg ccc gca cgg gtg cgt gaa ctg gcg gag aaa gcg caa ctg cct acc 720																	
Ala	Pro	Ala	Arg	Val	Arg	Glu	Leu	Ala	Glu	Lys	Ala	Gln	Leu	Pro	Thr		

225	230	235	240	
acc atg act tta atg gcg ctg ggc atg ttg cca aaa gcg cat ccg ttg				768
Thr Met Thr Leu Met Ala Leu Gly Met Leu Pro Lys Ala His Pro Leu	245	250	255	
tcg ctg ggt atg ctg ggg atg cac ggc gtg cgc agc acc aac tat att				816
Ser Leu Gly Met Leu Gly Met His Gly Val Arg Ser Thr Asn Tyr Ile	260	265	270	
ttg cag gag gcg gat ttg ttg ata gtg ctc ggt gcg cgt ttt gat gac				864
Leu Gln Glu Ala Asp Leu Leu Ile Val Leu Gly Ala Arg Phe Asp Asp	275	280	285	
cgg gcg att ggc aaa acc gag cag ttc tgt ccg aat gcc aaa atc att				912
Arg Ala Ile Gly Lys Thr Glu Gln Phe Cys Pro Asn Ala Lys Ile Ile	290	295	300	
cat gtc gat atc gac cgt gca gag ctg ggt aaa atc aag cag ccg cac				960
His Val Asp Ile Asp Arg Ala Glu Leu Gly Lys Ile Lys Gln Pro His	305	310	315	320
gtg gcg att cag gcg gat gtt gat gac gtg ctg gcg cag ttg atc ccg				1008
Val Ala Ile Gln Ala Asp Val Asp Asp Val Leu Ala Gln Leu Ile Pro	325	330	335	
ctg gtg gaa gcg caa ccg cgt gca gag tgg cac cag ttg gta gcg gat				1056
Leu Val Glu Ala Gln Pro Arg Ala Glu Trp His Gln Leu Val Ala Asp	340	345	350	
ttg cag cgt gag ttt ccg tgt cca atc ccg aaa gcg tgc gat ccg tta				1104
Leu Gln Arg Glu Phe Pro Cys Pro Ile Pro Lys Ala Cys Asp Pro Leu	355	360	365	
agc cat tac ggc ctg atc aac gcc gtt gcc gcc tgt gtc gat gac aat				1152
Ser His Tyr Gly Leu Ile Asn Ala Val Ala Ala Cys Val Asp Asp Asn	370	375	380	
gca att atc acc acc gac gtt ggt cag cat cag atg tgg acc gcg caa				1200
Ala Ile Ile Thr Thr Asp Val Gly Gln His Gln Met Trp Thr Ala Gln	385	390	395	400
gct tat ccg ctc aat cgc cca cgc cag tgg ctg acc tcc ggt ggg ctg				1248
Ala Tyr Pro Leu Asn Arg Pro Arg Gln Trp Leu Thr Ser Gly Gly Leu	405	410	415	
ggc acg atg ggt ttt ggc ctg cct gcg gcg att ggc gct gcg ctg gcg				1296
Gly Thr Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ala Leu Ala	420	425	430	
aac ccg gat cgc aaa gtg ttg tgt ttc tcc ggc gac ggc agc ctg atg				1344
Asn Pro Asp Arg Lys Val Leu Cys Phe Ser Gly Asp Gly Ser Leu Met	435	440	445	
atg aat att cag gag atg gcg acc gcc agt gaa aat cag ctg gat gtc				1392
Met Asn Ile Gln Glu Met Ala Thr Ala Ser Glu Asn Gln Leu Asp Val	450	455	460	

<220>

<221> CDS

<222> (1)...(1017)

<400> 172

atg	ttt	gtc	atc	tgg	agc	cat	aga	aca	ggg	ttc	atc	atg	agt	cat	caa	48
Met	Phe	Val	Ile	Trp	Ser	His	Arg	Thr	Gly	Phe	Ile	Met	Ser	His	Gln	
1				5					10					15		
ctt	acc	ttc	gcc	gac	agt	gaa	ttc	agc	agt	aag	cgc	cgt	cag	acc	aga	96
Leu	Thr	Phe	Ala	Asp	Ser	Glu	Phe	Ser	Ser	Lys	Arg	Arg	Gln	Thr	Arg	
			20					25					30			
aaa	gag	att	ttc	ttg	tcc	cgc	atg	gag	cag	att	ctg	cca	tgg	caa	aac	144
Lys	Glu	Ile	Phe	Leu	Ser	Arg	Met	Glu	Gln	Ile	Leu	Pro	Trp	Gln	Asn	
		35					40					45				
atg	gtg	gaa	gtc	atc	gag	ccg	ttt	tac	ccc	aag	gct	ggc	aat	ggc	cgg	192
Met	Val	Glu	Val	Ile	Glu	Pro	Phe	Tyr	Pro	Lys	Ala	Gly	Asn	Gly	Arg	
	50					55					60					
cga	cct	tat	ccg	ctg	gaa	acc	atg	cta	cgc	att	cac	tgc	atg	cag	cat	240
Arg	Pro	Tyr	Pro	Leu	Glu	Thr	Met	Leu	Arg	Ile	His	Cys	Met	Gln	His	
	65				70				75					80		
tgg	tac	aac	ctg	agc	gat	ggc	gcg	atg	gaa	gat	gct	ctg	tac	gaa	atc	288
Trp	Tyr	Asn	Leu	Ser	Asp	Gly	Ala	Met	Glu	Asp	Ala	Leu	Tyr	Glu	Ile	
				85				90					95			
gcc	tcc	atg	cgt	ctg	ttt	gcc	cgg	tta	tcc	ctg	gat	agc	gcc	ttg	ccg	336
Ala	Ser	Met	Arg	Leu	Phe	Ala	Arg	Leu	Ser	Leu	Asp	Ser	Ala	Leu	Pro	
			100					105					110			
gac	cgc	acc	acc	atc	atg	aat	ttc	cgc	cac	ctg	ctg	gag	cag	cat	caa	384
Asp	Arg	Thr	Thr	Ile	Met	Asn	Phe	Arg	His	Leu	Leu	Glu	Gln	His	Gln	
		115				120						125				
ctg	gcc	cgc	caa	ttg	ttc	aag	acc	atc	aat	cgc	tgg	ctg	gcc	gaa	gca	432
Leu	Ala	Arg	Gln	Leu	Phe	Lys	Thr	Ile	Asn	Arg	Trp	Leu	Ala	Glu	Ala	
	130					135				140						
ggc	gtc	atg	atg	act	caa	ggc	acc	ttg	gtc	gat	gcc	acc	atc	att	gag	480
Gly	Val	Met	Met	Thr	Gln	Gly	Thr	Leu	Val	Asp	Ala	Thr	Ile	Ile	Glu	
	145				150				155					160		
gca	ccc	agc	tcg	acc	aag	aac	aaa	gag	cag	caa	cgc	gat	ccg	gag	atg	528
Ala	Pro	Ser	Ser	Thr	Lys	Asn	Lys	Glu	Gln	Gln	Arg	Asp	Pro	Glu	Met	
				165				170					175			
cat	cag	acc	aag	aaa	ggc	aat	cag	tgg	cac	ttt	ggc	atg	aag	gcc	cac	576
His	Gln	Thr	Lys	Lys	Gly	Asn	Gln	Trp	His	Phe	Gly	Met	Lys	Ala	His	
			180					185					190			
att	ggc	gtc	gat	gcc	aag	agt	ggc	ctg	acc	cac	agc	ctg	gtc	acc	acc	624
Ile	Gly	Val	Asp	Ala	Lys	Ser	Gly	Leu	Thr	His	Ser	Leu	Val	Thr	Thr	
		195				200						205				

gcg gcc aac gag cat gac ctc aat cag ctg ggt aat ctg ctg cat gga	672
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly	
210 215 220	
gag gag caa ttt gtc tca gcc gat gcc ggc tac caa ggg gcg cca cag	720
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln	
225 230 235 240	
cgc gag gag ctg gcc gag gtg gat gtg gac tgg ctg atc gcc gag cgc	768
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg	
245 250 255	
ccc ggc aag gta aga acc ttg aaa cag cat cca cgc aag aac aaa acg	816
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr	
260 265 270	
gcc atc aac atc gaa tac atg aaa gcc agc atc cgg gcc agg gtg gag	864
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu	
275 280 285	
cac cca ttt cgc atc atc aag cga cag ttc ggc ttc gtg aaa gcc aga	912
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg	
290 295 300	
tac aag ggg ttg ctg aaa aac gat aac caa ctg gcg atg tta ttc acg	960
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr	
305 310 315 320	
ctg gcc aac ctg ttt cgg gcg gac caa atg ata cgt cag tgg gag aga	1008
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg	
325 330 335	
tct cac taa	1017
Ser His *	

<210> 173
 <211> 474
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(474)

<400> 173	
atg gta tat ata ata atc gtt tcc cac gga cat gaa gac tac atc aaa	48
Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys	
1 5 10 15	
aaa tta ctc gaa aat ctt aat gct gac gat gag cac tac aag att atc	96
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile	
20 25 30	
gta cgc gac aac aaa gac tct cta tta ttg aaa caa ata tgc cag cat	144

Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
35 40 45

tat gca ggc ctg gac tat att agt gga ggt gta tac ggc ttt ggt cat 192
Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
50 55 60

aat aat aat att gcg gtg gcg tat gta aag gaa aaa tat aga ccc gca 240
Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
65 70 75 80

gat gat gat tac att ttg ttt ttg aat ccc gat atc atc atg aag cat 288
Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
85 90 95

gat gat ttg ctg aca tat att aaa tat gtc gaa agt aag cgt tat gct 336
Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
100 105 110

ttt agt aca tta tgc ctg ttc cga gat gaa gcg aaa tct tta cat gat 384
Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
115 120 125

tat tcc gta aga aaa ttt cct gtg ctt tct gat ttt att gtg tca ttt 432
Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
130 135 140

atg tta ggg att aag gaa ggt gcg aac aag tcc ctg ata tga 474
Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile *
145 150 155

<210> 174
<211> 1119
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1119)

<400> 174

atg gga aaa agc ata gtc gtt gtt tct gcg gtc aat ttt acc act ggc 48
Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
1 5 10 15

ggt cca ttt acc att ttg aaa aaa ttt ttg gca gca act aat aat aaa 96
Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
20 25 30

gaa aat gtc agt ttt atc gca tta gtc cat tct gct aaa gag tta aaa 144
Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
35 40 45

gaa agt tat cca tgg gtt aaa ttc att gag ttt cct gag gtt aaa ggg 192
Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly

50	55	60	
tcg tgg cta aaa cgt ttg cac ttt gaa tat gta gtt tgt aaa aaa ctt			240
Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu			
65	70	75	80
tca aaa gag ctg aat gct acg cat tgg att tgt ctg cat gat att acg			288
Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr			
	85	90	95
gcc aat gtc gtc act aaa aaa aga tat gtg tat tgt cat aac cct gca			336
Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala			
	100	105	110
cct ttt tat aaa gga att tta ttc cgt gaa att ctt atg gag cct agc			384
Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser			
	115	120	125
ttt ttc tta ttt aaa atg cta tac ggg ctg ata tat aaa ata aac att			432
Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile			
	130	135	140
aaa aaa aat act gca gtg ttt gtt caa caa ttc tgg atg aaa gaa aaa			480
Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys			
	145	150	155
ttt atc aag aaa tat tct ata aat aac atc att gtc agt cgg cca gaa			528
Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu			
	165	170	175
att aaa tta tct gat aaa agc caa ctt act gat gat gat tct caa ttt			576
Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe			
	180	185	190
aag aat aac cct tct gag ttg aca ata ttt tac cct gct gtt cca cga			624
Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg			
	195	200	205
gta ttt aaa aat tac gag ctt att att agt gca gca agg aaa ttg aaa			672
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys			
	210	215	220
gaa caa tcc aat att aaa ttt ctg ctt act atc agt ggt aca gaa aat			720
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn			
	225	230	235
gcg tat gca aaa tat att atc agt ctt gca gaa gga ctg gat aat gtt			768
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val			
	245	250	255
cat ttc ctc ggg tac ttg gat aaa gaa aaa atc gat cat tgt tat aat			816
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn			
	260	265	270
att tca gat ata gtt tgt ttt ccc tct agg tta gaa aca tgg gga ttg			864
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu			
	275	280	285

His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile	
85 90 95	
gca agt aaa gta ttt att acc gat cat aat cac ggt tcc ttt aag cac	336
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His	
100 105 110	
tct gat cca atg agt tcg cca aat ata cct cca gac atg cgc acg ttg	384
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu	
115 120 125	
gaa tct tca gct gtt gta att ggc cag agg gtt tgg ttg ggt gag aat	432
Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn	
130 135 140	
gtg acg gtt ttg cct gga aca att att ggt aat gga gtc gta gtc ggc	480
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly	
145 150 155 160	
gcc aat tct gtt gtt aga ggt tct att ccc gaa aat act gtc att gcg	528
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala	
165 170 175	
gga gta cca gca aaa atc ata aag aaa tac aat cat gag acc aaa tta	576
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu	
180 185 190	
tgg gaa aaa gca tag	591
Trp Glu Lys Ala *	
195	
<210> 176	
<211> 993	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(993)	
<400> 176	
atg tat ttt ttg aat gat tta aat ttc tct aga cgc gat gct gga ttt	48
Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe	
1 5 10 15	
aaa gca aga aaa gat gca ctg gac att gct tca gat tat gaa aac att	96
Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile	
20 25 30	
tct gtt gtt aac att cct cta tgg ggt gga gta gtc cag aga att att	144
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile	
35 40 45	
agt tct gtt aag ctt agt aca ttt ctc tgc ggt ctt gaa aat aaa gat	192
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp	
50 55 60	

gtt tta att ttc aat ttc ccg atg gcc aaa cca ttt tgg cat ata ttg	240
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu	
65 70 75 80	
tca ttc ttt cac cgc ctt cta aaa ttt aga ata gta cct ctg att cat	288
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His	
85 90 95	
gat att gat gaa tta aga gga gga ggg ggt agt gat tct gtg cgg ctt	336
Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu	
100 105 110	
gct acc tgt gat atg gtc ata agt cac aat cca caa atg aca aag tac	384
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr	
115 120 125	
ctt agt aaa tat atg tct cag gat aaa atc aaa gac ata aaa ata ttt	432
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe	
130 135 140	
gat tac ctc gtc tca tct gat gtg gag cat cga gat gtt acg gat aag	480
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys	
145 150 155 160	
caa cga ggg gtc ata tat gct ggc aac ctt tct agg cat aaa tgt tct	528
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser	
165 170 175	
ttc ata tat act gaa gga tgc gat ttt act ctc ttt ggt gtc aac tat	576
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr	
180 185 190	
gaa aat aaa gat aat cct aaa tat ctt gga agt ttt gat gct caa tct	624
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser	
195 200 205	
ccg gaa aag att aac ctc cca ggc atg caa ttt gga ctc att tgg gat	672
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp	
210 215 220	
gga gat tct gtc gaa acc tgt agt ggt gcc ttt ggc gac tat tta aag	720
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys	
225 230 235 240	
ttt aat aac cct cat aag aca tct ctt tat ctt tca atg gaa ctt cca	768
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro	
245 250 255	
gta ttt ata tgg gat aaa gcc gcc ctt gcg gat ttc att gta gat aat	816
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn	
260 265 270	
aga ata gga tat gca gtg gga tca atc aaa gaa atg caa gag att gtt	864
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val	
275 280 285	

gac	tcc	atg	aca	ata	gaa	act	tat	aag	caa	att	agt	gag	aat	aca	aaa	912
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys	
	290					295					300					

att	att	tct	cag	aaa	att	cga	aca	gga	agt	tac	ttc	agg	gat	gtt	ctt	960
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu	
305					310					315					320	

gaa	gag	gtg	atc	gat	gat	ctt	aaa	act	cgc	taa						993
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg	*						
				325					330							

<210> 177

<211> 1167

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1167)

<400> 177

atg	atc	tat	ctt	gta	att	agt	gtc	ttt	ctc	att	aca	gca	ttt	atc	tgt	48
Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys	
1				5					10					15		

tta	tat	ctt	aag	aag	gat	ata	ttt	tat	cca	gcc	gta	tgc	gtt	aat	atc	96
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile	
			20					25					30			

atc	ttc	gca	ctg	gtc	tta	ttg	gga	tat	gaa	ata	acg	tca	gat	ata	tat	144
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr	
		35					40					45				

gct	ttt	cag	tta	aat	gac	gct	acg	ttg	att	ttt	cta	ctt	tgc	aat	gtt	192
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val	
	50					55					60					

ttg	aca	ttt	acc	ctg	tca	tgt	tta	ttg	acg	gaa	agt	gta	tta	gat	cta	240
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu	
65					70				75					80		

aat	atc	aga	aaa	gtc	aat	aat	gct	att	tat	agc	ata	cca	tcg	aag	aaa	288
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys	
				85					90					95		

gtg	cat	aat	gta	ggc	ttg	tta	gtt	att	tct	ttt	tcg	atg	ata	tat	ata	336
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile	
			100					105					110			

tgc	atg	agg	tta	agt	aac	tac	cag	ttc	ggg	act	agc	tta	ctt	agc	tat	384
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr	
		115					120					125				

atg	aat	ttg	ata	aga	gat	gct	gat	gtt	gaa	gac	aca	tca	aga	aat	ttc	432
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe	

130					135					140									
tca Ser 145	gca Ala	tac Tyr	atg Met	cag Gln	cca Pro	atc Ile	att Ile	cta Leu	act Thr	act Thr	ttt Phe	gct Ala	tta Leu	ttt Phe	att Ile	480			
					150					155					160				
tgg Trp	tct Ser	aaa Lys	aaa Lys	ttt Phe	act Thr	aat Asn	aca Thr	aag Lys	gta Val	agt Ser	aaa Lys	aca Thr	ttt Phe	act Thr	tta Leu	528			
					165					170					175				
ctt Leu	gtt Val	ttt Phe	att Ile	gta Val	ttc Phe	atc Ile	ttt Phe	gca Ala	att Ile	ata Ile	ctg Leu	aat Asn	act Thr	ggg Gly	aag Lys	576			
					180					185					190				
caa Gln	att Ile	gtc Val	ttt Phe	atg Met	gtt Val	atc Ile	atc Ile	tct Ser	tat Tyr	gca Ala	ttc Phe	atc Ile	gta Val	ggg Gly	gtt Val	624			
					195					200					205				
aat Asn	aga Arg	gta Val	aaa Lys	cat His	tat Tyr	gtt Val	tat Tyr	ctt Leu	att Ile	aca Thr	gct Ala	gta Val	ggg Gly	gtt Val	cta Leu	672			
					210					215					220				
ttc Phe	tcc Ser	ttg Leu	tat Tyr	atg Met	ctc Leu	ttt Phe	tta Leu	cgt Arg	gga Gly	ctg Leu	cct Pro	ggg Gly	ggg Gly	atg Met	gca Ala	720			
					225					230					235				
tat Tyr	tat Tyr	cta Leu	tcc Ser	atg Met	tat Tyr	ttg Leu	gtc Val	agc Ser	cct Pro	ata Ile	atc Ile	gcg Ala	ttt Phe	cag Gln	gag Glu	768			
					245					250					255				
ttt Phe	tat Tyr	ttt Phe	cag Gln	caa Gln	gta Val	tct Ser	aac Asn	tct Ser	gcc Ala	agt Ser	tct Ser	cat His	gtc Val	ttt Phe	tgg Trp	816			
					260					265					270				
ttt Phe	ttt Phe	gaa Glu	agg Arg	ctg Leu	atg Met	ggg Gly	cta Leu	tta Leu	aca Thr	ggg Gly	gga Gly	gtc Val	tct Ser	atg Met	tcg Ser	864			
					275					280					285				
ttg Leu	cat His	aaa Lys	gaa Glu	ttt Phe	gtg Val	tgg Trp	gtg Val	ggg Gly	ttg Leu	cca Pro	aca Thr	aat Asn	gtt Val	tat Tyr	act Thr	912			
					290					295					300				
gct Ala	ttt Phe	tcg Ser	gat Asp	tat Tyr	gtt Val	tat Tyr	att Ile	tcc Ser	gcg Ala	gag Glu	cta Leu	agc Ser	tat Tyr	ttg Leu	atg Met	960			
					305					310					315				
atg Met	gtt Val	att Ile	cat His	ggc Gly	tgt Cys	att Ile	tca Ser	ggg Gly	gtt Val	tta Leu	tgg Trp	aga Arg	ttg Leu	tct Ser	cga Arg	1008			
					325					330					335				
aat Asn	tac Tyr	ata Ile	tct Ser	gtg Val	aaa Lys	ata Ile	ttt Phe	tat Tyr	tca Ser	tat Tyr	ttt Phe	att Ile	tat Tyr	acc Thr	ttt Phe	1056			
					340					345					350				
tct Ser	ttc Phe	att Ile	ttt Phe	tat Tyr	cat His	gaa Glu	agc Ser	ttc Phe	atg Met	act Thr	aat Asn	att Ile	agc Ser	agt Ser	tgg Trp	1104			
					355					360					365				

ata caa ata act ctt tgt atc ata gta ttc tct caa ttt ctt aag gcc 1152
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380

cag aaa ata aag tga 1167
 Gln Lys Ile Lys *
 385

<210> 178
 <211> 1104
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1104)

<400> 178
 atg tac gat tat atc att gtt ggt tct ggt ttg ttt ggt gcc gtt tgt 48
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15
 gcg aat gag tta aaa aag cta aac aaa aaa gtt tta gtg att gag aaa 96
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30
 aga aat cat atc ggt gga aat gcg tac aca gag gac tgt gag ggt atc 144
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45
 cag att cat aaa tat ggt gca cat att ttt cat acc aat gat aaa tat 192
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60
 ata tgg gat tac gtt aat gat tta gta gaa ttt aat cgt ttt act aat 240
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80
 tct cca ctg gcg att tat aaa gac aaa tta ttc aac ctt cct ttt aat 288
 Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95
 atg aat act ttc cac caa atg tgg gga gtt aaa gat cct caa gaa gct 336
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110
 caa aat atc att aat gct cag aaa aaa aag tat ggt gac aag gta cct 384
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125
 gaa aat ttg gag gag cag gcg att tca tta gtt ggg gag gac tta tac 432
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140
 caa gca ttg ata aag ggt tat acg gag aag cag tgg gga aga agt gca 480

Gln	Ala	Leu	Ile	Lys	Gly	Tyr	Thr	Glu	Lys	Gln	Trp	Gly	Arg	Ser	Ala		
145					150					155					160		
aaa	gaa	ttg	cct	gca	ttt	att	att	aag	cga	atc	cca	gtg	aga	ttt	acg	528	
Lys	Glu	Leu	Pro	Ala	Phe	Ile	Ile	Lys	Arg	Ile	Pro	Val	Arg	Phe	Thr		
				165					170					175			
ttt	gat	aac	aat	tat	ttt	tcc	gat	cgc	tat	caa	ggt	att	ccg	gtg	gga	576	
Phe	Asp	Asn	Asn	Tyr	Phe	Ser	Asp	Arg	Tyr	Gln	Gly	Ile	Pro	Val	Gly		
			180					185					190				
ggc	tac	act	aag	ctt	att	gaa	aaa	atg	ctt	gaa	ggt	gtg	gac	gta	aaa	624	
Gly	Tyr	Thr	Lys	Leu	Ile	Glu	Lys	Met	Leu	Glu	Gly	Val	Asp	Val	Lys		
		195					200					205					
tta	ggc	att	gat	ttt	ttg	aaa	gac	aaa	gat	tct	cta	gcg	agt	aaa	gcc	672	
Leu	Gly	Ile	Asp	Phe	Leu	Lys	Asp	Lys	Asp	Ser	Leu	Ala	Ser	Lys	Ala		
	210					215					220						
cat	aga	atc	atc	tac	act	gga	ccc	att	gat	cag	tac	ttc	gac	tat	agg	720	
His	Arg	Ile	Ile	Tyr	Thr	Gly	Pro	Ile	Asp	Gln	Tyr	Phe	Asp	Tyr	Arg		
	225				230					235					240		
ttt	gga	gcg	tta	gaa	tat	cgc	tct	tta	aaa	ttt	gag	acg	gaa	cgc	cat	768	
Phe	Gly	Ala	Leu	Glu	Tyr	Arg	Ser	Leu	Lys	Phe	Glu	Thr	Glu	Arg	His		
			245					250						255			
gaa	ttt	cca	aac	ttc	caa	ggg	aat	gca	gta	ata	aat	ttc	act	gat	gct	816	
Glu	Phe	Pro	Asn	Phe	Gln	Gly	Asn	Ala	Val	Ile	Asn	Phe	Thr	Asp	Ala		
			260					265					270				
aat	gta	cca	tat	acc	aga	ata	att	gag	cat	aaa	cat	ttt	gac	tat	gtt	864	
Asn	Val	Pro	Tyr	Thr	Arg	Ile	Ile	Glu	His	Lys	His	Phe	Asp	Tyr	Val		
		275					280					285					
gag	aca	aag	cat	acg	gtt	gtt	aca	aaa	gaa	tat	cca	tta	gag	tggt	aaa	912	
Glu	Thr	Lys	His	Thr	Val	Val	Thr	Lys	Glu	Tyr	Pro	Leu	Glu	Trp	Lys		
	290					295					300						
gtt	ggc	gac	gaa	ccc	tac	tat	cca	gtt	aat	gat	aat	aaa	aac	atg	gag	960	
Val	Gly	Asp	Glu	Pro	Tyr	Tyr	Pro	Val	Asn	Asp	Asn	Lys	Asn	Met	Glu		
	305				310					315				320			
ctt	ttt	aag	aaa	tat	aga	gag	tta	gct	agc	aga	gaa	gac	aag	gtt	ata	1008	
Leu	Phe	Lys	Lys	Tyr	Arg	Glu	Leu	Ala	Ser	Arg	Glu	Asp	Lys	Val	Ile		
			325						330					335			
ttt	ggc	ggg	cgt	ttg	gcc	gag	tat	aaa	tat	tat	gat	atg	cat	caa	gtg	1056	
Phe	Gly	Gly	Arg	Leu	Ala	Glu	Tyr	Lys	Tyr	Tyr	Asp	Met	His	Gln	Val		
			340					345					350				
ata	tct	gcc	gct	ctt	tat	caa	gtg	aaa	aat	ata	atg	agt	acg	gat	taa	1104	
Ile	Ser	Ala	Ala	Leu	Tyr	Gln	Val	Lys	Asn	Ile	Met	Ser	Thr	Asp	*		
		355					360					365					

<210> 179
 <211> 693
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(693)

<400> 179

ttg aca tca tca ata acc aat gaa att atg caa tta tat acg gat agg	48
Met Thr Ser Ser Ile Thr Asn Glu Ile Met Gln Leu Tyr Thr Asp Arg	
1 5 10 15	
gag gtt ctt aac atg ggg ctt tgt agt cgt tat aaa agt ctt aca tgc	96
Glu Val Leu Asn Met Gly Leu Cys Ser Arg Tyr Lys Ser Leu Thr Cys	
20 25 30	
aat agt tgc tca atg cat tgc caa ata atg cca gaa gag tca ccg cgt	144
Asn Ser Cys Ser Met His Cys Gln Ile Met Pro Glu Glu Ser Pro Arg	
35 40 45	
ttg cag tat tgc gca aac tcg tgt ttt tgt atg tgg ccc gaa gaa agt	192
Leu Gln Tyr Cys Ala Asn Ser Cys Phe Cys Met Trp Pro Glu Glu Ser	
50 55 60	
tca tat ttt aat cgt ggt gtg gta gaa ggt atc tta aca aaa aac cac	240
Ser Tyr Phe Asn Arg Gly Val Val Glu Gly Ile Leu Thr Lys Asn His	
65 70 75 80	
aat gcg aga tta agc gga tat att ttt gtc gat ttt tca gta agt ttt	288
Asn Ala Arg Leu Ser Gly Tyr Ile Phe Val Asp Phe Ser Val Ser Phe	
85 90 95	
tta cgt cta ttc ctt gaa aaa gac tgg att gac tat ctt gca agt act	336
Leu Arg Leu Phe Leu Glu Lys Asp Trp Ile Asp Tyr Leu Ala Ser Thr	
100 105 110	
gac atg ggg att gtt tta gtc agc gac cgc aat atg caa tcg tta gct	384
Asp Met Gly Ile Val Leu Val Ser Asp Arg Asn Met Gln Ser Leu Ala	
115 120 125	
aat tac tgg cga aaa cac aac tca gca ata tct gct gtc ata tat aat	432
Asn Tyr Trp Arg Lys His Asn Ser Ala Ile Ser Ala Val Ile Tyr Asn	
130 135 140	
gat gat ggt ctt gat gtt gcc aat gaa aag atc aga caa cta ttt att	480
Asp Asp Gly Leu Asp Val Ala Asn Glu Lys Ile Arg Gln Leu Phe Ile	
145 150 155 160	
ggt cgt tat tta tca ttt acc gga ggt aac aca tta act cag atg gaa	528
Gly Arg Tyr Leu Ser Phe Thr Gly Gly Asn Thr Leu Thr Gln Met Glu	
165 170 175	
ttc acc ata atg ggg tat atg gtt tct ggt tat aat cca tat cag att	576
Phe Thr Ile Met Gly Tyr Met Val Ser Gly Tyr Asn Pro Tyr Gln Ile	
180 185 190	

gct gaa gtt ctg gat atg gat atc cgt agc atc tac gcg tac aag caa 624
Ala Glu Val Leu Asp Met Asp Ile Arg Ser Ile Tyr Ala Tyr Lys Gln
195 200 205

cga atc gaa aag aga atg ggt ggt aaa ata aac gaa tta ttt att cgt 672
Arg Ile Glu Lys Arg Met Gly Gly Lys Ile Asn Glu Leu Phe Ile Arg
210 215 220

tca cat tcg gtc caa cat tga 693
Ser His Ser Val Gln His *
225 230

<210> 180

<211> 1176

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1176)

<400> 180

atg caa aaa ctc att aac tca gtg caa aac tat gcc tgg ggc agc aaa 48
Met Gln Lys Leu Ile Asn Ser Val Gln Asn Tyr Ala Trp Gly Ser Lys
1 5 10 15

acg gcg ttg act gaa ctt tat ggt atg gaa aat ccg tcc agc cag ccg 96
Thr Ala Leu Thr Glu Leu Tyr Gly Met Glu Asn Pro Ser Ser Gln Pro
20 25 30

atg gcc gag ctg tgg atg ggc gca cat ccg aaa agc agt tca cga gtg 144
Met Ala Glu Leu Trp Met Gly Ala His Pro Lys Ser Ser Ser Arg Val
35 40 45

cag aat gcc gcc gga gat atc gtt tca ctg cgt gat gtg att gag agt 192
Gln Asn Ala Ala Gly Asp Ile Val Ser Leu Arg Asp Val Ile Glu Ser
50 55 60

gat aaa tcg act ctg ctc gga gag gcc gtt gcc aaa cgc ttt ggc gaa 240
Asp Lys Ser Thr Leu Leu Gly Glu Ala Val Ala Lys Arg Phe Gly Glu
65 70 75 80

ctg cct ttc ctg ttc aaa gta tta tgc gca gca cag cca ctc tcc att 288
Leu Pro Phe Leu Phe Lys Val Leu Cys Ala Ala Gln Pro Leu Ser Ile
85 90 95

cag gtt cat cca aac aaa cac aat tct gaa atc ggt ttt gcc aaa gaa 336
Gln Val His Pro Asn Lys His Asn Ser Glu Ile Gly Phe Ala Lys Glu
100 105 110

aat gcc gca ggt atc ccg atg gat gcc gcc gag cgt aac tat aaa gat 384
Asn Ala Ala Gly Ile Pro Met Asp Ala Ala Glu Arg Asn Tyr Lys Asp
115 120 125

cct aac cac aag ccg gag ctg gtt ttt gcg ctg acg cct ttc ctt gcg 432

Pro	Asn	His	Lys	Pro	Glu	Leu	Val	Phe	Ala	Leu	Thr	Pro	Phe	Leu	Ala	
130						135					140					
atg	aac	gcg	ttt	cgt	gaa	ttt	tcc	gag	att	gtc	tcc	cta	ctc	cag	ccg	480
Met	Asn	Ala	Phe	Arg	Glu	Phe	Ser	Glu	Ile	Val	Ser	Leu	Leu	Gln	Pro	
145					150					155					160	
gtc	gca	ggg	gca	cat	ccg	gcg	att	gct	cac	ttt	tta	caa	cag	cct	gat	528
Val	Ala	Gly	Ala	His	Pro	Ala	Ile	Ala	His	Phe	Leu	Gln	Gln	Pro	Asp	
				165					170					175		
gcc	gaa	cgt	tta	agc	gaa	ctg	ttc	gcc	agc	ctg	ttg	aat	atg	cag	ggg	576
Ala	Glu	Arg	Leu	Ser	Glu	Leu	Phe	Ala	Ser	Leu	Leu	Asn	Met	Gln	Gly	
			180					185					190			
gaa	gaa	aaa	tcc	cgc	gcg	ctg	gcg	att	tta	aaa	tcg	gcc	ctc	gat	agc	624
Glu	Glu	Lys	Ser	Arg	Ala	Leu	Ala	Ile	Leu	Lys	Ser	Ala	Leu	Asp	Ser	
		195					200					205				
cag	cag	ggg	gaa	ccg	tgg	caa	acg	att	cgt	tta	att	tct	gaa	ttt	tac	672
Gln	Gln	Gly	Glu	Pro	Trp	Gln	Thr	Ile	Arg	Leu	Ile	Ser	Glu	Phe	Tyr	
		210				215					220					
ccg	gaa	gac	agc	ggg	ctg	ttc	tcc	ccg	cta	ttg	ctg	aat	gtg	gtg	aaa	720
Pro	Glu	Asp	Ser	Gly	Leu	Phe	Ser	Pro	Leu	Leu	Leu	Asn	Val	Val	Lys	
225					230					235					240	
ttg	aac	cct	ggc	gaa	gcg	atg	ttc	ctg	ttc	gct	gaa	aca	ccg	cac	gct	768
Leu	Asn	Pro	Gly	Glu	Ala	Met	Phe	Leu	Phe	Ala	Glu	Thr	Pro	His	Ala	
				245					250					255		
tac	ctg	caa	ggc	gtg	gcg	ctg	gaa	gtg	atg	gca	aac	tcc	gat	aac	gtg	816
Tyr	Leu	Gln	Gly	Val	Ala	Leu	Glu	Val	Met	Ala	Asn	Ser	Asp	Asn	Val	
			260					265					270			
ctg	cgt	gcg	ggg	ctg	acg	cct	aaa	tac	att	gat	att	ccg	gaa	ctg	gtt	864
Leu	Arg	Ala	Gly	Leu	Thr	Pro	Lys	Tyr	Ile	Asp	Ile	Pro	Glu	Leu	Val	
		275					280					285				
gcc	aat	gtg	aaa	ttc	gaa	gcc	aaa	ccg	gct	aac	cag	ttg	ttg	acc	cag	912
Ala	Asn	Val	Lys	Phe	Glu	Ala	Lys	Pro	Ala	Asn	Gln	Leu	Leu	Thr	Gln	
		290				295					300					
ccg	gtg	aaa	caa	ggg	gca	gaa	ctg	gac	ttc	ccg	att	cca	gtg	gat	gat	960
Pro	Val	Lys	Gln	Gly	Ala	Glu	Leu	Asp	Phe	Pro	Ile	Pro	Val	Asp	Asp	
305					310					315					320	
ttt	gcc	ttc	tcg	ctg	cat	gac	ctt	agt	gat	aaa	gaa	acc	acc	att	agc	1008
Phe	Ala	Phe	Ser	Leu	His	Asp	Leu	Ser	Asp	Lys	Glu	Thr	Thr	Ile	Ser	
				325					330					335		
cag	cag	agt	gcc	gcc	att	ttg	ttc	tgc	gtc	gaa	ggc	gat	gca	acg	ttg	1056
Gln	Gln	Ser	Ala	Ala	Ile											


```

355          360          365
att gcc gcc aac gaa tca ccg gtg act gtc aaa ggc cac ggc cgt tta 1152
Ile Ala Ala Asn Glu Ser Pro Val Thr Val Lys Gly His Gly Arg Leu
370          375          380

gcg cgt gtt tac aac aag ctg taa 1176
Ala Arg Val Tyr Asn Lys Leu *
385          390

<210> 181
<211> 795
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(795)

<400> 181
atg aaa cag tat tta gaa ctg atg caa aaa gtg ctc gac gaa ggc aca 48
Met Lys Gln Tyr Leu Glu Leu Met Gln Lys Val Leu Asp Glu Gly Thr
1          5          10          15

cag aaa aac gac cgt acc gga acc gga acg ctt tcc att ttt ggt cat 96
Gln Lys Asn Asp Arg Thr Gly Thr Gly Thr Leu Ser Ile Phe Gly His
20          25          30

cag atg cgt ttt aac ctg caa gat gga ttc ccg ctg gtg aca act aaa 144
Gln Met Arg Phe Asn Leu Gln Asp Gly Phe Pro Leu Val Thr Thr Lys
35          40          45

cgt tgc cac ctg cgt tcc atc atc cat gaa ctg ctg tgg ttt ctg cag 192
Arg Cys His Leu Arg Ser Ile Ile His Glu Leu Leu Trp Phe Leu Gln
50          55          60

ggc gac act aac att gct tat cta cac gaa aac aat gtc acc atc tgg 240
Gly Asp Thr Asn Ile Ala Tyr Leu His Glu Asn Asn Val Thr Ile Trp
65          70          75          80

gac gaa tgg gcc gat gaa aac ggc gac ctc ggg cca gtg tat ggt aaa 288
Asp Glu Trp Ala Asp Glu Asn Gly Asp Leu Gly Pro Val Tyr Gly Lys
85          90          95

cag tgg cgc gcc tgg cca acg cca gat ggt cgt cat att gac cag atc 336
Gln Trp Arg Ala Trp Pro Thr Pro Asp Gly Arg His Ile Asp Gln Ile
100          105          110

act acg gta ctg aac cag ctg aaa aac gac ccg gat tcg cgc cgc att 384
Thr Thr Val Leu Asn Gln Leu Lys Asn Asp Pro Asp Ser Arg Arg Ile
115          120          125

att gtt tca gcg tgg aac gta ggc gaa ctg gat aaa atg gcg ctg gca 432
Ile Val Ser Ala Trp Asn Val Gly Glu Leu Asp Lys Met Ala Leu Ala
130          135          140

```


50	55	60	
ttc ctc ggc gtc ttc ctc ggg gga cgt att ggt tat gtt ctg ttc tac			240
Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr			
65	70	75	80
aat ttc ccg cag ttt atg gcc gat ccg ctg tat ctg ttc cgt gtc tgg			288
Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp			
	85	90	95
gac ggc ggc atg tct ttc cac ggc ggc ctg att ggc gtt atc gtg gtg			336
Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val			
	100	105	110
atg att atc ttc gcc cgc cgt act aaa cgt tcc ttc ttc cag gtc tct			384
Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser			
	115	120	125
gat ttt atc gca cca ctc att ccg ttt ggt ctt ggt gcc ggg cgt ctg			432
Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu			
	130	135	140
ggc aac ttt att aac ggt gaa ttg tgg ggc cgc gtt gac ccg aac ttc			480
Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe			
	145	150	155
ccg ttt gcc atg ctg ttc cct ggc tcc cgt aca gaa gat att ttg ctg			528
Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu			
	165	170	175
ctg caa acc aac ccg cag tgg caa tcc att ttc gac act tac ggt gtg			576
Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val			
	180	185	190
ctg ccg cgc cac cca tca cag ctt tac gag ctg ctg ctg gaa ggt gtg			624
Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val			
	195	200	205
gtg ctg ttt att atc ctc aac ctg tat att cgt aaa cca cgc cca atg			672
Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met			
	210	215	220
gga gct gtc tca ggt ttg ttc ctg att ggt tac ggc gcg ttt cgc atc			720
Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile			
	225	230	235
att gtt gag ttt ttc cgc cag ccc gac gcg cag ttt acc ggt gcc tgg			768
Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp			
	245	250	255
gtg cag tac atc agc atg ggg caa att ctt tcc atc ccg atg att gtc			816
Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val			
	260	265	270
gcg ggt gtg atc atg atg gtc tgg gca tat cgt cgc agc cca cag caa			864
Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln			
	275	280	285

cac gtt tcc tga
His Val Ser *
290

876

<210> 183
<211> 726
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(726)

<400> 183
atg gac agt ctc aat ctt aat aaa cat att tcc ggc cag ttc aac gcc 48
Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
1 5 10 15
gaa ctg gaa agt atc cgc acg cag gtg atg acc atg ggc ggc atg gtg 96
Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
20 25 30
gag cag cag ctt tct gat gca atc acc gcg atg cat aac cag gac agc 144
Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
35 40 45
gat ctg gcg aag cgc gtc atc gaa ggc gac aag aac gtc aac atg atg 192
Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
50 55 60
gaa gtg gcg atc gat gaa gcc tgc gtg cgc att atc gcc aaa cgt cag 240
Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
65 70 75 80
ccg acg gcg agc gac ctg cga ctg gtt atg gtg atc agt aaa acc att 288
Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
85 90 95
gcc gag ctg gag cgt att ggc gac gtg gcg gac aaa atc tgc cgt act 336
Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
100 105 110
gcg ctg gag aaa ttc tcc cag cag cat cag ccg ttg ctg gta agt ctg 384
Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
115 120 125
gag tcg ctg ggc cgt cat acc atc cag atg ctg cac gac gtg ctg gac 432
Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
130 135 140
gcg ttc gcg cgg atg gac att gac gaa gcg gta cgt att tat cgt gaa 480
Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
145 150 155 160
gat aaa aaa gtc gat cag gaa tac gaa ggt att gtt cgt caa ctg atg 528

ttc cag aaa ccg acg ccg ttt ccg atg tcc atc tac gac aac atc gct	336
Phe Gln Lys Pro Thr Pro Phe Pro Met Ser Ile Tyr Asp Asn Ile Ala	
100 105 110	
ttt ggc gtt cgt ctg ttt gag aag ctc tcc cgt gcc gac atg gac gag	384
Phe Gly Val Arg Leu Phe Glu Lys Leu Ser Arg Ala Asp Met Asp Glu	
115 120 125	
cgc gtg cag tgg gca ttg acc aaa gcc gca ttg tgg aac gaa acc aaa	432
Arg Val Gln Trp Ala Leu Thr Lys Ala Ala Leu Trp Asn Glu Thr Lys	
130 135 140	
gat aaa ttg cac cag agc ggt tac tct ctc tct ggt ggt cag caa cag	480
Asp Lys Leu His Gln Ser Gly Tyr Ser Leu Ser Gly Gly Gln Gln Gln	
145 150 155 160	
cgt ctg tgt att gcg cgt ggt atc gcc att cgc ccg gaa gtg ctg ctg	528
Arg Leu Cys Ile Ala Arg Gly Ile Ala Ile Arg Pro Glu Val Leu Leu	
165 170 175	
ctc gac gaa ccg tgt tcg gcg ctc gac cct atc tct acc ggg cgt att	576
Leu Asp Glu Pro Cys Ser Ala Leu Asp Pro Ile Ser Thr Gly Arg Ile	
180 185 190	
gaa gag ctg atc acc gaa ctg aag cag gat tac acc gtg gtg atc gtc	624
Glu Glu Leu Ile Thr Glu Leu Lys Gln Asp Tyr Thr Val Val Ile Val	
195 200 205	
acc cac aac atg cag cag gct gcg cgt tgt tcc gac cac acg gcg ttt	672
Thr His Asn Met Gln Gln Ala Ala Arg Cys Ser Asp His Thr Ala Phe	
210 215 220	
atg tac ctg ggc gaa ttg att gag ttc agc aac acg gac gat ctg ttc	720
Met Tyr Leu Gly Glu Leu Ile Glu Phe Ser Asn Thr Asp Asp Leu Phe	
225 230 235 240	
acc aag cca gcg aag aaa caa aca gaa gac tac atc acc ggt cgt tac	768
Thr Lys Pro Ala Lys Lys Gln Thr Glu Asp Tyr Ile Thr Gly Arg Tyr	
245 250 255	
ggt tga	774
Gly *	

<210> 185
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> .CDS
 <222> (1)...(891)

<400> 185
 atg gct atg gtt gaa atg caa acc act gcg gcg ctg gct gaa tct cgc 48

Met 1	Ala	Met	Val	Glu 5	Met	Gln	Thr	Thr	Ala 10	Ala	Leu	Ala	Glu	Ser 15	Arg	
cgc Arg	aaa Lys	atg Met	cag Gln 20	gcg Ala	cgt Arg	cgc Arg	cgc Arg	ctc Leu 25	aaa Lys	aac Asn	cgt Arg	att Ile 30	gcg Ala	ctg Leu	acg Thr	96
ctc Leu	tcg Ser	atg Met 35	gcg Ala	acg Thr	atg Met	gcc Ala	ttc Phe 40	ggc Gly	ctg Leu	ttc Phe	tgg Trp 45	ctg Leu	atc Ile	tgg Trp	att Ile	144
tta Leu	atg Met 50	tcc Ser	acc Thr	atc Ile	act Thr	cgc Arg 55	ggg Gly	atc Ile	gac Asp	ggg Gly	atg Met 60	tcg Ser	ctg Leu	gcg Ala	ctg Leu	192
ttc Phe 65	act Thr	gaa Glu	atg Met	acg Thr	ccg Pro 70	ccg Pro	ccc Pro	aat Asn	acg Thr	gaa Glu 75	ggg Gly	ggg Gly	ggg Gly	ctg Leu	gcg Ala 80	240
aac Asn	gct Ala	ctg Leu	gcg Ala	ggg Gly 85	agc Ser	ggg Gly	ctg Leu	tta Leu	att Ile 90	ttg Leu	tgg Trp	gcc Ala	acg Thr	gta Val 95	ttc Phe	288
ggg Gly	acg Thr	ccg Pro	ctg Leu 100	ggc Gly	att Ile	atg Met	gcg Ala	ggg Gly 105	att Ile	tat Tyr	ctg Leu	gcg Ala	gaa Glu 110	tat Tyr	ggg Gly	336
cgt Arg	aaa Lys	tcc Ser 115	tgg Trp	ctg Leu	gca Ala	gaa Glu	gtg Val 120	att Ile	cgc Arg	ttc Phe	att Ile 125	aac Asn	gac Asp	att Ile	ctg Leu	384
ctc Leu 130	tct Ser	gcg Ala	ccg Pro	tcg Ser	att Ile	gtg Val 135	gtt Val	ggg Gly	ctg Leu	ttt Phe	gtt Val 140	tac Tyr	acc Thr	att Ile	gtg Val	432
gtg Val 145	gcg Ala	cag Gln	atg Met	gag Glu	cac His 150	ttc Phe	tcc Ser	ggc Gly	tgg Trp	gcg Ala 155	ggc Gly	gtg Val	att Ile	gcc Ala	ctg Leu 160	480
gcg Ala	ttg Leu	ttg Leu	cag Gln	gtg Val 165	ccg Pro	att Ile	gtt Val	atc Ile	cgc Arg 170	acc Thr	acc Thr	gag Glu	aac Asn	atg Met 175	ctg Leu	528
aaa Lys	ctg Leu	gtg Val 180	ccg Pro	tac Tyr	agc Ser	ctg Leu	cgt Arg	gaa Glu 185	gcg Ala	gct Ala	tat Tyr	gcg Ala	ctg Leu 190	ggg Gly	aca Thr	576
ccg Pro	aag Lys	tgg Trp 195	aag Lys	atg Met	atc Ile	tct Ser	gcg Ala 200	att Ile	acg Thr	ctg Leu	aaa Lys 205	gcg Ala	tcg Ser	gtg Val	tcc Ser	624
ggg Gly 210	att Ile	atg Met	acc Thr	ggg Gly	atc Ile	ctg Leu 215	ctg Leu	gcg Ala	att Ile	gcc Ala 220	cgt Arg	att Ile	gct Ala	ggg Gly	gaa Glu	672
acc Thr	gcg Ala	ccg Pro	ctg Leu	ctg Leu	ttt Phe	acc Thr	gcg Ala	ctc Leu	tcc Ser	aac Asn	cag Gln	ttc Phe	tgg Trp	agc Ser	acg Thr	720

```

225                230                235                240
gac atg atg cag ccg atc gcc aac ctg ccg gtg acg atc ttt aag ttt 768
Asp Met Met Gln Pro Ile Ala Asn Leu Pro Val Thr Ile Phe Lys Phe
                245                250                255

gcg atg agc ccg ttt gcg gaa tgg cag caa ttg gcc tgg gcc ggg gta 816
Ala Met Ser Pro Phe Ala Glu Trp Gln Gln Leu Ala Trp Ala Gly Val
                260                265                270

ttg atc att acc ctg tgc gta ctg ctg ctg aac att ctg gcg cgc gtt 864
Leu Ile Ile Thr Leu Cys Val Leu Leu Leu Asn Ile Leu Ala Arg Val
                275                280                285

gtt ttt gcg aag aat aaa cac ggt tga 891
Val Phe Ala Lys Asn Lys His Gly *
                290                295

<210> 186
<211> 960
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(960)

<400> 186
atg gct gca acc aag cct gct ttt aac cca ccg ggt aaa aag ggc gac 48
Met Ala Ala Thr Lys Pro Ala Phe Asn Pro Pro Gly Lys Lys Gly Asp
 1                5                10                15

ata att ttc agc gtg ctg gta aaa ctg gcg gcg ctg att gtg cta ttg 96
Ile Ile Phe Ser Val Leu Val Lys Leu Ala Ala Leu Ile Val Leu Leu
                20                25                30

atg ttg ggt ggc att att gtc tct ctg atc atc tcc tcc tgg ccg agc 144
Met Leu Gly Gly Ile Ile Val Ser Leu Ile Ile Ser Ser Trp Pro Ser
                35                40                45

att cag aaa ttt ggt ctg gct ttc cta tgg acc aaa gag tgg gat gca 192
Ile Gln Lys Phe Gly Leu Ala Phe Leu Trp Thr Lys Glu Trp Asp Ala
                50                55                60

ccg aac gat atc tac ggg gcg ctg gtg ccg atc tac ggt acg ttg gtg 240
Pro Asn Asp Ile Tyr Gly Ala Leu Val Pro Ile Tyr Gly Thr Leu Val
                65                70                75                80

act tcg ttt atc gcg ctg ctg atc gcc gtc ccg gtg agt ttc ggt atc 288
Thr Ser Phe Ile Ala Leu Leu Ile Ala Val Pro Val Ser Phe Gly Ile
                85                90                95

gcc ctg ttc ctg act gag ctt gcg cct ggc tgg ctg aaa cgc ccg ctg 336
Ala Leu Phe Leu Thr Glu Leu Ala Pro Gly Trp Leu Lys Arg Pro Leu
                100                105                110

```



```

ggt atc gcc att gag ctg ctg gca gcc att cca agt atc gtt tac ggc 384
Gly Ile Ala Ile Glu Leu Leu Ala Ala Ile Pro Ser Ile Val Tyr Gly
      115                      120                      125

atg tgg ggc ctg ttt atc ttt gcg ccg ctg ttc gcc gtt tac ttt cag 432
Met Trp Gly Leu Phe Ile Phe Ala Pro Leu Phe Ala Val Tyr Phe Gln
      130                      135                      140

gag ccg gtc ggc aat atc atg tcg aat atc ccg att gtt ggc gcg ctg 480
Glu Pro Val Gly Asn Ile Met Ser Asn Ile Pro Ile Val Gly Ala Leu
      145                      150                      155                      160

ttc tct ggc ccc gca ttt ggt atc ggt atc ctc gcg gca ggc gtg atc 528
Phe Ser Gly Pro Ala Phe Gly Ile Gly Ile Leu Ala Ala Gly Val Ile
      165                      170                      175

ctc gcc atc atg att att ccg tac att gcg gcg gta atg cgt gat gtg 576
Leu Ala Ile Met Ile Ile Pro Tyr Ile Ala Ala Val Met Arg Asp Val
      180                      185                      190

ttc gaa caa acc ccg gtg atg atg aaa gag tcg gcc tac ggt att ggc 624
Phe Glu Gln Thr Pro Val Met Met Lys Glu Ser Ala Tyr Gly Ile Gly
      195                      200                      205

tgc acc acc tgg gaa gtt atc tgg cgt atc gtt ctt ccg ttc acc aaa 672
Cys Thr Thr Trp Glu Val Ile Trp Arg Ile Val Leu Pro Phe Thr Lys
      210                      215                      220

aat ggt gtt atc ggc ggc atc atg ctg ggg ctg ggc cgc gcg ctc ggt 720
Asn Gly Val Ile Gly Gly Ile Met Leu Gly Leu Gly Arg Ala Leu Gly
      225                      230                      235                      240

gaa acc atg gcg gtg acc ttt atc atc ggt aac acc tac cag ctc gac 768
Glu Thr Met Ala Val Thr Phe Ile Ile Gly Asn Thr Tyr Gln Leu Asp
      245                      250                      255

agc gcc tcg ctg tat atg ccg ggc aac agt atc acc tct gcg ctg gcg 816
Ser Ala Ser Leu Tyr Met Pro Gly Asn Ser Ile Thr Ser Ala Leu Ala
      260                      265                      270

aac gaa ttt gcg gaa gcg gaa tcc ggt ctg cac gtt gcc gca ctg atg 864
Asn Glu Phe Ala Glu Ala Glu Ser Gly Leu His Val Ala Ala Leu Met
      275                      280                      285

gaa ctg ggc ctg atc ctg ttt gtg att acc ttc atc gtc ctc gcc gca 912
Glu Leu Gly Leu Ile Leu Phe Val Ile Thr Phe Ile Val Leu Ala Ala
      290                      295                      300

tcg aag ttt atg att atg cgc ctg gct aag aat gag ggg gca cgc taa 960
Ser Lys Phe Met Ile Met Arg Leu Ala Lys Asn Glu Gly Ala Arg *
      305                      310                      315

```

<210> 187
 <211> 1041
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1041)

<400> 187

atg	aaa	ggt	atg	cgt	acc	acc	gtc	gca	act	ggt	gtc	gcc	gcg	acc	tta	48
Met	Lys	Val	Met	Arg	Thr	Thr	Val	Ala	Thr	Val	Val	Ala	Ala	Thr	Leu	
1				5					10					15		
tcg	atg	agt	gct	ttc	tct	gtg	ttt	gca	gaa	gca	agc	ctg	aca	ggt	gca	96
Ser	Met	Ser	Ala	Phe	Ser	Val	Phe	Ala	Glu	Ala	Ser	Leu	Thr	Gly	Ala	
			20					25					30			
ggt	gca	acc	ttc	cct	gcg	ccg	gtg	tat	gcc	aaa	tgg	gct	gac	act	tac	144
Gly	Ala	Thr	Phe	Pro	Ala	Pro	Val	Tyr	Ala	Lys	Trp	Ala	Asp	Thr	Tyr	
			35				40					45				
cag	aaa	gaa	acc	ggt	aat	aaa	ggt	aac	tac	cag	ggt	atc	ggt	tct	tcc	192
Gln	Lys	Glu	Thr	Gly	Asn	Lys	Val	Asn	Tyr	Gln	Gly	Ile	Gly	Ser	Ser	
	50					55					60					
ggt	ggc	gta	aaa	cag	att	atc	gct	aat	acc	ggt	gat	ttt	ggt	gcc	tct	240
Gly	Gly	Val	Lys	Gln	Ile	Ile	Ala	Asn	Thr	Val	Asp	Phe	Gly	Ala	Ser	
	65				70				75					80		
gac	gcg	ccg	ctg	tct	gac	gaa	aaa	ctg	gct	cag	gaa	ggt	ctg	ttc	cag	288
Asp	Ala	Pro	Leu	Ser	Asp	Glu	Lys	Leu	Ala	Gln	Glu	Gly	Leu	Phe	Gln	
				85					90					95		
ttc	ccg	acc	gtg	att	ggc	ggc	gtg	gtg	ctg	gcg	ggt	aac	att	cca	ggg	336
Phe	Pro	Thr	Val	Ile	Gly	Gly	Val	Val	Leu	Ala	Val	Asn	Ile	Pro	Gly	
			100					105					110			
ctg	aag	tct	ggc	gaa	ctg	gtg	ctg	gat	ggt	aaa	acc	ctc	ggc	gac	atc	384
Leu	Lys	Ser	Gly	Glu	Leu	Val	Leu	Asp	Gly	Lys	Thr	Leu	Gly	Asp	Ile	
		115					120					125				
tac	ctg	ggc	aaa	atc	aag	aag	tgg	gat	gat	gaa	gcc	atc	gcc	aaa	ctg	432
Tyr	Leu	Gly	Lys	Ile	Lys	Lys	Trp	Asp	Asp	Glu	Ala	Ile	Ala	Lys	Leu	
	130					135					140					
aat	ccg	ggt	ctg	aaa	ctg	cct	tca	caa	aac	att	gct	gta	gta	cgc	cgc	480
Asn	Pro	Gly	Leu	Lys	Leu	Pro	Ser	Gln	Asn	Ile	Ala	Val	Val	Arg	Arg	
	145				150					155				160		
gca	gat	ggc	tcc	ggg	act	tcc	ttc	gtc	ttc	acc	agc	tac	ctg	gcg	aaa	528
Ala	Asp	Gly	Ser	Gly	Thr	Ser	Phe	Val	Phe	Thr	Ser	Tyr	Leu	Ala	Lys	
			165					170						175		
gtg	aac	gaa	gag	tgg	aaa	aac	aac	ggt	ggt	act	ggc	tct	acc	gta	aaa	576
Val	Asn	Glu	Glu	Trp	Lys	Asn	Asn	Val	Gly	Thr	Gly	Ser	Thr	Val	Lys	
		180					185						190			
tgg	ccg	atc	ggt	ctg	ggc	ggt	aaa	ggt	aac	gac	ggt	atc	gcc	gcg	ttc	624
Trp	Pro	Ile	Gly	Leu	Gly	Gly	Lys	Gly	Asn	Asp	Gly	Ile	Ala	Ala	Phe	

195	200	205	
gtt cag cgt ctg ccg ggt gca att ggt tat gtt gaa tat gct tac gcg	672		
Val Gln Arg Leu Pro Gly Ala Ile Gly Tyr Val Glu Tyr Ala Tyr Ala			
210 215 220			
aag cag aac aac ctg gcg tac acc aaa ctg atc tcc gct gat ggt aaa	720		
Lys Gln Asn Asn Leu Ala Tyr Thr Lys Leu Ile Ser Ala Asp Gly Lys			
225 230 235 240			
ccg gtt agt ccg acc gaa gaa aac ttc gct aat gca gca aaa ggt gca	768		
Pro Val Ser Pro Thr Glu Glu Asn Phe Ala Asn Ala Ala Lys Gly Ala			
245 250 255			
gac tgg agc aaa acc ttc gct cag gat ctg acc aac cag aaa ggc gaa	816		
Asp Trp Ser Lys Thr Phe Ala Gln Asp Leu Thr Asn Gln Lys Gly Glu			
260 265 270			
gat gca tgg cct att acc tct acc acg ttc att ctg atc cac aaa gat	864		
Asp Ala Trp Pro Ile Thr Ser Thr Thr Phe Ile Leu Ile His Lys Asp			
275 280 285			
cag aag aaa cca gaa caa ggc aca gaa gtg ctg aaa ttc ttc gac tgg	912		
Gln Lys Lys Pro Glu Gln Gly Thr Glu Val Leu Lys Phe Phe Asp Trp			
290 295 300			
gcg tac aaa acc ggg gct aaa cag gcg aac gac ctg gat tac gcc agc	960		
Ala Tyr Lys Thr Gly Ala Lys Gln Ala Asn Asp Leu Asp Tyr Ala Ser			
305 310 315 320			
ctg ccg gat agt gta gtt gaa cag gtt cgc gct gcg tgg aag acc aat	1008		
Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn			
325 330 335			
att aaa gac agt agc ggt aag ccg ctg tac taa	1041		
Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr *			
340 345			

<210> 188
 <211> 711
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(711)

<400> 188	
atg gga tct gga ctg gtg aac gga ggt gat tat ttt tat aat aac ctt	48
Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu	
1 5 10 15	
tca ttc aca gtc acc agg tac aac ggc atc atg gca act gac tca aca	96
Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr	
20 25 30	

```

caa tgt gta aaa aaa agc cgt ggc cgc cca aaa gtg ttc gac agg gat 144
Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
      35                40                45

gcc gcg ctt gat aag gcc atg aaa ttg ttc tgg caa cac ggt tat gaa 192
Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
      50                55                60

gcg act tct ctt gcg gac ctc gtc gaa gcg acc gga gcc aaa gcg ccc 240
Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
      65                70                75                80

acg cta tac gcg gaa ttt acc aac aaa gag ggg tta ttt cgt gcc gtt 288
Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
      85                90                95

ctc gac cgc tat atc gat cgt ttt gcc gct aag cat gaa gca cag ctg 336
Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu
      100                105                110

ttt tgt gaa gag aaa agc gtg gag tct gcg ctg gct gac tat ttt gct 384
Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
      115                120                125

gcc atc gcc aac tgc ttt acc agc aaa gac acc ccg gca ggc tgc ttc 432
Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe
      130                135                140

atg atc aac aac tgc acc acc ctc tcc cca gat tca gga gat atc gcc 480
Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala
      145                150                155                160

aat acg ttg aaa tca cgc cat gcg atg caa gag cgc act ttg cag cag 528
Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln
      165                170                175

ttt tta tgt caa cga caa gcg cgc ggg gaa atc ccg ccc cac tgt gac 576
Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp
      180                185                190

gtg aca cat ctg gca gaa ttc ctt aat tgt att att cag ggg atg tcg 624
Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser
      195                200                205

atc agc gca cgc gaa ggt gca tcg ctg gaa aaa ctg atg cag att gcc 672
Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala
      210                215                220

gga acg act ttg cgt tta tgg ccc gaa ctg gtg aaa taa 711
Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys *
      225                230                235

```

<210> 189
 <211> 546
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(546)

<400> 189

gtg	cag	gcc	aaa	att	gcg	gca	tca	aat	acg	ggt	gaa	ctg	gat	gcc	ctg	48
Met	Gln	Ala	Lys	Ile	Ala	Ala	Ser	Asn	Thr	Gly	Glu	Leu	Asp	Ala	Leu	
1				5					10					15		

caa	cag	ctg	gga	ttc	tcc	ctg	gta	gaa	ggt	gaa	gtt	gat	ttg	gcg	cta	96
Gln	Gln	Leu	Gly	Phe	Ser	Leu	Val	Glu	Gly	Glu	Val	Asp	Leu	Ala	Leu	
		20						25					30			

ccc	gtg	aac	aat	gcc	agt	gat	agc	ggt	gct	gta	gtg	gca	caa	gag	acc	144
Pro	Val	Asn	Asn	Ala	Ser	Asp	Ser	Gly	Ala	Val	Val	Ala	Gln	Glu	Thr	
		35					40					45				

gat	att	ccc	gca	tta	cgt	cag	tta	gcc	agc	gcc	gca	ttt	gcg	caa	agc	192
Asp	Ile	Pro	Ala	Leu	Arg	Gln	Leu	Ala	Ser	Ala	Ala	Phe	Ala	Gln	Ser	
	50					55					60					

cgt	ttt	cgt	gcg	cgc	tgg	tat	gcg	cct	gac	gcc	agc	agt	cgc	ttt	tat	240
Arg	Phe	Arg	Ala	Pro	Trp	Tyr	Ala	Pro	Asp	Ala	Ser	Ser	Arg	Phe	Tyr	
65					70				75					80		

gca	cag	tgg	att	gaa	aat	gcc	gtg	cgc	ggc	acc	ttt	gat	cat	caa	tgt	288
Ala	Gln	Trp	Ile	Glu	Asn	Ala	Val	Arg	Gly	Thr	Phe	Asp	His	Gln	Cys	
			85						90					95		

ctg	att	tta	cgt	gcg	gcg	tcc	ggc	gat	att	cgc	ggc	tat	gtc	tct	tta	336
Leu	Ile	Leu	Arg	Ala	Ala	Ser	Gly	Asp	Ile	Arg	Gly	Tyr	Val	Ser	Leu	
		100						105					110			

cgg	gaa	ctc	aat	gcg	aca	gat	gcg	cga	att	ggc	ctg	ctg	gct	gga	cgc	384
Arg	Glu	Leu	Asn	Ala	Thr	Asp	Ala	Arg	Ile	Gly	Leu	Leu	Ala	Gly	Arg	
	115						120					125				

ggt	gca	ggt	gct	gag	ctg	atg	caa	acg	gcg	cta	aac	tgg	gcg	tat	cgt	432
Gly	Ala	Gly	Ala	Glu	Leu	Met	Gln	Thr	Ala	Leu	Asn	Trp	Ala	Tyr	Arg	
	130					135					140					

cgc	ggt	aaa	aca	act	ttg	cgg	gtg	gcg	acc	caa	atg	ggc	aac	acc	gcc	480
Arg	Gly	Lys	Thr	Thr	Leu	Arg	Val	Ala	Thr	Gln	Met	Gly	Asn	Thr	Ala	
145					150					155					160	

gcg	ctt	aaa	cga	tac	ata	caa	agt	ggt	gcg	aat	gta	gaa	agc	acc	gcg	528
Ala	Leu	Lys	Arg	Tyr	Ile	Gln	Ser	Gly	Ala	Asn	Val	Glu	Ser	Thr	Ala	
			165					170						175		

tac	tgg	tta	tac	agg	tga											546
Tyr	Trp	Leu	Tyr	Arg	*											
		180														

<210> 190

<211> 1131

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1131)

<400> 190

atg att cca ttt aac gca ccg ccg gtg gtg gga acc gaa ctc gac tat	48
Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr	
1 5 10 15	

atg cag tcg gca atg ggt agc ggc aaa ctg tgt ggc gat ggc ggt ttt	96
Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe	
20 25 30	

acc cgt cgc tgc cag cag tgg ctg gag caa cgt ttt ggc agc gcc aaa	144
Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys	
35 40 45	

gtg tta ctg acg ccg tcc tgc acc gct tcg ctg gag atg gcg gcg ctg	192
Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu	
50 55 60	

ctg ctc gat atc cag cct ggc gat gaa gtg atc atg ccg agc tac acc	240
Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr	
65 70 75 80	

ttt gtc tcc acc gcc aat gcc ttt gtg ctg cgt ggc gca aaa atc gtt	288
Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val	
85 90 95	

ttt gtg gat gtt cgc ccg gac acc atg aac atc gac gaa acg ctg att	336
Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile	
100 105 110	

gaa gcg gcg atc acc gac aaa acg cgc gtt atc gtg ccg gtc cat tac	384
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr	
115 120 125	

gcg ggt gtg gcc tgc gaa atg gac acc att atg gcg ttg gcg aaa aag	432
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys	
130 135 140	

cat aat ttg ttt gtg gta gaa gat gcc gct cag ggc gtg atg tcc act	480
His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr	
145 150 155 160	

tac aaa ggg cgt gca ctg gga acc att ggt cat att ggc tgc ttt agc	528
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser	
165 170 175	

ttc cat gaa acc aaa aac tac acg gcg ggc ggt gaa ggc ggc gcg acg	576
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr	
180 185 190	

ctg att aac gat aaa gcg tta atc gaa cga gcc gag atc atc cgt gaa	624
---	-----

Leu Ile Asn Asp Lys Ala Leu Ile Glu Arg Ala Glu Ile Ile Arg Glu	
195	200 205
aag ggc act aac cgc agc cag ttc ttc cgt ggt cag gtc gat aaa tat	672
Lys Gly Thr Asn Arg Ser Gln Phe Phe Arg Gly Gln Val Asp Lys Tyr	
210	215 220
acc tgg cgc gat att ggc tcc agc tat ttg atg tcc gat ctg caa gct	720
Thr Trp Arg Asp Ile Gly Ser Ser Tyr Leu Met Ser Asp Leu Gln Ala	
225	230 235 240
gca tac ctg tgg gcg caa ctg gaa gca gcg gat cgt atc aac cag caa	768
Ala Tyr Leu Trp Ala Gln Leu Glu Ala Ala Asp Arg Ile Asn Gln Gln	
	245 250 255
cgt ctg gcg ctg tgg caa aac tac tac gat gcg tta gcg cct ctg gcg	816
Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala	
	260 265 270
aaa gcc ggg cgt atc gag ctg ccg tgc att ccc gat ggc tgc gtg cag	864
Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln	
	275 280 285
aac gcg cat atg ttc tac att aaa ctg cgg gat att gat gac cgg agc	912
Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser	
	290 295 300
gcg ttg att aac ttt ctg aaa gaa gcg gaa atc atg gcg gtg ttt cat	960
Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His	
305	310 315 320
tac att ccg ctg cac ggt tgc cct gcg ggg gaa cac ttt ggt gag ttc	1008
Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe	
	325 330 335
cac ggt gaa gat cgc tac acc acc aaa gag agc gag cgc ctg ctg cgc	1056
His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg	
	340 345 350
ctg ccg ctg ttc tac aac ctg tgc ccc gtc aat cag cgt acg gta att	1104
Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile	
	355 360 365
gcg act ttg ttg aac tac ttt tcc tga	1131
Ala Thr Leu Leu Asn Tyr Phe Ser *	
370	375

<210> 191
 <211> 1251
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(1251)

```

<400> 191
atg tcg ttg gca aaa gcg tcc ttg tgg acg gcg gcc agt aca ctg gtc 48
Met Ser Leu Ala Lys Ala Ser Leu Trp Thr Ala Ala Ser Thr Leu Val
1 5 10 15

aag att ggt gcc ggg tta ctg gtc ggt aag ttg ctg gcg gtg tca ttt 96
Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
20 25 30

ggg ccg gcg ggg ctt ggg ctg gcg gca aat ttc cgc cag ttg att acc 144
Gly Pro Ala Gly Leu Gly Leu Ala Ala Asn Phe Arg Gln Leu Ile Thr
35 40 45

gtg ctc ggc gtg ctt gcc ggg gct ggc atc ttt aac ggt gta acc aaa 192
Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
50 55 60

tac gtt gcc cag tac cat gat aat ccg caa cag ctg cgc cgc gtg gtc 240
Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
65 70 75 80

ggc act tca tca gcg atg gta ctt ggt ttc tct acg ctg atg gcg ctg 288
Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
85 90 95

gtt ttt gtg ctg gca gct gcg cca atc agc cag gga ttg ttt ggt aat 336
Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
100 105 110

acc gac tat cag ggg ctg gtg cgt tta gtg gcg ctg gtg caa atg ggg 384
Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
115 120 125

atc gcc tgg ggc aac ctg tta ctg gcg ctg atg aaa ggc ttt cgc gat 432
Ile Ala Trp Gly Asn Leu Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
130 135 140

gcc gca ggt aat gcg tta tcg ctg att gtc ggc agc ttg att ggc gtt 480
Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
145 150 155 160

ctc gcg tac tac gtc agt tac cgt ttg ggc ggt tat gaa ggg gcg ttg 528
Leu Ala Tyr Tyr Val Ser Tyr Arg Leu Gly Tyr Glu Gly Ala Leu
165 170 175

ctg ggt ctg gcg ctg att ccc gcg ctg gtg gta att cct gcc gcc atc 576
Leu Gly Leu Ala Leu Ile Pro Ala Leu Val Val Ile Pro Ala Ala Ile
180 185 190

atg ttg atc aaa cgt ggt gtc atc ccg tta agc tat ctg aaa ccc agc 624
Met Leu Ile Lys Arg Gly Val Ile Pro Leu Ser Tyr Leu Lys Pro Ser
195 200 205

tgg gat aac ggt ctg gca ggg cag ttg agc aaa ttt acg ctc atg gcg 672
Trp Asp Asn Gly Leu Ala Gly Gln Leu Ser Lys Phe Thr Leu Met Ala
210 215 220

```


ttg att acg tcg gtg acc ttg cct gtt gct tac atc atg atg cgt aaa	720
Leu Ile Thr Ser Val Thr Leu Pro Val Ala Tyr Ile Met Met Arg Lys	
225 230 235 240	
ctg ctg gcg gcg cag tat agc tgg gat gag gtg ggg atc tgg caa ggg	768
Leu Leu Ala Ala Gln Tyr Ser Trp Asp Glu Val Gly Ile Trp Gln Gly	
245 250 255	
gtg agc agt att tcc gat gcc tac ctg caa ttt att acg gca tcg ttc	816
Val Ser Ser Ile Ser Asp Ala Tyr Leu Gln Phe Ile Thr Ala Ser Phe	
260 265 270	
agc gta tat ttg ctg ccc acg ttg tcg cgg cta acg gaa aag cgc gat	864
Ser Val Tyr Leu Leu Pro Thr Leu Ser Arg Leu Thr Glu Lys Arg Asp	
275 280 285	
atc acc cgg gaa gtg gtt aaa tcg ctg aaa ttc gtc tta ccg gca gtg	912
Ile Thr Arg Glu Val Val Lys Ser Leu Lys Phe Val Leu Pro Ala Val	
290 295 300	
gcg gcg gcg agt ttt acc gtc tgg ctg ctg cgt gat ttt gct atc tgg	960
Ala Ala Ala Ser Phe Thr Val Trp Leu Leu Arg Asp Phe Ala Ile Trp	
305 310 315 320	
ctg ctg ttg tcg aat aaa ttt acc gct atg cgc gat ctc ttt gcc tgg	1008
Leu Leu Leu Ser Asn Lys Phe Thr Ala Met Arg Asp Leu Phe Ala Trp	
325 330 335	
cag tta gtg ggt gat gtg tta aaa gtg ggc gct tat gtc ttt ggt tat	1056
Gln Leu Val Gly Asp Val Leu Lys Val Gly Ala Tyr Val Phe Gly Tyr	
340 345 350	
ctg gtg atc gcc aaa gcg tca ctg cgg ttt tat att ctg gcg gaa gtc	1104
Leu Val Ile Ala Lys Ala Ser Leu Arg Phe Tyr Ile Leu Ala Glu Val	
355 360 365	
agc cag ttc act tta ttg atg gta ttt gcc cac tgg cta atc cct gcg	1152
Ser Gln Phe Thr Leu Leu Met Val Phe Ala His Trp Leu Ile Pro Ala	
370 375 380	
cat ggt gca ctg ggc gcg gcg cag gca tat atg gca act tat atc gtc	1200
His Gly Ala Leu Gly Ala Ala Gln Ala Tyr Met Ala Thr Tyr Ile Val	
385 390 395 400	
tat ttt tct ctt tgt tgt ggc gtg ttt tta ctc tgg cgt agg cgg gca	1248
Tyr Phe Ser Leu Cys Cys Gly Val Phe Leu Leu Trp Arg Arg Arg Ala	
405 410 415	
tga	1251
*	

<210> 192
 <211> 1353
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1353)

<400> 192

atg agt ctg ctg caa ttc agt ggc ctg ttt gtt gtc tgg ctg ctc tgc	48
Met Ser Leu Leu Gln Phe Ser Gly Leu Phe Val Val Trp Leu Leu Cys	
1 5 10 15	
acg ctg ttt att gcc acg ctg acc tgg ttt gag ttt cgc cgt gtg cgc	96
Thr Leu Phe Ile Ala Thr Leu Thr Trp Phe Glu Phe Arg Arg Val Arg	
20 25 30	
ttt aac ttc aat gtc ttc ttt tca ttg ctg ttt ttg ctc acc ttt ttc	144
Phe Asn Phe Asn Val Phe Phe Ser Leu Leu Phe Leu Leu Thr Phe Phe	
35 40 45	
ttc ggc ttc ccg ctg acc agc gtg ctg gta ttt cgc ttt gat gtt ggt	192
Phe Gly Phe Pro Leu Thr Ser Val Leu Val Phe Arg Phe Asp Val Gly	
50 55 60	
gtc gcg ccg cca gaa atc ttg ttg cag gcg ttg ctt tct gcg ggc tgc	240
Val Ala Pro Pro Glu Ile Leu Leu Gln Ala Leu Leu Ser Ala Gly Cys	
65 70 75 80	
ttc tac gcg gtt tac tat gtc acc tac aaa acc cgc cta cgc aaa cgc	288
Phe Tyr Ala Val Tyr Tyr Val Thr Tyr Lys Thr Arg Leu Arg Lys Arg	
85 90 95	
gtt gct gat gta ccg cgc cgt ccg ctg ttt acc atg aac cgc gtg gag	336
Val Ala Asp Val Pro Arg Arg Pro Leu Phe Thr Met Asn Arg Val Glu	
100 105 110	
acc aat ctt acg tgg gtg atc ctg atg ggt atc gcg ctg gta agc gtc	384
Thr Asn Leu Thr Trp Val Ile Leu Met Gly Ile Ala Leu Val Ser Val	
115 120 125	
ggc atc ttc ttc atg cac aac ggc ttt ttg ctg ttc cgc ctt aac tcc	432
Gly Ile Phe Phe Met His Asn Gly Phe Leu Leu Phe Arg Leu Asn Ser	
130 135 140	
tac agt cag atc ttt tcc agt gaa gtc tcc ggc gtg gcg tta aaa cgc	480
Tyr Ser Gln Ile Phe Ser Ser Glu Val Ser Gly Val Ala Leu Lys Arg	
145 150 155 160	
ttc ttt tac ttt ttc atc ccg gcg atg ctg gtg gtc tac ttt ctg cgc	528
Phe Phe Tyr Phe Phe Ile Pro Ala Met Leu Val Val Tyr Phe Leu Arg	
165 170 175	
cag gac agc aaa gcg tgg ctg ttt ttc ctc gtc agc acg gtc gcc ttt	576
Gln Asp Ser Lys Ala Trp Leu Phe Phe Leu Val Ser Thr Val Ala Phe	
180 185 190	
ggc ttg ctg act tat atg att gtc ggc ggc act cgc gcc aat atc atc	624
Gly Leu Leu Thr Tyr Met Ile Val Gly Gly Thr Arg Ala Asn Ile Ile	
195 200 205	

atc gca ttc gct atc ttc ctg ttt att ggc att att cgc ggc tgg att	672
Ile Ala Phe Ala Ile Phe Leu Phe Ile Gly Ile Ile Arg Gly Trp Ile	
210 215 220	
tcg ttg tgg atg ctg gcg gcg gcg ggc gtg ctg ggg att gtt ggc atg	720
Ser Leu Trp Met Leu Ala Ala Ala Gly Val Leu Gly Ile Val Gly Met	
225 230 235 240	
ttc tgg ctg gca cta aaa cgc tat gga atg aat gtg agc ggc gat gaa	768
Phe Trp Leu Ala Leu Lys Arg Tyr Gly Met Asn Val Ser Gly Asp Glu	
245 250 255	
gcg ttc tat acg ttt ctc tat ctc act cgc gac acc ttc tcg ccg tgg	816
Ala Phe Tyr Thr Phe Leu Tyr Leu Thr Arg Asp Thr Phe Ser Pro Trp	
260 265 270	
gag aat ctg gcg ttg ctg ttg cag aac tac gac aac atc gac ttc cag	864
Glu Asn Leu Ala Leu Leu Leu Gln Asn Tyr Asp Asn Ile Asp Phe Gln	
275 280 285	
ggc ctg gct cca att gtc cgc gat ttc tat gtc ttt atc cct tcc tgg	912
Gly Leu Ala Pro Ile Val Arg Asp Phe Tyr Val Phe Ile Pro Ser Trp	
290 295 300	
ctg tgg ccg ggt cgc ccg agt atg gtg ctg aac tca gcc aac tac ttt	960
Leu Trp Pro Gly Arg Pro Ser Met Val Leu Asn Ser Ala Asn Tyr Phe	
305 310 315 320	
acc tgg gaa gtg ctg aat aac cac tcc gga ctg gcg atc tcg cct acg	1008
Thr Trp Glu Val Leu Asn Asn His Ser Gly Leu Ala Ile Ser Pro Thr	
325 330 335	
ctt ata ggc tca ctg gtg gtg atg ggc ggc gcg ttg ttc atc ccg ctc	1056
Leu Ile Gly Ser Leu Val Val Met Gly Gly Ala Leu Phe Ile Pro Leu	
340 345 350	
ggg gcg atc gtg gtt ggt ctg atc atc aaa tgg ttc gac tgg ctg tat	1104
Gly Ala Ile Val Val Gly Leu Ile Ile Lys Trp Phe Asp Trp Leu Tyr	
355 360 365	
gag ctg ggc aac cgc gag cct aat cgc tat aaa gct gcg ata ttg cac	1152
Glu Leu Gly Asn Arg Glu Pro Asn Arg Tyr Lys Ala Ala Ile Leu His	
370 375 380	
agt ttc tgc ttt ggg gcg atc ttc aat atg atc gtg ctg gcg cgt gaa	1200
Ser Phe Cys Phe Gly Ala Ile Phe Asn Met Ile Val Leu Ala Arg Glu	
385 390 395 400	
ggg ctg gat tcg ttt gtc tca cgc gtg gtc ttt ttt atc gtg gtc ttc	1248
Gly Leu Asp Ser Phe Val Ser Arg Val Val Phe Phe Ile Val Val Phe	
405 410 415	
ggc gca tgt ctg atg atc gca aaa ctg ttg tac tgg ctt ttt gaa agc	1296
Gly Ala Cys Leu Met Ile Ala Lys Leu Leu Tyr Trp Leu Phe Glu Ser	
420 425 430	

gcc gga ctc att cat aaa cgt aca aaa tca tcg ctc cgg acg cag gtt	1344
Ala Gly Leu Ile His Lys Arg Thr Lys Ser Ser Leu Arg Thr Gln Val	
435 440 445	
gaa gga taa	1353
Glu Gly *	
450	
<210> 193	
<211> 741	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(741)	
<400> 193	
atg aat aac aac acc acg gca cca acc tat acg ctg cgt ggc tta cag	48
Met Asn Asn Asn Thr Thr Ala Pro Thr Tyr Thr Leu Arg Gly Leu Gln	
1 5 10 15	
ttg att ggt tgg cgt gat atg cag cac gcc ctc gat tat ctg ttt gct	96
Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Tyr Leu Phe Ala	
20 25 30	
gac ggg cag ctt aag cag gga acg ctg gtt gcc att aat gct gaa aaa	144
Asp Gly Gln Leu Lys Gln Gly Thr Leu Val Ala Ile Asn Ala Glu Lys	
35 40 45	
atg ctg act att gaa gat aac gcc gag gtc agg gag tta att aac gct	192
Met Leu Thr Ile Glu Asp Asn Ala Glu Val Arg Glu Leu Ile Asn Ala	
50 55 60	
gcc gaa ttt aaa tat gcg gat ggc atc agc gtt gta cgt tca gta cgt	240
Ala Glu Phe Lys Tyr Ala Asp Gly Ile Ser Val Val Arg Ser Val Arg	
65 70 75 80	
aaa aag tac ccg cag gcg cag gtt tcc cgc gtt gcc ggt gcc gat ctc	288
Lys Lys Tyr Pro Gln Ala Gln Val Ser Arg Val Ala Gly Ala Asp Leu	
85 90 95	
tgg gaa gag ctg atg gcg cgc gca ggc aaa gaa ggg acg ccg gta ttt	336
Trp Glu Glu Leu Met Ala Arg Ala Gly Lys Glu Gly Thr Pro Val Phe	
100 105 110	
ctt gtg ggc ggt aaa cct gaa gtg ctg gcg caa act gaa gct aaa ctg	384
Leu Val Gly Gly Lys Pro Glu Val Leu Ala Gln Thr Glu Ala Lys Leu	
115 120 125	
cgc aac cag tgg aat gtg aat atc gtt ggc agt cag gat ggt tat ttt	432
Arg Asn Gln Trp Asn Val Asn Ile Val Gly Ser Gln Asp Gly Tyr Phe	
130 135 140	
aaa ccc gag cag cgt cag gcg ctg ttt gaa cgc att cat gcc agc ggt	480
Lys Pro Glu Gln Arg Gln Ala Leu Phe Glu Arg Ile His Ala Ser Gly	

145	150	155	160	
gcg caa atc gtc acc gtt gcg atg gga tgc cca aag cag gag atc atc				528
Ala Gln Ile Val Thr Val Ala Met Gly Ser Pro Lys Gln Glu Ile Ile	165	170	175	
atg cgc gac tgc cgt ctg gta cat cca gat gcg ctg tat atg ggc gtt				576
Met Arg Asp Cys Arg Leu Val His Pro Asp Ala Leu Tyr Met Gly Val	180	185	190	
ggc ggg act tac gat gtt ttc acc ggt cac gta aaa cgc gca ccg aaa				624
Gly Gly Thr Tyr Asp Val Phe Thr Gly His Val Lys Arg Ala Pro Lys	195	200	205	
atc tgg caa acg ctg ggg ctg gag tgg ctc tac cgc ctg ctt tcg cag				672
Ile Trp Gln Thr Leu Gly Leu Glu Trp Leu Tyr Arg Leu Leu Ser Gln	210	215	220	
ccg agc cgc att aag cgt cag ctt cgt ttg ctg cgt tat tta cgc tgg				720
Pro Ser Arg Ile Lys Arg Gln Leu Arg Leu Leu Arg Tyr Leu Arg Trp	225	230	235	240
cac tac acc ggc aac cta tga				741
His Tyr Thr Gly Asn Leu *	245			
<210> 194				
<211> 225				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(225)				
<400> 194				
atg act gta ctg att cac gta ctg gga tgc gat atc cct cac cat aac				48
Met Thr Val Leu Ile His Val Leu Gly Ser Asp Ile Pro His His Asn	1	5	10	15
cga acc gtt ttg cgg ttt ttc aat gac gcg ctg gcc gcg acg agc gag				96
Arg Thr Val Leu Arg Phe Phe Asn Asp Ala Leu Ala Ala Thr Ser Glu	20	25	30	
cac gcg cgc gag ttt atg gtt gtt ggc aag gac gac ggc tta agt gat				144
His Ala Arg Glu Phe Met Val Val Gly Lys Asp Asp Gly Leu Ser Asp	35	40	45	
agc tgt ccg gcg ctt tct gtg caa ttt ttc ccc tgg gaa aaa atc gct				192
Ser Cys Pro Ala Leu Ser Val Gln Phe Phe Pro Trp Glu Lys Ile Ala	50	55	60	
ggc gga agc ggt cat cgc gaa agc aaa agc taa				225
Gly Gly Ser Gly His Arg Glu Ser Lys Ser *	65	70		

<210> 195
 <211> 615
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(615)

<400> 195

gtg cgg ggc gaa ctg ctg ttc ttc ccg acg cgg atg gac cct tcg ctc	48
Met Arg Gly Glu Leu Leu Phe Phe Pro Thr Arg Met Asp Pro Ser Leu	
1 5 10 15	
aat acg atg gcg aac gat cgg caa cgt gaa ggg aaa atg acc att ctg	96
Asn Thr Met Ala Asn Asp Arg Gln Arg Glu Gly Lys Met Thr Ile Leu	
20 25 30	
gtg ggg aac tcc ggc gac cgc agc aat gag cat att gct gcc ttg cgc	144
Val Gly Asn Ser Gly Asp Arg Ser Asn Glu His Ile Ala Ala Leu Arg	
35 40 45	
gcc gtt cat cag caa ttt ggc gat acg gta aaa gtg gtg gtg ccg atg	192
Ala Val His Gln Gln Phe Gly Asp Thr Val Lys Val Val Val Pro Met	
50 55 60	
gga tat ccg cct aat aac gaa gcg tac att gag gaa gtt cgt cag gcg	240
Gly Tyr Pro Pro Asn Asn Glu Ala Tyr Ile Glu Glu Val Arg Gln Ala	
65 70 75 80	
ggg ctg gag tta ttc agc gaa gaa aat cta caa att ctg agc gaa aaa	288
Gly Leu Glu Leu Phe Ser Glu Glu Asn Leu Gln Ile Leu Ser Glu Lys	
85 90 95	
ctg gaa ttt gac gcc tat ctg gcg cta ctt cgt cag tgc gat ctt ggt	336
Leu Glu Phe Asp Ala Tyr Leu Ala Leu Leu Arg Gln Cys Asp Leu Gly	
100 105 110	
tac ttt att ttt gcc cgc cag cag ggc att ggt acg ctg tgc tta ctg	384
Tyr Phe Ile Phe Ala Arg Gln Gln Gly Ile Gly Thr Leu Cys Leu Leu	
115 120 125	
att cag gcg ggc att cct tgt gtg ctt aac cgg gaa aat ccg ttc tgg	432
Ile Gln Ala Gly Ile Pro Cys Val Leu Asn Arg Glu Asn Pro Phe Trp	
130 135 140	
cag gat atg acg gaa caa cat ttg ccg gtg ctg ttt act acc gac gat	480
Gln Asp Met Thr Glu Gln His Leu Pro Val Leu Phe Thr Thr Asp Asp	
145 150 155 160	
ctc aac gag gat att gtg cgt gaa gcg cag cgc cag ttg gcg tcg gtg	528
Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val	
165 170 175	
gat aaa aac acc att gcc ttc ttt agc cct aac tat cta caa ggc tgg	576
Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp	

	180	185	190	
	cag cgg gcg ttg gcg att gcc gcc agg gag gtc gca tga			615
	Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala *			
	195	200		
<210>	196			
<211>	549			
<212>	DNA			
<213>	Escherichia coli			
<220>				
<221>	CDS			
<222>	(1)...(549)			
<400>	196			
	atg att cgg caa cgt cgt cgt gcg tta acg ccg gaa caa cag cag gaa			48
	Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Glu			
	1 5 10 15			
	atg ggt caa caa gcc gct acc cgg atg atg act tat ccc ccg gtg gtg			96
	Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val			
	20 25 30			
	atg gca cat acg gtc gct gta ttc ctc tct ttt gat ggc gaa ctc gac			144
	Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp			
	35 40 45			
	acc cag cca ctc ata gaa caa ctc tgg cgc gcc ggt aag cgc gta tat			192
	Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr			
	50 55 60			
	ctt cca gtt ttg cat ccc ttt agt gcc ggt aat ttg ctg ttc ctg aat			240
	Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn			
	65 70 75 80			
	tac cat ccg caa agc gaa ctg gtg atg aac agg ttg aag atc cat gag			288
	Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu			
	85 90 95			
	cca aaa ttg gat gtg cgt gac gtg cta ccc ctt tcc cga tta gac gtg			336
	Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val			
	100 105 110			
	ctg atc aca ccg ctg gtc gcc ttt gat gag tac ggt cag cgc ctg gga			384
	Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly			
	115 120 125			
	atg ggc ggt ggt ttt tat gat cgg acc tta caa aac tgg cag cac tat			432
	Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr			
	130 135 140			
	aaa acg caa ccg gtg ggt tat gcg cat gat tgt cag ttg gtg gaa aaa			480
	Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys			
	145 150 155 160			

ctc ccc gtt gaa gag tgg gat atc cct ctt cct gcg gtg gtt aca ccg	528
Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro	
165 170 175	

tcg aaa gtc tgg gag tgg taa	549
Ser Lys Val Trp Glu Trp *	
180	

<210> 197
 <211> 276
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(276)

<400> 197															
atg gca cgc gta act gtt cag gac gct gta gag aaa att ggt aac cgt	48														
Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg															
1 5 10 15															
ttt gac ctg gta ctg gtc gcc gcg cgt cgc gct cgt cag atg cag gta	96														
Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val															
20 25 30															
ggc gga aag gat ccg ctg gta ccg gaa gaa aac gat aaa acc act gta	144														
Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val															
35 40 45															
atc gcg ctg cgc gaa atc gaa gaa ggt ctg atc aac aac cag atc ctc	192														
Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu															
50 55 60															
gac gtt cgc gaa cgc cag gaa cag caa gag cag gaa gcc gct gaa tta	240														
Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu															
65 70 75 80															
caa gcc gtt acc gct att gct gaa ggt cgt cgt taa	276														
Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg *															
85 90															

<210> 198
 <211> 2109
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2109)

<400> 198															
ttg tat ctg ttt gaa agc ctg aat caa ctg att caa acc tac ctg ccg	48														
Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro															
1 5 10 15															

gaa gac caa atc aag cgt ctg cgg cag gcg tat ctc gtt gca cgt gat	96
Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp	
20 25 30	
gct cac gag ggg caa aca cgt tca agc ggt gaa ccc tat atc acg cac	144
Ala His Glu Gly Gln Thr Arg Ser Ser Gly Glu Pro Tyr Ile Thr His	
35 40 45	
ccg gta gcg gtt gcc tgc att ctg gcc gag atg aaa ctc gac tat gaa	192
Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu	
50 55 60	
acg ctg atg gcg gcg ctg ctg cat gac gtg att gaa gat act ccc gcc	240
Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala	
65 70 75 80	
acc tac cag gat atg gaa cag ctt ttt ggt aaa agc gtc gcc gag ctg	288
Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu	
85 90 95	
gta gag ggg gtg tgc aaa ctt gat aaa ctc aag ttc cgc gat aag aaa	336
Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys	
100 105 110	
gag gcg cag gcc gaa aac ttt cgc aag atg att atg gcg atg gtg cag	384
Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln	
115 120 125	
gat atc cgc gtc atc ctc atc aaa ctt gcc gac cgt acc cac aac atg	432
Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met	
130 135 140	
cgc acg ctg ggc tca ctt cgc ccg gac aaa cgt cgc cgc atc gcc cgt	480
Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg	
145 150 155 160	
gaa act ctc gaa att tat agc ccg ctg gcg cac cgt tta ggt atc cac	528
Glu Thr Leu Glu Ile Tyr Ser Pro Leu Ala His Arg Leu Gly Ile His	
165 170 175	
cac att aaa acc gaa ctc gaa gag ctg ggt ttt gag gcg ctg tat ccc	576
His Ile Lys Thr Glu Leu Glu Glu Leu Gly Phe Glu Ala Leu Tyr Pro	
180 185 190	
aac cgt tat cgc gta atc aaa gaa gtg gtg aaa gcc gcg cgc ggc aac	624
Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn	
195 200 205	
cgt aaa gag atg atc cag aag att ctt tct gaa atc gaa ggg cgt ttg	672
Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu	
210 215 220	
cag gaa gcg gga ata ccg tgc cgc gtc agt ggt cgc gag aag cat ctt	720
Gln Glu Ala Gly Ile Pro Cys Arg Val Ser Gly Arg Glu Lys His Leu	
225 230 235 240	

tat tcg att tac tgc aaa atg gtg ctc aaa gag cag cgt ttt cac tcg	768
Tyr Ser Ile Tyr Cys Lys Met Val Leu Lys Glu Gln Arg Phe His Ser	
245 250 255	
atc atg gac atc tac gct ttc cgc gtg atc gtc aat gat tct gac acc	816
Ile Met Asp Ile Tyr Ala Phe Arg Val Ile Val Asn Asp Ser Asp Thr	
260 265 270	
tgt tat cgc gtg ctg ggc cag atg cac agc ctg tac aag ccg cgt ccg	864
Cys Tyr Arg Val Leu Gly Gln Met His Ser Leu Tyr Lys Pro Arg Pro	
275 280 285	
ggc cgc gtg aaa gac tat atc gcc att cca aaa gcg aac ggc tat cag	912
Gly Arg Val Lys Asp Tyr Ile Ala Ile Pro Lys Ala Asn Gly Tyr Gln	
290 295 300	
tct ttg cac acc tcg atg atc ggc ccg cac ggt gtg ccg gtt gag gtc	960
Ser Leu His Thr Ser Met Ile Gly Pro His Gly Val Pro Val Glu Val	
305 310 315 320	
cag atc cgt acc gaa gat atg gac cag atg gcg gag atg ggt gtt gcc	1008
Gln Ile Arg Thr Glu Asp Met Asp Gln Met Ala Glu Met Gly Val Ala	
325 330 335	
gcg cac tgg gct tat aaa gag cac ggc gaa acc agt act acc gca caa	1056
Ala His Trp Ala Tyr Lys Glu His Gly Glu Thr Ser Thr Thr Ala Gln	
340 345 350	
atc cgc gcc cag cgc tgg atg caa agc ctg ctg gag ctg caa cag agc	1104
Ile Arg Ala Gln Arg Trp Met Gln Ser Leu Leu Glu Leu Gln Gln Ser	
355 360 365	
gcc ggt agt tcg ttt gaa ttt atc gag agc gtt aaa tcc gat ctc ttc	1152
Ala Gly Ser Ser Phe Glu Phe Ile Glu Ser Val Lys Ser Asp Leu Phe	
370 375 380	
ccg gat gag att tac gtt ttc aca ccg gaa ggg cgc att gtc gag ctg	1200
Pro Asp Glu Ile Tyr Val Phe Thr Pro Glu Gly Arg Ile Val Glu Leu	
385 390 395 400	
cct gcc ggt gca acg ccc gtc gac ttc gct tat gca gtg cat acc gat	1248
Pro Ala Gly Ala Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Asp	
405 410 415	
atc ggt cat gcc tgc gtg ggc gca cgc gtt gac cgc cag cct tac ccg	1296
Ile Gly His Ala Cys Val Gly Ala Arg Val Asp Arg Gln Pro Tyr Pro	
420 425 430	
ctg tcg cag ccg ctt acc agc ggt caa acc gtt gaa atc att acc gct	1344
Leu Ser Gln Pro Leu Thr Ser Gly Gln Thr Val Glu Ile Ile Thr Ala	
435 440 445	
ccg ggc gct cgc ccg aat gcc gct tgg ctg aac ttt gtc gtt agc tcg	1392
Pro Gly Ala Arg Pro Asn Ala Ala Trp Leu Asn Phe Val Val Ser Ser	
450 455 460	
aaa gcg cgc gcc aaa att cgt cag ttg ctg aaa aac ctc aag cgt gat	1440

Lys	Ala	Arg	Ala	Lys	Ile	Arg	Gln	Leu	Leu	Lys	Asn	Leu	Lys	Arg	Asp	
465					470					475					480	
gat	tct	gta	agc	ctg	ggc	cgt	cgt	ctg	ctc	aac	cat	gct	ttg	ggg	ggg	1488
Asp	Ser	Val	Ser	Leu	Gly	Arg	Arg	Leu	Leu	Asn	His	Ala	Leu	Gly	Gly	
				485					490					495		
agc	cgt	aag	ctg	aat	gaa	atc	ccg	cag	gaa	aat	att	cag	cgc	gag	ctg	1536
Ser	Arg	Lys	Leu	Asn	Glu	Ile	Pro	Gln	Glu	Asn	Ile	Gln	Arg	Glu	Leu	
			500					505					510			
gat	cgc	atg	aag	ctg	gca	acg	ctt	gac	gat	ctg	ctg	gca	gaa	atc	gga	1584
Asp	Arg	Met	Lys	Leu	Ala	Thr	Leu	Asp	Asp	Leu	Leu	Ala	Glu	Ile	Gly	
		515					520					525				
ctt	ggg	aac	gca	atg	agc	gtg	gtg	gtc	gcg	aaa	aat	ctg	caa	cat	ggg	1632
Leu	Gly	Asn	Ala	Met	Ser	Val	Val	Val	Ala	Lys	Asn	Leu	Gln	His	Gly	
	530					535					540					
gac	gcc	tcc	att	cca	ccg	gca	acc	caa	agc	cac	gga	cat	ctg	ccc	att	1680
Asp	Ala	Ser	Ile	Pro	Pro	Ala	Thr	Gln	Ser	His	Gly	His	Leu	Pro	Ile	
	545				550				555						560	
aaa	ggg	gcc	gat	ggc	gtg	ctg	atc	acc	ttt	gcg	aaa	tgc	tgc	cgc	cct	1728
Lys	Gly	Ala	Asp	Gly	Val	Leu	Ile	Thr	Phe	Ala	Lys	Cys	Cys	Arg	Pro	
				565					570					575		
att	cct	ggc	gac	ccg	att	atc	gcc	cac	gtc	agc	ccc	ggg	aaa	ggg	ctg	1776
Ile	Pro	Gly	Asp	Pro	Ile	Ile	Ala	His	Val	Ser	Pro	Gly	Lys	Gly	Leu	
			580					585					590			
gtg	atc	cac	cat	gaa	tcc	tgc	cgt	aat	atc	cgt	ggc	tac	cag	aaa	gag	1824
Val	Ile	His	His	Glu	Ser	Cys	Arg	Asn	Ile	Arg	Gly	Tyr	Gln	Lys	Glu	
		595					600					605				
cca	gag	aag	ttt	atg	gct	gtg	gaa	tgg	gat	aaa	gag	acg	gcg	cag	gag	1872
Pro	Glu	Lys	Phe	Met	Ala	Val	Glu	Trp	Asp	Lys	Glu	Thr	Ala	Gln	Glu	
	610					615					620					
ttc	atc	acc	gaa	atc	aag	gtg	gag	atg	ttc	aat	cat	cag	ggg	gcg	ctg	1920
Phe	Ile	Thr	Glu	Ile	Lys	Val	Glu	Met	Phe	Asn	His	Gln	Gly	Ala	Leu	
	625				630					635					640	
gca	aac	ctg	acg	gcg	gca	att	aac	acc	acg	act	tcg	aat	att	caa	agt	1968
Ala	Asn	Leu	Thr	Ala	Ala	Ile	Asn	Thr	Thr	Thr	Ser	Asn	Ile	Gln	Ser	
			645						650					655		
ttg	aat	acg	gaa	gag	aaa	gat	ggg	cgc	gtc	tac	agc	gcc	ttt	att	cgt	2016
Leu	Asn	Thr	Glu	Glu	Lys	Asp	Gly	Arg	Val	Tyr	Ser	Ala	Phe	Ile	Arg	
			660					665					670			
ctg	acc	gct	cgt	gac	cgt	gtg	cat	ctg	gcg	aat	atc	atg	cgc	aaa	atc	2064
Leu	Thr	Ala	Arg	Asp	Arg	Val	His	Leu	Ala	Asn	Ile	Met	Arg	Lys	Ile	
		675					680					685				
cgc	gtg	atg	cca	gac	gtg	att	aaa	gtc	acc	cga	aac	cga	aat	taa		2109
Arg	Val	Met	Pro	Asp	Val	Ile	Lys	Val	Thr	Arg	Asn	Arg	Asn	*		

690

695

700

<210> 199

<211> 690

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(690)

<400> 199

atg aac cca aca cgt tat gca cgc atc tgc gaa atg ctc gcc agg cgg	48
Met Asn Pro Thr Arg Tyr Ala Arg Ile Cys Glu Met Leu Ala Arg Arg	
1 5 10 15	

cag cct gat ctg acc gtc tgc atg gag cag gtc cac aaa cct cat aac	96
Gln Pro Asp Leu Thr Val Cys Met Glu Gln Val His Lys Pro His Asn	
20 25 30	

gtt tct gcg att att cgt acc gca gat gcc gtt ggc gta cat gaa gtt	144
Val Ser Ala Ile Ile Arg Thr Ala Asp Ala Val Gly Val His Glu Val	
35 40 45	

cac gcc gtc tgg cct ggt agc cgc atg cgc acc atg gct tcg gca gcg	192
His Ala Val Trp Pro Gly Ser Arg Met Arg Thr Met Ala Ser Ala Ala	
50 55 60	

gcg ggt agt aac agc tgg gta cag gtg aaa aca cac cgc acc att ggc	240
Ala Gly Ser Asn Ser Trp Val Gln Val Lys Thr His Arg Thr Ile Gly	
65 70 75 80	

gat gcc gtc gct cat ctc aaa ggc cag ggc atg cag att ctg gca acc	288
Asp Ala Val Ala His Leu Lys Gly Gln Gly Met Gln Ile Leu Ala Thr	
85 90 95	

cat ctt tct gat aac gct gtc gat ttc cgc gaa att gat tac act cgc	336
His Leu Ser Asp Asn Ala Val Asp Phe Arg Glu Ile Asp Tyr Thr Arg	
100 105 110	

ccg acc tgc att ttg atg gga cag gag aaa acg ggc atc acg cag gaa	384
Pro Thr Cys Ile Leu Met Gly Gln Glu Lys Thr Gly Ile Thr Gln Glu	
115 120 125	

gca ttg gcc ctg gcg gat cag gac atc atc att ccg atg atc ggc atg	432
Ala Leu Ala Leu Ala Asp Gln Asp Ile Ile Ile Pro Met Ile Gly Met	
130 135 140	

gtg cag tcg ctg aat gtt tcc gtt gcc tca gcc ctc att ctt tac gaa	480
Val Gln Ser Leu Asn Val Ser Val Ala Ser Ala Leu Ile Leu Tyr Glu	
145 150 155 160	

gcc cag cgt cag cgg caa aat gca ggc atg tac ctg cgt gaa aac agc	528
Ala Gln Arg Gln Arg Gln Asn Ala Gly Met Tyr Leu Arg Glu Asn Ser	
165 170 175	

atg ttg ccg gaa gca gag caa caa cgc ctg ttg ttt gaa ggc ggc tat	576
Met Leu Pro Glu Ala Glu Gln Gln Arg Leu Leu Phe Glu Gly Gly Tyr	
180 185 190	
ccg gtg ctg gcg aaa gtc gca aaa cgc aaa ggc ctg cct tat ccc cac	624
Pro Val Leu Ala Lys Val Ala Lys Arg Lys Gly Leu Pro Tyr Pro His	
195 200 205	
gtc aat cag caa ggc gag atc gaa gct gat gcc gac tgg tgg gct act	672
Val Asn Gln Gln Gly Glu Ile Glu Ala Asp Ala Asp Trp Trp Ala Thr	
210 215 220	
atg cag gct gca ggg taa	690
Met Gln Ala Ala Gly *	
225	
<210> 200	
<211> 2082	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(2082)	
<400> 200	
atg aaa ggt cgc ctg tta gat gct gtc cca ctc agt tcc cta acg ggc	48
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly	
1 5 10 15	
gtt ggc gca gca ctt agt aac aaa ctg gcg aaa atc aac ctg cat acc	96
Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr	
20 25 30	
gtg cag gat cta ctc tta cac ctt ccc ctg cgc tac gaa gat cgc acc	144
Val Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr	
35 40 45	
cat ctc tac ccc atc gga gaa cta ctg ccg ggc gtt tat gcc acg gtg	192
His Leu Tyr Pro Ile Gly Glu Leu Leu Pro Gly Val Tyr Ala Thr Val	
50 55 60	
gaa ggc gaa gtg ctg aac tgc aat atc tcc ttc ggc ggt cgg cgg atg	240
Glu Gly Glu Val Leu Asn Cys Asn Ile Ser Phe Gly Gly Arg Arg Met	
65 70 75 80	
atg acc tgc cag atc agc gac ggt tcc ggc atc ctc acc atg cgc ttt	288
Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Ile Leu Thr Met Arg Phe	
85 90 95	
ttc aat ttc agc gcg gca atg aaa aat agc ctg gcg gcg ggc cgc cgt	336
Phe Asn Phe Ser Ala Ala Met Lys Asn Ser Leu Ala Ala Gly Arg Arg	
100 105 110	
gta ctg gct tat ggc gaa gca aag cgc ggt aaa tat ggt gcg gag atg	384

Val	Leu	Ala	Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Lys	Tyr	Gly	Ala	Glu	Met	
	115						120					125				
atc	cac	ccg	gaa	tac	cgc	gtg	cag	ggc	gat	ctc	agc	acg	cca	gaa	tta	432
Ile	His	Pro	Glu	Tyr	Arg	Val	Gln	Gly	Asp	Leu	Ser	Thr	Pro	Glu	Leu	
	130					135				140						
cag	gaa	acg	ctc	acg	ccg	gtt	tat	cca	aca	acg	gaa	ggc	gta	aag	cag	480
Gln	Glu	Thr	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Val	Lys	Gln	
	145				150					155					160	
gcc	acg	ctg	cgt	aaa	tta	acc	gac	cag	gcg	ctg	gat	ctg	ctc	gac	acc	528
Ala	Thr	Leu	Arg	Lys	Leu	Thr	Asp	Gln	Ala	Leu	Asp	Leu	Leu	Asp	Thr	
				165					170					175		
tgc	gcc	att	gaa	gaa	ctc	ctg	ccg	ccg	gaa	ctg	tca	caa	gga	atg	atg	576
Cys	Ala	Ile	Glu	Glu	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Gln	Gly	Met	Met	
		180						185					190			
acg	cta	ccg	gaa	gcg	ttg	cgc	act	ttg	cac	cgc	ccg	cca	ccg	acg	cta	624
Thr	Leu	Pro	Glu	Ala	Leu	Arg	Thr	Leu	His	Arg	Pro	Pro	Pro	Thr	Leu	
		195					200					205				
cag	ctt	agc	gat	ctg	gaa	acc	ggg	cag	cat	ccg	gcg	caa	cgt	cgt	ctg	672
Gln	Leu	Ser	Asp	Leu	Glu	Thr	Gly	Gln	His	Pro	Ala	Gln	Arg	Arg	Leu	
	210					215				220						
att	ctg	gaa	gaa	ctg	ctg	gcg	cac	aac	ctc	agc	atg	tta	gcc	tta	cgt	720
Ile	Leu	Glu	Glu	Leu	Leu	Ala	His	Asn	Leu	Ser	Met	Leu	Ala	Leu	Arg	
	225				230					235					240	
gcc	gga	gca	cag	cgt	ttt	cat	gcc	cag	ccg	ctg	agc	gcc	aat	gac	acg	768
Ala	Gly	Ala	Gln	Arg	Phe	His	Ala	Gln	Pro	Leu	Ser	Ala	Asn	Asp	Thr	
				245					250					255		
ctg	aaa	aat	aaa	ctc	ctc	gcc	gcc	tta	ccg	ttc	aag	cca	acg	ggc	gca	816
Leu	Lys	Asn	Lys	Leu	Leu	Ala	Ala	Leu	Pro	Phe	Lys	Pro	Thr	Gly	Ala	
			260					265					270			
cag	gca	cgc	gta	gtg	gcg	gag	atc	gag	cgc	gat	atg	gcg	ctg	gat	gtg	864
Gln	Ala	Arg	Val	Val	Ala	Glu	Ile	Glu	Arg	Asp	Met	Ala	Leu	Asp	Val	
		275					280					285				
ccg	atg	atg	cgt	ctg	gtg	cag	ggc	gat	gta	ggg	tcc	ggg	aaa	acg	ctg	912
Pro	Met	Met	Arg	Leu	Val	Gln	Gly	Asp	Val	Gly	Ser	Gly	Lys	Thr	Leu	
	290					295					300					
gtc	gcc	gcc	ctc	gcc	gcg	ttg	cgt	gcg	att	gcc	cac	ggc	aaa	cag	gta	960
Val	Ala	Ala	Leu	Ala	Ala	Leu	Arg	Ala	Ile	Ala	His	Gly	Lys	Gln	Val	
	305				310					315					320	
gca	ttg	atg	gca	cca	acc	gaa	tta	ctc	gcc	gag	cag	cac	gcc	aat	aac	1008
Ala	Leu	Met	Ala	Pro	Thr	Glu	Leu	Leu	Ala	Glu	Gln	His	Ala	Asn	Asn	
				325					330				335			
ttc	cgc	aac	tgg	ttt	gca	ccg	ctc	ggg	atc	gaa	gtg	ggc	tgg	ctc	gcc	1056
Phe	Arg	Asn	Trp	Phe	Ala	Pro	Leu	Gly	Ile	Glu	Val	Gly	Trp	Leu	Ala	

340						345						350						
ggt	aag	cag	aaa	ggt	aaa	gca	cgg	ctg	gca	cag	cag	gaa	gcc	atc	gcc	1104		
Gly	Lys	Gln	Lys	Gly	Lys	Ala	Arg	Leu	Ala	Gln	Gln	Glu	Ala	Ile	Ala			
355						360						365						
agc	ggt	cag	gtg	cag	atg	att	gtc	ggt	aca	cac	gcc	atc	ttc	cag	gaa	1152		
Ser	Gly	Gln	Val	Gln	Met	Ile	Val	Gly	Thr	His	Ala	Ile	Phe	Gln	Glu			
370						375						380						
cag	gtg	cag	ttt	aac	ggc	ctg	gcg	ctg	gtg	att	atc	gac	gaa	cag	cat	1200		
Gln	Val	Gln	Phe	Asn	Gly	Leu	Ala	Leu	Val	Ile	Ile	Asp	Glu	Gln	His			
385						390						395						400
cgt	ttt	ggc	gtg	cat	cag	cgt	ctg	gca	ttg	tgg	gag	aaa	ggc	cag	cag	1248		
Arg	Phe	Gly	Val	His	Gln	Arg	Leu	Ala	Leu	Trp	Glu	Lys	Gly	Gln	Gln			
405						410						415						
cag	ggc	ttc	cat	ccg	cat	cag	ttg	atc	atg	acc	gcc	acg	ccg	atc	ccc	1296		
Gln	Gly	Phe	His	Pro	His	Gln	Leu	Ile	Met	Thr	Ala	Thr	Pro	Ile	Pro			
420						425						430						
cgc	acg	ctg	gca	atg	act	gcg	tat	gcc	gat	ctc	gat	acc	tcg	gtg	ata	1344		
Arg	Thr	Leu	Ala	Met	Thr	Ala	Tyr	Ala	Asp	Leu	Asp	Thr	Ser	Val	Ile			
435						440						445						
gat	gag	ctg	ccg	cca	ggc	cgc	acg	cca	gtg	act	acg	gtc	gct	att	cct	1392		
Asp	Glu	Leu	Pro	Pro	Gly	Arg	Thr	Pro	Val	Thr	Thr	Val	Ala	Ile	Pro			
450						455						460						
gat	acc	cgc	cgt	acc	gac	atc	att	gac	cgc	gtg	cac	cac	gcc	tgc	ata	1440		
Asp	Thr	Arg	Arg	Thr	Asp	Ile	Ile	Asp	Arg	Val	His	His	Ala	Cys	Ile			
465						470						475						480
act	gaa	ggt	cgt	cag	gca	tac	tgg	gtt	tgt	acg	ttg	att	gaa	gag	tcg	1488		
Thr	Glu	Gly	Arg	Gln	Ala	Tyr	Trp	Val	Cys	Thr	Leu	Ile	Glu	Glu	Ser			
485						490						495						
gaa	ttg	ctg	gaa	gcg	cag	gcg	gcg	gaa	gct	acc	tgg	gaa	gag	ttg	aaa	1536		
Glu	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Glu	Ala	Thr	Trp	Glu	Glu	Leu	Lys			
500						505						510						
ctg	gcg	cta	cca	gag	ttg	aac	gtt	ggc	ctg	gta	cac	ggg	cgg	atg	aaa	1584		
Leu	Ala	Leu	Pro	Glu	Leu	Asn	Val	Gly	Leu	Val	His	Gly	Arg	Met	Lys			
515						520						525						
cct	gcc	gag	aaa	cag	gcg	gtg	atg	gcg	tcg	ttt	aaa	caa	ggt	gag	cta	1632		
Pro	Ala	Glu	Lys	Gln	Ala	Val	Met	Ala	Ser	Phe	Lys	Gln	Gly	Glu	Leu			
530						535						540						
cac	ctg	ctg	gtt	gcc	aca	acc	gtt	att	gaa	gtc	ggc	gtt	gat	gtg	cct	1680		
His	Leu	Leu	Val	Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Val	Asp	Val	Pro			
545						550						555						560
aac	gcc	agt	ctg	atg	att	atc	gaa	aac	ccg	gag	cgt	ctg	ggt	ctg	gcg	1728		
Asn	Ala	Ser	Leu	Met	Ile	Ile	Glu	Asn	Pro	Glu	Arg	Leu	Gly	Leu	Ala			
565						570						575						

cag tta cac cag ctg cgc ggg cgc gta ggt cgt ggc gcg gtg gct tct 1776
Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
580 585 590

cac tgc gtg ctg ctc tac aaa acg ccg ctt tct aaa acg gcg caa att 1824
His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Ile
595 600 605

cgc ctg caa gtg ctg cgc gac agt aac gac ggt ttt gtg att gcg caa 1872
Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
610 615 620

aaa gat ctg gag att cgc ggc cct ggc gaa ttg tta ggc acg cgt cag 1920
Lys Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
625 630 635 640

acg ggt aat gct gaa ttt aaa gtg gcg gat tta ctg cgc gat cag gcg 1968
Thr Gly Asn Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
645 650 655

atg atc ccg gaa gtt cag cgc ctg gca cgc cat att cac gaa cgt tac 2016
Met Ile Pro Glu Val Gln Arg Leu Ala Arg His Ile His Glu Arg Tyr
660 665 670

cca caa cag gca aaa gcc ctg ata gaa cgc tgg atg ccg gag acg gaa 2064
Pro Gln Gln Ala Lys Ala Leu Ile Glu Arg Trp Met Pro Glu Thr Glu
675 680 685

cgt tac tcg aat gcg taa 2082
Arg Tyr Ser Asn Ala *
690

<210> 201
<211> 1287
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1287)

<400> 201
atg aaa acc tct ctg ttt aaa agc ctt tac ttt cag gtc ctg aca gcg 48
Met Lys Thr Ser Leu Phe Lys Ser Leu Tyr Phe Gln Val Leu Thr Ala
1 5 10 15

ata gcc att ggt att ctc ctt ggc cat ttc tat cct gaa ata ggc gag 96
Ile Ala Ile Gly Ile Leu Leu Gly His Phe Tyr Pro Glu Ile Gly Glu
20 25 30

caa atg aaa ccg ctt ggc gac ggc ttc gtt aag ctc att aag atg atc 144
Gln Met Lys Pro Leu Gly Asp Gly Phe Val Lys Leu Ile Lys Met Ile
35 40 45

atc gct cct gtc atc ttt tgt acc gtc gta acg ggc att gcg ggc atg 192

Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met	
50						55					60					
gaa	agc	atg	aag	gcg	gtc	ggg	cgt	acc	ggc	gca	gtc	gca	ctg	ctt	tac	240
Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr	
65					70				75						80	
ttt	gaa	att	gtc	agt	acc	atc	gcg	ctg	att	att	ggg	ctt	atc	atc	gtt	288
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val	
				85					90					95		
aac	gtc	gtg	cag	cct	ggg	gcc	gga	atg	aac	gtc	gat	ccg	gca	acg	ctt	336
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu	
			100					105					110			
gat	gcg	aaa	gcg	gta	gcg	gtt	tac	gcc	gat	cag	gcg	aaa	gac	cag	ggc	384
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly	
		115					120					125				
att	gtc	gcc	ttc	att	atg	gat	gtc	atc	ccg	gcg	agc	gtc	att	ggc	gca	432
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala	
	130					135					140					
ttt	gcc	agc	ggg	aac	att	ctg	cag	gtg	ctg	ctg	ttt	gcc	gta	ctg	ttt	480
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe	
145					150				155						160	
ggg	ttt	gcg	ctc	cac	cgt	ctg	ggc	agc	aaa	ggc	caa	ctg	att	ttt	aac	528
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn	
				165				170						175		
gtc	atc	gaa	agt	ttc	tcg	cag	gtc	atc	ttc	ggc	atc	atc	aat	atg	atc	576
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile	
			180					185					190			
atg	cgt	ctg	gca	cct	att	ggg	gcg	ttc	ggg	gca	atg	gcg	ttt	acc	atc	624
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile	
		195				200						205				
ggg	aaa	tac	ggc	gtc	ggc	aca	ctg	gtg	caa	ctg	ggg	cag	ctg	att	atc	672
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile	
	210					215					220					
tgt	ttc	tac	att	acc	tgt	atc	ctg	ttt	gtg	gtg	ctg	gta	ttg	ggg	tca	720
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser	
225					230					235					240	
atc	gct	aaa	gcg	act	ggg	ttc	agt	atc	ttc	aaa	ttt	atc	cgc	tac	atc	768
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile	
				245					250					255		
cgt	gaa	gaa	ctg	ctg	att	gta	ctg	ggg	act	tca	tct	tcc	gag	tcg	gcg	816
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu									

cta	ccg	gta	att	tca	gcg	cag	ttt	ggc	gta	ccg	gcg	ggc	agt	acg	cag	144
Leu	Pro	Val	Ile	Ser	Ala	Gln	Phe	Gly	Val	Pro	Ala	Gly	Ser	Thr	Gln	
		35					40					45				
atg	acc	ctc	agt	act	tat	att	ctg	ggc	ttt	gcg	ttg	ggg	cag	tta	atc	192
Met	Thr	Leu	Ser	Thr	Tyr	Ile	Leu	Gly	Phe	Ala	Leu	Gly	Gln	Leu	Ile	
		50				55					60					
tac	ggg	ccg	atg	gca	gac	agc	ttc	ggg	cgt	aag	ccg	gtg	gtg	ctc	ggc	240
Tyr	Gly	Pro	Met	Ala	Asp	Ser	Phe	Gly	Arg	Lys	Pro	Val	Val	Leu	Gly	
		65			70					75					80	
ggt	acg	ctg	gtg	ttt	gcc	gcc	gcc	gcg	gtg	gcg	tgt	gcg	ttg	gca	aac	288
Gly	Thr	Leu	Val	Phe	Ala	Ala	Ala	Ala	Val	Ala	Cys	Ala	Leu	Ala	Asn	
				85					90					95	,	
acc	atc	gat	cag	ctg	att	gtg	atg	cgt	ttc	ttc	cac	ggg	ctg	gct	gcg	336
Thr	Ile	Asp	Gln	Leu	Ile	Val	Met	Arg	Phe	Phe	His	Gly	Leu	Ala	Ala	
			100					105					110			
gct	gcg	gcc	agc	gtg	gtc	att	aac	gcc	ctg	atg	cgc	gat	att	tac	ccg	384
Ala	Ala	Ala	Ser	Val	Val	Ile	Asn	Ala	Leu	Met	Arg	Asp	Ile	Tyr	Pro	
			115				120					125				
aaa	gaa	gag	ttc	tcg	cgg	atg	atg	tcg	ttt	gtc	atg	ctg	gtg	aca	acc	432
Lys	Glu	Glu	Phe	Ser	Arg	Met	Met	Ser	Phe	Val	Met	Leu	Val	Thr	Thr	
		130				135					140					
att	gca	ccg	ctg	atg	gca	ccg	ata	gtt	ggc	ggc	tgg	gtg	ctg	gtg	tgg	480
Ile	Ala	Pro	Leu	Met	Ala	Pro	Ile	Val	Gly	Gly	Trp	Val	Leu	Val	Trp	
		145			150					155					160	
ctg	agc	tgg	cat	tac	atc	ttc	tgg	atc	ctg	gca	tta	gcg	gcg	att	ctg	528
Leu	Ser	Trp	His	Tyr	Ile	Phe	Trp	Ile	Leu	Ala	Leu	Ala	Ala	Ile	Leu	
			165						170					175		
gct	tcg	gca	atg	att	ttc	ttc	ctg	att	aaa	gaa	acc	tta	cca	ccg	gag	576
Ala	Ser	Ala	Met	Ile	Phe	Phe	Leu	Ile	Lys	Glu	Thr	Leu	Pro	Pro	Glu	
			180					185				190				
cgt	cgt	cag	cca	ttt	cac	att	cgt	acc	act	att	ggt	aac	ttt	gcg	gcg	624
Arg	Arg	Gln	Pro	Phe	His	Ile	Arg	Thr	Thr	Ile	Gly	Asn	Phe	Ala	Ala	
		195					200					205				
ctg	ttc	cgc	cat	aaa	cgt	gtc	ctg	agc	tac	atg	ctt	gcc	agt	ggt	ttc	672
Leu	Phe	Arg	His	Lys	Arg	Val	Leu	Ser	Tyr	Met	Leu	Ala	Ser	Gly	Phe	
		210				215					220					
agc	ttt	gcc	ggg	atg	ttc	tca	ttc	tta	agc	gcc	gga	ccg	ttt	gtt	tat	720
Ser	Phe	Ala	Gly	Met	Phe	Ser	Phe	Leu	Ser	Ala	Gly	Pro	Phe	Val	Tyr	
		225			230					235					240	
att	gaa	att	aac	cac	gtc	gcg	ccg									

Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
260 265 270

gtc cgc cgc att ggc gcg tta aat atg ttc cgc tcg ggg ttg tgg ata 864
Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
275 280 285

caa ttt att atg gca gcg tgg atg gtc atc agt gcg ctg ctg ggg ctg 912
Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
290 295 300

gga ttt tgg tcg ctg gtg gtt ggc gtt gcg gcg ttt gtg ggc tgc gtg 960
Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
305 310 315 320

tcg atg gtg tca tcc aat gcg atg gcg gtc att ctt gat gag ttt ccc 1008
Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro
325 330 335

cat atg gcg gga acg gca tct tcg ctg gca gga acc ttc cgt ttt ggc 1056
His Met Ala Gly Thr Ala Ser Ser Leu Ala Gly Thr Phe Arg Phe Gly
340 345 350

ata ggg gca att gtt ggc gca ttg ctt tct ctt gcg acc ttt aac tct 1104
Ile Gly Ala Ile Val Gly Ala Leu Leu Ser Leu Ala Thr Phe Asn Ser
355 360 365

gca tgg ccg atg att tgg tca att gca ttc tgc gca acc agc tcc att 1152
Ala Trp Pro Met Ile Trp Ser Ile Ala Phe Cys Ala Thr Ser Ser Ile
370 375 380

ctc ttc tgt ctg tac gcc agt cgg ccg aaa aaa cgg tga 1191
Leu Phe Cys Leu Tyr Ala Ser Arg Pro Lys Lys Arg *
385 390 395

<210> 203
<211> 696
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(696)

<400> 203
atg cga ctt gat aaa ttt atc gca cag caa ctc ggc gtt agc cgt gct 48
Met Arg Leu Asp Lys Phe Ile Ala Gln Gln Leu Gly Val Ser Arg Ala
1 5 10 15

att gcc ggg cgt gaa atc cgc ggc aat cgt gtc acc gtc gat ggc gaa 96
Ile Ala Gly Arg Glu Ile Arg Gly Asn Arg Val Thr Val Asp Gly Glu
20 25 30

atc gtc cgt aat gca gcg ttc aaa ctg ctt cct gaa cat gat gtc gct 144
Ile Val Arg Asn Ala Ala Phe Lys Leu Leu Pro Glu His Asp Val Ala
35 40 45

[illegible]

atg Met 1	aaa Lys	aaa Lys	att Ile	gaa Glu 5	tgc Cys	gct Ala	tgc Cys	aat Asn	ttt Phe 10	ctg Leu	atg Met	gat Asp	aaa Lys	gat Asp 15	gcg Ala	48
cag Gln	ggg Gly	tat Tyr	atc Ile 20	gac Asp	ctg Leu	tct Ser	gat Asp	ttg Leu 25	gat Asp	tta Leu	aca Thr	agt Ser	tgt Cys 30	cat His	ttt Phe	96
aaa Lys	ggt Gly	gac Asp 35	gtt Val	ata Ile	tcg Ser	aag Lys	gtg Val 40	tct Ser	ttt Phe	tta Leu	tca Ser	tca Ser 45	aat Asn	cta Leu	caa Gln	144
cat His	gta Val 50	aca Thr	ttc Phe	gaa Glu	tgt Cys	aaa Lys 55	gaa Glu	att Ile	ggg Gly	gat Asp	tgc Cys 60	aat Asn	ttt Phe	act Thr	act Thr	192
gca Ala 65	ata Ile	gtt Val	gat Asp	aat Asn	gtc Val 70	ata Ile	ttt Phe	aga Arg	tgt Cys 75	cga Arg	cgt Arg	tta Leu	cac His	aat Asn	gtg Val 80	240
att Ile	ttt Phe	atc Ile	aaa Lys 85	gcg Ala	agt Ser	ggg Gly	gaa Glu	tgt Cys	gtc Val 90	gat Asp	ttc Phe	agc Ser	aaa Lys	aat Asn 95	att Ile	288
ctt Leu	gat Asp	aca Thr 100	gtt Val	gac Asp	ttc Phe	tcg Ser	cag Gln 105	agt Ser	caa Gln	ctt Leu	ggg Gly	cat His 110	agt Ser	aat Asn	ttt Phe	336
cgc Arg	gaa Glu 115	tgt Cys	cag Gln	att Ile	aga Arg	aat Asn	tca Ser 120	aac Asn	ttc Phe	gat Asp	aat Asn	tgt Cys 125	tat Tyr	ctt Leu	tac Tyr	384
gct Ala 130	tcg Ser	cac His	ttc Phe	acc Thr	aga Arg	gca Ala 135	gag Glu	ttt Phe	ctg Leu	tct Ser	gcc Ala 140	aaa Lys	gaa Glu	ata Ile	tca Ser	432
ttt Phe 145	att Ile	aaa Lys	tcg Ser	aat Asn	ttg Leu 150	aca Thr	gct Ala	gtt Val	atg Met 155	ttt Phe	gat Asp	tat Tyr	gtg Val	cga Arg	atg Met 160	480
tcg Ser	aca Thr	ggg Gly	aat Asn 165	ttt Phe	aaa Lys	gat Asp	tgc Cys	att Ile	aca Thr 170	gaa Glu	caa Gln	ttg Leu	gaa Glu	tta Leu 175	act Thr	528
att Ile	gat Asp	tat Tyr 180	tca Ser	gat Asp	ata Ile	ttt Phe	tgg Trp 185	aat Asn	gaa Glu	gat Asp	ctc Leu	gat Asp	ggg Gly 190	tat Tyr	atc Ile	576
aat Asn	aac Asn 195	att Ile	ata Ile	aaa Lys	atg Met	att Ile	gat Asp 200	aca Thr	ttg Leu	cca Pro	gat Asp	aat Asn 205	gca Ala	atg Met	ata Ile	624
ttg Leu	aaa Lys	tcc Ser	gtt Val	ctg Leu	gcc Ala	gta Val	aaa Lys	ctg Leu	gtg Val	atg Met	caa Gln	tta Leu	aaa Lys	ata Ile	ctt Leu	672

210				215				220									
aat	att	gtt	aat	aaa	aac	ttt	att	gag	aat	atg	aag	aaa	ata	ttt	agc	720	
Asn	Ile	Val	Asn	Lys	Asn	Phe	Ile	Glu	Asn	Met	Lys	Lys	Ile	Phe	Ser		
225				230				235				240					
cat	tgt	cct	tat	ata	aaa	gat	ccc	att	ata	cgc	agt	tat	atc	cat	tct	768	
His	Cys	Pro	Tyr	Ile	Lys	Asp	Pro	Ile	Ile	Arg	Ser	Tyr	Ile	His	Ser		
245				250				255									
gat	gaa	gat	aac	aag	ttc	gat	gat	ttt	atg	cgt	caa	cat	cga	ttc	agt	816	
Asp	Glu	Asp	Asn	Lys	Phe	Asp	Asp	Phe	Met	Arg	Gln	His	Arg	Phe	Ser		
260				265				270									
gag	gtg	aat	ttc	gat	acc	caa	cag	atg	atc	gat	ttt	att	aac	aga	ttt	864	
Glu	Val	Asn	Phe	Asp	Thr	Gln	Gln	Met	Ile	Asp	Phe	Ile	Asn	Arg	Phe		
275				280				285									
aat	acg	aat	aaa	tgg	cta	att	gat	aaa	aat	aac	aat	ttt	ttt	atc	caa	912	
Asn	Thr	Asn	Lys	Trp	Leu	Ile	Asp	Lys	Asn	Asn	Asn	Phe	Phe	Ile	Gln		
290				295				300									
ctt	atc	gat	cag	gcc	tta	cga	tca	acg	gat	gat	atg	atc	aaa	gca	aat	960	
Leu	Ile	Asp	Gln	Ala	Leu	Arg	Ser	Thr	Asp	Asp	Met	Ile	Lys	Ala	Asn		
305				310				315				320					
gtt	tgg	cat	ctt	tat	aaa	gag	tgg	att	cgt	agt	gat	gat	gtt	tca	cct	1008	
Val	Trp	His	Leu	Tyr	Lys	Glu	Trp	Ile	Arg	Ser	Asp	Asp	Val	Ser	Pro		
325				330				335									
ata	ttt	ata	gaa	act	gaa	gat	aat	tta	aga	acc	ttt	aac	acg	aat	gaa	1056	
Ile	Phe	Ile	Glu	Thr	Glu	Asp	Asn	Leu	Arg	Thr	Phe	Asn	Thr	Asn	Glu		
340				345				350									
tta	aca	cga	aac	gat	aat	atc	ttt	atc	ctg	ttc	tcc	tca	gtc	gat	gat	1104	
Leu	Thr	Arg	Asn	Asp	Asn	Ile	Phe	Ile	Leu	Phe	Ser	Ser	Val	Asp	Asp		
355				360				365									
ggg	cca	gtt	atg	gtg	gta	agc	tcc	cag	cgc	tta	cat	gat	atg	ttg	aat	1152	
Gly	Pro	Val	Met	Val	Val	Ser	Ser	Gln	Arg	Leu	His	Asp	Met	Leu	Asn		
370				375				380									
cct	aca	aaa	gat	acc	aat	tgg	aat	tcc	acg	tat	atc	tac	aaa	tcc	aga	1200	
Pro	Thr	Lys	Asp	Thr	Asn	Trp	Asn	Ser	Thr	Tyr	Ile	Tyr	Lys	Ser	Arg		
385				390				395				400					
cat	gag	atg	ttg	cct	gtt	aat	ctt	act	cag	gaa	aca	ctt	ttc	agc	tcc	1248	
His	Glu	Met	Leu	Pro	Val	Asn	Leu	Thr	Gln	Glu	Thr	Leu	Phe	Ser	Ser		
405				410				415									
aaa	tct	cat	ggt	aaa	tat	gcg	ctt	ttc	ccc	att	ttt	act	gcg	agt	tgg	1296	
Lys	Ser	His	Gly	Lys	Tyr	Ala	Leu	Phe	Pro	Ile	Phe	Thr	Ala	Ser	Trp		
420				425				430									
cga	gct	cat	cgt	ata	atg	aat	aag	ggt	gtt	taa							1329
Arg	Ala	His	Arg	Ile	Met	Asn	Lys	Gly	Val	*							
435				440													

<210> 205
 <211> 717
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(717)

<400> 205

gtg gga cgt aaa tgg gcc aat att gtt gct aaa aaa acg gct aaa gac	48
Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp	
1 5 10 15	
ggt gca acg tct aaa att tat gca aaa ttc ggt gta gaa atc tat gct	96
Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala	
20 25 30	
gct gct aaa caa ggt gaa ccc gat cca gaa tta aac aca tct tta aaa	144
Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys	
35 40 45	
ttc gtt att gaa cgt gca aag cag gca caa gtt cca aag cac gtt att	192
Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile	
50 55 60	
gat aaa gca att gat aaa gcc aaa ggc ggc gga gat gaa acg ttc gtg	240
Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val	
65 70 75 80	
cag gga cgt tat gaa ggc ttt ggt cct aat ggc tca atg att atc gcc	288
Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala	
85 90 95	
gag aca ttg act tca aat gtt aac cgt acg att gct aac gtt cgc aca	336
Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr	
100 105 110	
att ttc aat aaa aaa ggc ggc aat atc gga gcg gca ggt tct gtc agc	384
Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser	
115 120 125	
tat atg ttt gac aat acg ggt gtg att gta ttt aaa ggg aca gac cct	432
Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro	
130 135 140	
gac cat att ttt gaa att tta ctt gaa gct gaa gtt gat gtt cgt gat	480
Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp	
145 150 155 160	
gtg act gaa gaa gaa ggt aac att gtt att tat act gaa cct act gac	528
Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp	
165 170 175	
ctt cat aaa gga atc gcg gct cta aaa gca gct gga atc act gag ttc	576

Leu His Lys Gly Ile Ala Ala Leu Lys Ala Ala Gly Ile Thr Glu Phe
180 185 190

tca aca aca gaa tta gaa atg att gct caa tct gaa gtt gag ctt tcc 624
Ser Thr Thr Glu Leu Glu Met Ile Ala Gln Ser Glu Val Glu Leu Ser
195 200 205

cca gaa gat tta gaa atc ttt gaa ggg ctt gtt gat gcc ctt gaa gat 672
Pro Glu Asp Leu Glu Ile Phe Glu Gly Leu Val Asp Ala Leu Glu Asp
210 215 220

gac gac gat gta caa aaa gtt tat cat aac gtc gca aat ctc taa 717
Asp Asp Asp Val Gln Lys Val Tyr His Asn Val Ala Asn Leu *
225 230 235

<210> 206

<211> 786

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(786)

<400> 206

gtg gtt ctt atg tcc gaa aca aaa aac gaa ctt gaa gac ctg ctg gaa 48
Met Val Leu Met Ser Glu Thr Lys Asn Glu Leu Glu Asp Leu Leu Glu
1 5 10 15

aaa gca gca act gaa ccg gcg cac cgc ccg gcc ttt ttc cgt act cta 96
Lys Ala Ala Thr Glu Pro Ala His Arg Pro Ala Phe Phe Arg Thr Leu
20 25 30

ctg gaa tcc acc gtc tgg gtg cct ggt acg gcg gcg cag ggc gag gct 144
Leu Glu Ser Thr Val Trp Val Pro Gly Thr Ala Ala Gln Gly Glu Ala
35 40 45

gtg gtt gaa gat agc gcg ctt gat tta cag cac tgg gaa aaa gaa gac 192
Val Val Glu Asp Ser Ala Leu Asp Leu Gln His Trp Glu Lys Glu Asp
50 55 60

ggc acc agc gtc att cct ttt ttc acc tcg tta gaa gca ctt caa cag 240
Gly Thr Ser Val Ile Pro Phe Phe Thr Ser Leu Glu Ala Leu Gln Gln
65 70 75 80

gcg gtt gaa gac gaa cag gca ttt gtc gta atg ccc gtt cgc acg ctg 288
Ala Val Glu Asp Glu Gln Ala Phe Val Val Met Pro Val Arg Thr Leu
85 90 95

ttt gag atg aca ctt ggc gaa acg ctc ttc ctt aat gcc aaa ctg cca 336
Phe Glu Met Thr Leu Gly Glu Thr Leu Phe Leu Asn Ala Lys Leu Pro
100 105 110

acc ggt aaa gaa ttt atg ccg cgt gaa atc agt ttg ttg att ggt gaa 384
Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu

115						120						125						
gag	gga	aat	ccg	ctg	agc	agc	cag	gaa	atc	ctg	gaa	ggc	ggt	gaa	tcg	432		
Glu	Gly	Asn	Pro	Leu	Ser	Ser	Gln	Glu	Ile	Leu	Glu	Gly	Gly	Glu	Ser			
130					135					140								
ctg	ata	tta	tcg	gaa	gtc	gca	gag	ccg	cca	gca	caa	atg	att	gat	tca	480		
Leu	Ile	Leu	Ser	Glu	Val	Ala	Glu	Pro	Pro	Ala	Gln	Met	Ile	Asp	Ser			
145					150					155					160			
ctc	acc	acc	tta	ttt	aaa	acc	att	aag	ccg	gtg	aag	cgt	gct	ttt	att	528		
Leu	Thr	Thr	Leu	Phe	Lys	Thr	Ile	Lys	Pro	Val	Lys	Arg	Ala	Phe	Ile			
165					170					175								
tgt	tca	att	aaa	gag	aac	gaa	gag	gca	cag	cct	aat	tta	ctt	att	ggc	576		
Cys	Ser	Ile	Lys	Glu	Asn	Glu	Glu	Ala	Gln	Pro	Asn	Leu	Leu	Ile	Gly			
180					185					190								
att	gaa	gcc	gat	ggt	gat	atc	gaa	gaa	att	att	cag	gcg	acg	gga	agt	624		
Ile	Glu	Ala	Asp	Gly	Asp	Ile	Glu	Glu	Ile	Ile	Gln	Ala	Thr	Gly	Ser			
195					200					205								
gta	gcg	acc	gat	aca	tta	cct	ggc	gat	gaa	cca	atc	gat	att	tgt	cag	672		
Val	Ala	Thr	Asp	Thr	Leu	Pro	Gly	Asp	Glu	Pro	Ile	Asp	Ile	Cys	Gln			
210					215					220								
gtg	aaa	aaa	ggg	gaa	aaa	gga	att	agc	cac	ttt	att	acc	gaa	cat	att	720		
Val	Lys	Lys	Gly	Glu	Lys	Gly	Ile	Ser	His	Phe	Ile	Thr	Glu	His	Ile			
225					230					235					240			
gcg	cca	ttc	tat	gaa	cgt	cgc	tgg	ggt	ggt	ttt	ttg	cgt	gac	ttt	aaa	768		
Ala	Pro	Phe	Tyr	Glu	Arg	Arg	Trp	Gly	Gly	Phe	Leu	Arg	Asp	Phe	Lys			
245					250					255								
cag	aat	cgg	ata	atc	taa											786		
Gln	Asn	Arg	Ile	Ile	*													
260																		

<210> 207

<211> 1266

<212> DNA

<213> Escherichia coli

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (1266)$

<400> 207

atg ctc acg aaa aag aaa tgg gcg tta ttt agt cta tta aca ctg tgt 48
Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys
1 5 10 15

ggc ggt aca att tat aaa tta ccg tcg ctg aaa gat gcg ttt tat atc 96
Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile
20 25 30

ccg atg cag gaa tat ttc cat ttg acc aat ggt caa att ggt aat gct	144
Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala	
35 40 45	
atg tcg gta aac tca ttt gtc acc aca gtg ggc ttt ttt ctg tct att	192
Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile	
50 55 60	
tat ttt gcc gat aaa cta ccg cgc aga tac acc atg tca ttc tca ctc	240
Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu	
65 70 75 80	
att gcg aca gga tta ctg ggt gtt tat ttg acg aca atg ccg ggg tat	288
Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr	
85 90 95	
tgg ggc atc ctc ttt gtc tgg gcg cta ttt ggc gtt act tgc gac atg	336
Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met	
100 105 110	
atg aac tgg ccg gtc ttg ctc aag tcg gta agt cga ttg ggc aat agc	384
Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser	
115 120 125	
gaa caa caa ggt cgg ttg ttt ggc ttc ttc gaa aca ggg cgt ggc att	432
Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile	
130 135 140	
gtc gat acc gtg gtg gca ttt tct gcg ttg gca gta ttt acc tgg ttt	480
Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe	
145 150 155 160	
ggc agt ggc tta tta ggt ttt aaa gca ggc atc tgg ttc tat tcc ctt	528
Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu	
165 170 175	
att gtg att gcc gta ggc att att att ttc ttt gtc ctg aat gac aaa	576
Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys	
180 185 190	
gaa gag gca ccg tcc gtt gag gtg aaa aaa gaa gac gga gca tcg aaa	624
Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys	
195 200 205	
aac acc agt atg acc tcg gtg ctg aaa gac aaa act atc tgg ctt atc	672
Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile	
210 215 220	
gct ttt aac gtc ttc ttc gtt tac gcg gtt tac tgt ggc ctg aca ttc	720
Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe	
225 230 235 240	
ttc att cca ttc ctg aaa aac atc tat cta ttg ccc gtt gcg ctg gtg	768
Phe Ile Pro Phe Leu Lys Asn Ile Tyr Leu Leu Pro Val Ala Leu Val	
245 250 255	
ggg gct tac ggc atc att aac caa tac tgt ctg aaa atg att ggt gga	816

gcg ccc ttt ctc ctt ttt ctt gca gcg tgg gga gca gat aaa ctc tgg	96
Ala Pro Phe Leu Leu Phe Leu Ala Ala Trp Gly Ala Asp Lys Leu Trp	
20 25 30	
cct cta ccg ctg cat gaa gtc aat ccc gca cga gtg gtc gtg gcg cag	144
Pro Leu Pro Leu His Glu Val Asn Pro Ala Arg Val Val Val Ala Gln	
35 40 45	
gat ggt acg ccg ctc tgg cgc ttc gcc gat gct gac ggc atc tgg cgt	192
Asp Gly Thr Pro Leu Trp Arg Phe Ala Asp Ala Asp Gly Ile Trp Arg	
50 55 60	
tat ccg gta aca atc gaa gat gtt tct cca cgt tac ctt gaa gcg ctg	240
Tyr Pro Val Thr Ile Glu Asp Val Ser Pro Arg Tyr Leu Glu Ala Leu	
65 70 75 80	
atc aat tat gaa gat cgc tgg ttc tgg aag cat ccg ggg gtg aat cca	288
Ile Asn Tyr Glu Asp Arg Trp Phe Trp Lys His Pro Gly Val Asn Pro	
85 90 95	
ttc tcg gtg gcg cgc gca gca tgg caa gat ctc act tcg gga ccg gtt	336
Phe Ser Val Ala Arg Ala Ala Trp Gln Asp Leu Thr Ser Gly Arg Val	
100 105 110	
att tcc ggt ggc agc acg ctc act atg cag gtt gct cgt ctg ctt gat	384
Ile Ser Gly Gly Ser Thr Leu Thr Met Gln Val Ala Arg Leu Leu Asp	
115 120 125	
cct cac ccc aaa aca ttt ggc ggc aaa att cgc cag ctc tgg cgc gcg	432
Pro His Pro Lys Thr Phe Gly Gly Lys Ile Arg Gln Leu Trp Arg Ala	
130 135 140	
ttg caa ctg gaa tgg cat ctg tct aag cgt gaa att ctg acc ttg tat	480
Leu Gln Leu Glu Trp His Leu Ser Lys Arg Glu Ile Leu Thr Leu Tyr	
145 150 155 160	
ctt aac cgc gct ccg ttt ggc ggt acg ttg cag ggg atc ggt gcg gca	528
Leu Asn Arg Ala Pro Phe Gly Gly Thr Leu Gln Gly Ile Gly Ala Ala	
165 170 175	
agt tgg gct tat ctc gga aaa tcg cct gcg aat tta agc tat tcc gag	576
Ser Trp Ala Tyr Leu Gly Lys Ser Pro Ala Asn Leu Ser Tyr Ser Glu	
180 185 190	
gcg gca atg ctg gcg gtt ttg ccg caa gcg ccc agc cgt ctt cgc ccg	624
Ala Ala Met Leu Ala Val Leu Pro Gln Ala Pro Ser Arg Leu Arg Pro	
195 200 205	
gat cgt tgg ccg gag cgt gcc gaa gcc gcg cgt aat aaa gtg ctc gaa	672
Asp Arg Trp Pro Glu Arg Ala Glu Ala Ala Arg Asn Lys Val Leu Glu	
210 215 220	
cgg atg gcc gtg caa ggt gtg tgg tcc cgt gag cag gta aaa gag tca	720
Arg Met Ala Val Gln Gly Val Trp Ser Arg Glu Gln Val Lys Glu Ser	
225 230 235 240	

agg	gaa	gaa	ccc	atc	tgg	ctg	gcc	ccc	cga	caa	atg	ccg	caa	ctg	gca	768
Arg	Glu	Glu	Pro	Ile	Trp	Leu	Ala	Pro	Arg	Gln	Met	Pro	Gln	Leu	Ala	
			245						250					255		
ccg	ctg	ttt	tcg	cgc	atg	atg	ctc	ggt	aaa	agc	aaa	agc	gac	aaa	atc	816
Pro	Leu	Phe	Ser	Arg	Met	Met	Leu	Gly	Lys	Ser	Lys	Ser	Asp	Lys	Ile	
			260					265					270			
act	act	acg	ttg	gat	gcc	ggt	ctt	caa	cga	cgt	ctg	gaa	gaa	ctg	gcg	864
Thr	Thr	Thr	Leu	Asp	Ala	Gly	Leu	Gln	Arg	Arg	Leu	Glu	Glu	Leu	Ala	
		275					280					285				
caa	aac	tgg	aaa	ggg	cgg	ttg	cca	ccg	cgc	agc	tca	ctg	gcg	atg	atc	912
Gln	Asn	Trp	Lys	Gly	Arg	Leu	Pro	Pro	Arg	Ser	Ser	Leu	Ala	Met	Ile	
		290				295					300					
gtg	gtt	gat	cat	acc	gat	atg	cgt	gtt	cgc	ggc	tgg	gtg	gga	tcg	gtt	960
Val	Val	Asp	His	Thr	Asp	Met	Arg	Val	Arg	Gly	Trp	Val	Gly	Ser	Val	
305					310					315					320	
gat	ctc	aac	gat	gat	tca	cgc	ttt	ggt	cat	gtt	gat	atg	gtc	aat	tcg	1008
Asp	Leu	Asn	Asp	Asp	Ser	Arg	Phe	Gly	His	Val	Asp	Met	Val	Asn	Ser	
			325						330					335		
atc	cga	tcg	cca	gga	tca	gtg	ctc	aaa	ccg	ttt	gtt	tat	ggg	ctg	gcg	1056
Ile	Arg	Ser	Pro	Gly	Ser	Val	Leu	Lys	Pro	Phe	Val	Tyr	Gly	Leu	Ala	
			340					345					350			
ctg	gat	gaa	ggc	ttg	atc	cac	ccg	gca	tca	ctg	ctg	caa	gac	gtc	ccc	1104
Leu	Asp	Glu	Gly	Leu	Ile	His	Pro	Ala	Ser	Leu	Leu	Gln	Asp	Val	Pro	
		355					360					365				
cgg	cgc	acc	ggt	gat	tat	cga	cca	ggt	aac	ttt	gat	agc	ggg	ttt	cat	1152
Arg	Arg	Thr	Gly	Asp	Tyr	Arg	Pro	Gly	Asn	Phe	Asp	Ser	Gly	Phe	His	
		370				375					380					
ggc	ccg	atc	agc	atg	agc	gag	gcg	ctg	gtg	cgc	tcg	ctg	aac	tta	cct	1200
Gly	Pro	Ile	Ser	Met	Ser	Glu	Ala	Leu	Val	Arg	Ser	Leu	Asn	Leu	Pro	
385					390					395				400		
gct	gtg	cag	gtg	ctg	gaa	gcc	tat	gga	ccg	aaa	cgg	ttt	gcg	gca	aag	1248
Ala	Val	Gln	Val	Leu	Glu	Ala	Tyr	Gly	Pro	Lys	Arg	Phe	Ala	Ala	Lys	
			405					410					415			
tta	cgc	aat	gtt	gga	ttg	ccg	tta	tat	ttg	ccc	aac	ggg	gct	gcg	ccg	1296
Leu	Arg	Asn	Val	Gly	Leu	Pro	Leu	Tyr	Leu	Pro	Asn	Gly	Ala	Ala	Pro	
			420				425					430				
aat	ctt	tca	ctc	att	ctc	ggc	ggc	gct	ggg	gca	aaa	ctg	gaa	gat	atg	1344
Asn	Leu	Ser	Leu	Ile	Leu	Gly	Gly	Ala	Gly	Ala	Lys	Leu	Glu	Asp	Met	
		435				440						445				
gcg	gca	gcg	tat	acc	gcg											

690	695	700	
cgt tta ccg ggc gca gcg gaa gcg act ttg ccg ttg caa tca agt gga			2160
Arg Leu Pro Gly Ala Ala Glu Ala Thr Leu Pro Leu Gln Ser Ser Gly			
705	710	715	720
ggg gca ggt gaa cgc tgg tgg ttt ctg aat ggc gaa ccg tta act gaa			2208
Gly Ala Gly Glu Arg Trp Trp Phe Leu Asn Gly Glu Pro Leu Thr Glu			
	725	730	735
cgc ggg cgc aac gtg acc ctg cat ttg acg gat aaa ggt gat tat caa			2256
Arg Gly Arg Asn Val Thr Leu His Leu Thr Asp Lys Gly Asp Tyr Gln			
	740	745	750
ttg ctg gtg atg gat gac gtg ggg caa atc gcg aca gtg aaa ttt gtc			2304
Leu Leu Val Met Asp Asp Val Gly Gln Ile Ala Thr Val Lys Phe Val			
	755	760	765
atg caa tag			2313
Met Gln *			
770			
<210> 209			
<211> 4962			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(4962)			
<400> 209			
atg aaa aag tta cgc gta gcc gcc tgc atg cta atg ctg gcg ctg gca			48
Met Lys Lys Leu Arg Val Ala Ala Cys Met Leu Met Leu Ala Leu Ala			
1	5	10	15
ggg tgc gac aac aac gat aac gcg cca aca gcg gtg aaa aaa gat gcg			96
Gly Cys Asp Asn Asn Asp Asn Ala Pro Thr Ala Val Lys Lys Asp Ala			
	20	25	30
cct tct gaa gtt act aaa gcg gcc tct tca gaa aac gcg agt tca gca			144
Pro Ser Glu Val Thr Lys Ala Ala Ser Ser Glu Asn Ala Ser Ser Ala			
	35	40	45
aaa ctc tcc gtg ccg gag aga caa aaa ctg gcc caa cag agt gcc ggt			192
Lys Leu Ser Val Pro Glu Arg Gln Lys Leu Ala Gln Gln Ser Ala Gly			
	50	55	60
aag gtg ctg aca ttg ctg gat ctc tct gaa gtc caa ctt gat ggt gca			240
Lys Val Leu Thr Leu Leu Asp Leu Ser Glu Val Gln Leu Asp Gly Ala			
	65	70	75
gcc acg ctg gtg ctg acg ttc tcc atc cct ctc gac ccg gat cag gat			288
Ala Thr Leu Val Leu Thr Phe Ser Ile Pro Leu Asp Pro Asp Gln Asp			
	85	90	95

ttc tca cgc gtt att cat gtc gtc gat aaa aaa agc ggc aaa gtg gat	336
Phe Ser Arg Val Ile His Val Val Asp Lys Lys Ser Gly Lys Val Asp	
100 105 110	
ggt gcc tgg gag ctg tca gat aat ctt aaa gag tta cgt tta cgc cac	384
Gly Ala Trp Glu Leu Ser Asp Asn Leu Lys Glu Leu Arg Leu Arg His	
115 120 125	
ctc gaa ccg aaa cgt gat ttg atc gtt act att ggc aag gag gtc aaa	432
Leu Glu Pro Lys Arg Asp Leu Ile Val Thr Ile Gly Lys Glu Val Lys	
130 135 140	
gca ctc aac aac gca acc ttc agt aaa gat tac gaa aaa act ata act	480
Ala Leu Asn Asn Ala Thr Phe Ser Lys Asp Tyr Glu Lys Thr Ile Thr	
145 150 155 160	
acc cgc gac atc caa ccc agc gtc ggt ttt gcc agc cgt ggt tcg ctg	528
Thr Arg Asp Ile Gln Pro Ser Val Gly Phe Ala Ser Arg Gly Ser Leu	
165 170 175	
ctg cct ggc aaa gtc gtt gaa ggg ctg ccg gta atg gcg ctc aac gtt	576
Leu Pro Gly Lys Val Val Glu Gly Leu Pro Val Met Ala Leu Asn Val	
180 185 190	
aat aat gtc gat gtt aac ttc ttc cgc gtt aag cca gaa tct ctg cca	624
Asn Asn Val Asp Val Asn Phe Phe Arg Val Lys Pro Glu Ser Leu Pro	
195 200 205	
gca ttc att agc caa tgg gaa tac cgc aat tcg ctg gcg aac tgg cag	672
Ala Phe Ile Ser Gln Trp Glu Tyr Arg Asn Ser Leu Ala Asn Trp Gln	
210 215 220	
tca gac aaa ctg ctg cag atg gcg gat ctg gtc tac acc gga cgg ttt	720
Ser Asp Lys Leu Leu Gln Met Ala Asp Leu Val Tyr Thr Gly Arg Phe	
225 230 235 240	
gat ctc aat cct gcg cgt aac acc cgt gaa aaa tta ttg ctg ccg ctg	768
Asp Leu Asn Pro Ala Arg Asn Thr Arg Glu Lys Leu Leu Leu Pro Leu	
245 250 255	
ggc gat atc aaa ccg ctt cag cag gcg ggc gtg tat ctg gct gtg atg	816
Gly Asp Ile Lys Pro Leu Gln Gln Ala Gly Val Tyr Leu Ala Val Met	
260 265 270	
aat cag gct gga cgt tac gat tac agt aat ccc gcg acg ctg ttt acg	864
Asn Gln Ala Gly Arg Tyr Asp Tyr Ser Asn Pro Ala Thr Leu Phe Thr	
275 280 285	
tta agt gat atc ggc gtt tca gct cac cgt tat cac aat cgt ctg gat	912
Leu Ser Asp Ile Gly Val Ser Ala His Arg Tyr His Asn Arg Leu Asp	
290 295 300	
atc ttt acc caa agt ctg gaa aac ggc gcg gcc cag caa gga att gaa	960
Ile Phe Thr Gln Ser Leu Glu Asn Gly Ala Ala Gln Gln Gly Ile Glu	
305 310 315 320	
gtc tct tta tta aat gag aaa ggg cag act ctg act cag gca acc agt	1008

Val Ser Leu Leu Asn Glu Lys Gly Gln Thr Leu Thr Gln Ala Thr Ser	
325 330 335	
gac gct cag ggg cat gtg cag ctg gaa aat gat aaa aac gcg gca tta	1056
Asp Ala Gln Gly His Val Gln Leu Glu Asn Asp Lys Asn Ala Ala Leu	
340 345 350	
ctg ttg gcg cgt aaa gac ggt cag aca acg cta ctc gat tta aaa ctt	1104
Leu Leu Ala Arg Lys Asp Gly Gln Thr Thr Leu Leu Asp Leu Lys Leu	
355 360 365	
ccg gcg ctg gac tta gca gaa ttt aac att gct ggc gcg cca ggc tat	1152
Pro Ala Leu Asp Leu Ala Glu Phe Asn Ile Ala Gly Ala Pro Gly Tyr	
370 375 380	
agc aaa cag ttt ttc atg ttt ggc cca cgc gat ctt tat cgc cca ggt	1200
Ser Lys Gln Phe Phe Met Phe Gly Pro Arg Asp Leu Tyr Arg Pro Gly	
385 390 395 400	
gaa acg gta atc ctc aat ggt ttg ctg cgt gat gca gac ggt aaa gcg	1248
Glu Thr Val Ile Leu Asn Gly Leu Leu Arg Asp Ala Asp Gly Lys Ala	
405 410 415	
ttg ccc aat caa ccc atc aag tta gac gtg att aaa ccc gat ggg cag	1296
Leu Pro Asn Gln Pro Ile Lys Leu Asp Val Ile Lys Pro Asp Gly Gln	
420 425 430	
gta ctc agg agc gtc gtt agt cag ccg gag aat ggc ctc tac cac ttt	1344
Val Leu Arg Ser Val Val Ser Gln Pro Glu Asn Gly Leu Tyr His Phe	
435 440 445	
acc tgg cca ctc gat agc aat gcg gca acc ggt atg tgg cat att cgc	1392
Thr Trp Pro Leu Asp Ser Asn Ala Ala Thr Gly Met Trp His Ile Arg	
450 455 460	
gct aac acg ggc gat aat cag tat cgg atg tgg gat ttc cac gtc gaa	1440
Ala Asn Thr Gly Asp Asn Gln Tyr Arg Met Trp Asp Phe His Val Glu	
465 470 475 480	
gat ttt atg cca gag cgc atg gcg ctg aat ctg acc ggt gag aaa acc	1488
Asp Phe Met Pro Glu Arg Met Ala Leu Asn Leu Thr Gly Glu Lys Thr	
485 490 495	
ccg cta acg ccg aaa gat gaa gtg aaa ttc tcc gtg gtg ggg tac tac	1536
Pro Leu Thr Pro Lys Asp Glu Val Lys Phe Ser Val Val Gly Tyr Tyr	
500 505 510	
ctg tat ggt gca cct gct aat ggt aat act ttg caa ggg caa ctt ttc	1584
Leu Tyr Gly Ala Pro Ala Asn Gly Asn Thr Leu Gln Gly Gln Leu Phe	
515 520 525	
ctg cgc cca ctg cgt gaa gct gtg tca gcc tta cct ggt ttt gaa ttc	1632
Leu Arg Pro Leu Arg Glu Ala Val Ser Ala Leu Pro Gly Phe Glu Phe	
530 535 540	
ggc gat ata gct gcc gaa aat ctt tcc cgc acg ctg gat gaa gtt cag	1680
Gly Asp Ile Ala Ala Glu Asn Leu Ser Arg Thr Leu Asp Glu Val Gln	

545	550	555	560	
ttg acg ctg gat gat Leu Thr Leu Asp Asp	aaa ggg cgc ggc Lys Gly Arg Gly	gaa gtt tct aca Val Ser Thr	gaa agc cag Glu Ser Gln	1728
	565	570	575	
tgg aag gaa acg cat tcc cca tta cag gtt att ttc cag ggt agt ttg Trp Lys Glu Thr His Ser Pro Leu Gln Val Ile Phe Gln Gly Ser Leu				1776
	580	585	590	
ctg gaa tcg ggc ggt cgc ccg gtg acg cgc cgc gct gag cag gct atc Leu Glu Ser Gly Gly Arg Pro Val Thr Arg Arg Ala Glu Gln Ala Ile				1824
	595	600	605	
tgg cct gcc gat gca ttg ccg ggg atc cgt ccg cag ttc gcc tcg aaa Trp Pro Ala Asp Ala Leu Pro Gly Ile Arg Pro Gln Phe Ala Ser Lys				1872
	610	615	620	
tcg gtt tac gat tat cgt act gac agc acg gtg aaa cag ccc att gtt Ser Val Tyr Asp Tyr Arg Thr Asp Ser Thr Val Lys Gln Pro Ile Val				1920
	625	630	635	640
gat gaa ggc agt aac gcc gct ttt gac atc gtt tat agc gat gcg caa Asp Glu Gly Ser Asn Ala Ala Phe Asp Ile Val Tyr Ser Asp Ala Gln				1968
	645	650	655	
ggc gtg aaa aaa gcc gtg tcg ggc ttg cag gtg cgc ctg att cgc gaa Gly Val Lys Lys Ala Val Ser Gly Leu Gln Val Arg Leu Ile Arg Glu				2016
	660	665	670	
cgc cgc gat tac tac tgg aac tgg tca gaa gat gaa ggc tgg cag tca Arg Arg Asp Tyr Tyr Trp Asn Trp Ser Glu Asp Glu Gly Trp Gln Ser				2064
	675	680	685	
cag ttt gat caa aaa gat ctg atc gaa aat gaa caa act ctg gat ctg Gln Phe Asp Gln Lys Asp Leu Ile Glu Asn Glu Gln Thr Leu Asp Leu				2112
	690	695	700	
aaa gcg gac gaa acc ggc aag gtc agt ttt ccg gta gag tgg ggc gct Lys Ala Asp Glu Thr Gly Lys Val Ser Phe Pro Val Glu Trp Gly Ala				2160
	705	710	715	720
tat cgt ctg gaa gtc aaa gcg ccg aat gaa gcg gtc agt agt gtt cgt Tyr Arg Leu Glu Val Lys Ala Pro Asn Glu Ala Val Ser Ser Val Arg				2208
	725	730	735	
ttc tgg gct ggc tat agc tgg cag gac aac agc gac ggt agc ggc gca Phe Trp Ala Gly Tyr Ser Trp Gln Asp Asn Ser Asp Gly Ser Gly Ala				2256
	740	745	750	
gtg cga ccc gac cgt gtc acg ctg aaa ctg gat aaa gcc agt tat cgc Val Arg Pro Asp Arg Val Thr Leu Lys Leu Asp Lys Ala Ser Tyr Arg				2304
	755	760	765	
cct ggc gac acc att aag ttg cat atc gcc gcg cca acg gcg ggt aaa Pro Gly Asp Thr Ile Lys Leu His Ile Ala Ala Pro Thr Ala Gly Lys				2352
	770	775	780	

ggt tat gcg atg gtc gag tcc agt gaa ggg ccg ctg tgg tgg caa gag	2400
Gly Tyr Ala Met Val Glu Ser Ser Glu Gly Pro Leu Trp Trp Gln Glu	
785 790 795 800	
att gat gtt cgg gct caa ggg ctg gat ctg acg att ccg gtc gat aaa	2448
Ile Asp Val Arg Ala Gln Gly Leu Asp Leu Thr Ile Pro Val Asp Lys	
805 810 815	
acc tgg aat cgt cat gat ctg tat tta agt acg ctg gtg gta cgt cct	2496
Thr Trp Asn Arg His Asp Leu Tyr Leu Ser Thr Leu Val Val Arg Pro	
820 825 830	
ggc gat aaa tct cgc tcc gcg acg cca aaa cgc gcg gtt ggt gtg ttg	2544
Gly Asp Lys Ser Arg Ser Ala Thr Pro Lys Arg Ala Val Gly Val Leu	
835 840 845	
cat ctg ccg ctt ggc gat gaa aac cgt cgc ctc gat ctg gcg ctg gaa	2592
His Leu Pro Leu Gly Asp Glu Asn Arg Arg Leu Asp Leu Ala Leu Glu	
850 855 860	
aca cca gca aaa atg cgt ccc aat caa cca tta acc gtg aaa att aaa	2640
Thr Pro Ala Lys Met Arg Pro Asn Gln Pro Leu Thr Val Lys Ile Lys	
865 870 875 880	
gcc agc act aaa aat ggc gag aag cct aaa cag gtg aat gtg ctg gtg	2688
Ala Ser Thr Lys Asn Gly Glu Lys Pro Lys Gln Val Asn Val Leu Val	
885 890 895	
tct gcc gtt gat agt ggt gtg ctg aat att act gac tac gtc acg cca	2736
Ser Ala Val Asp Ser Gly Val Leu Asn Ile Thr Asp Tyr Val Thr Pro	
900 905 910	
gat ccg tgg cag gcg ttc ttt ggt cag aaa cgc tat ggc gca gac att	2784
Asp Pro Trp Gln Ala Phe Phe Gly Gln Lys Arg Tyr Gly Ala Asp Ile	
915 920 925	
tac gat att tac ggt cag gtt att gaa ggt cag ggg cgt ctg gca gct	2832
Tyr Asp Ile Tyr Gly Gln Val Ile Glu Gly Gln Gly Arg Leu Ala Ala	
930 935 940	
ctg cgt ttc ggt ggc gat ggt gat gag ctg aaa cgt ggt ggt aaa ccg	2880
Leu Arg Phe Gly Gly Asp Gly Asp Glu Leu Lys Arg Gly Gly Lys Pro	
945 950 955 960	
ccg gtc aat cac gtc aat att gtc gtg cag cag gcg ctg ccg gta acg	2928
Pro Val Asn His Val Asn Ile Val Val Gln Gln Ala Leu Pro Val Thr	
965 970 975	
ctc aac gaa cag ggc gaa ggc tcg gtt aca ctg ccg att ggc gat ttt	2976
Leu Asn Glu Gln Gly Glu Gly Ser Val Thr Leu Pro Ile Gly Asp Phe	
980 985 990	
aac ggt gaa ttg cgc gtc atg gcg caa gcc tgg acg gca gat gac ttc	3024
Asn Gly Glu Leu Arg Val Met Ala Gln Ala Trp Thr Ala Asp Asp Phe	
995 1000 1005	

ggt Gly	agc Ser	aac Asn	gaa Glu	agt Ser	aaa Lys	gtg Val	ata Ile	gtt Val	gcc Ala	gca Ala	ccg Pro	gtg Val	att Ile	gct Ala	gaa Glu	3072
1010			1015			1020										
ctg Leu	aac Asn	atg Met	ccg Pro	cgc Arg	ttt Phe	atg Met	gcg Ala	agt Ser	ggc Gly	gat Asp	acc Thr	tcg Ser	cgt Arg	ctg Leu	acg Thr	3120
1025			1030			1035			1040							
ctg Leu	gat Asp	atc Ile	act Thr	aat Asn	ctt Leu	acc Thr	gat Asp	aaa Lys	ccg Pro	caa Gln	aaa Lys	ctg Leu	aac Asn	gtt Val	gcc Ala	3168
1045			1050			1055										
ctg Leu	acc Thr	gcc Ala	agt Ser	ggt Gly	ttg Leu	ctt Leu	gaa Glu	ctg Leu	gtc Val	agc Ser	gat Asp	tca Ser	ccc Pro	gca Ala	gcc Ala	3216
1060			1065			1070										
gtt Val	gaa Glu	tta Leu	gcg Ala	cca Pro	ggt Gly	gtg Val	cgt Arg	act Thr	acg Thr	ctg Leu	ttt Phe	atc Ile	ccg Pro	gtg Val	cga Arg	3264
1075			1080			1085										
gca Ala	ttg Leu	ccg Pro	ggt Gly	tat Tyr	ggc Gly	gat Asp	gga Gly	gaa Glu	att Ile	cag Gln	gcc Ala	acc Thr	att Ile	agc Ser	ggg Gly	3312
1090			1095			1100										
tta Leu	gcg Ala	tta Leu	ccg Pro	ggt Gly	gaa Glu	acc Thr	gtt Val	gcc Ala	gat Asp	cag Gln	cat His	aag Lys	cag Gln	tgg Trp	aaa Lys	3360
1105			1110			1115			1120							
atc Ile	ggc Gly	gtc Val	cgt Arg	ccg Pro	gcg Ala	ttc Phe	ccg Pro	gca Ala	caa Gln	acg Thr	gtt Val	aat Asn	tac Tyr	ggt Gly	acg Thr	3408
1125			1130			1135										
gcg Ala	tta Leu	cag Gln	cct Pro	ggt Gly	gag Glu	aca Thr	tgg Trp	gcg Ala	att Ile	ccg Pro	gcg Ala	gat Asp	gga Gly	ttg Leu	caa Gln	3456
1140			1145			1150										
aac Asn	ttc Phe	tcg Ser	cct Pro	gtt Val	acg Thr	ctg Leu	gaa Glu	ggg Gly	caa Gln	ttg Leu	ttg Leu	ttg Leu	agc Ser	ggc Gly	aaa Lys	3504
1155			1160			1165										
cca Pro	cog Pro	ctg Leu	aac Asn	atc Ile	gca Ala	cgt Arg	tat Tyr	atc Ile	aaa Lys	gag Glu	tta Leu	aaa Lys	gcg Ala	tat Tyr	ccg Pro	3552
1170			1175			1180										
tac Tyr	ggc Gly	tgt Cys	ctt Leu	gag Glu	caa Gln	acc Thr	gcc Ala	agc Ser	ggc Gly	ctg Leu	ttt Phe	ccg Pro	tca Ser	ctt Leu	tat Tyr	3600
1185			1190			1195			1200							
acc Thr	aac Asn	gca Ala	gcc Ala	caa Gln	ctg Leu	cag Gln	gcg Ala	ttg Leu	ggc Gly	atc Ile	aaa Lys	ggc Gly	gac Asp	agt Ser	gat Asp	3648
1205			1210			1215										
gag Glu	aaa Lys	gcg Arg	cgt Arg	gca Ala	tcg Ser	gtc Val	gat Asp	atc Ile	ggc Gly	att Ile	tcc Ser	cgt Arg	ttg Leu	ctg Leu	caa Gln	3696
1220			1225			1230										
atg Val	caa Glu	cgt Glu	gat Asp	aac Glu	ggc Glu	ggc Glu	ttt Val	gcg Val	ctg Val	tgg Val	gat Val	aaa Val	aac Val	ggt Val	gac Val	3744

Met	Gln	Arg	Asp	Asn	Gly	Gly	Phe	Ala	Leu	Trp	Asp	Lys	Asn	Gly	Asp		
		1235					1240					1245					
gaa	gag	tac	tgg	ctg	acg	gct	tac	gtg	atg	gat	ttc	ctg	gtc	cgc	gca	3792	
Glu	Glu	Tyr	Trp	Leu	Thr	Ala	Tyr	Val	Met	Asp	Phe	Leu	Val	Arg	Ala		
		1250				1255				1260							
ggc	gaa	cag	ggt	tac	agc	gtg	ccg	aca	gac	gcc	att	aac	cgg	ggt	aat	3840	
Gly	Glu	Gln	Gly	Tyr	Ser	Val	Pro	Thr	Asp	Ala	Ile	Asn	Arg	Gly	Asn		
		1265			1270				1275					1280			
gag	cgt	ctg	ctg	cgc	tat	tta	caa	gat	ccg	ggc	atg	atg	tcg	atc	ccg	3888	
Glu	Arg	Leu	Leu	Arg	Tyr	Leu	Gln	Asp	Pro	Gly	Met	Met	Ser	Ile	Pro		
				1285				1290						1295			
tac	gcg	gat	aat	ctc	aaa	gcc	agt	aaa	ttc	gcc	gta	cag	tct	tac	gct	3936	
Tyr	Ala	Asp	Asn	Leu	Lys	Ala	Ser	Lys	Phe	Ala	Val	Gln	Ser	Tyr	Ala		
			1300					1305					1310				
gcg	ctg	gtg	ttg	gcc	cgt	cag	caa	aag	gct	ccg	ctg	ggt	gcg	ctg	cgt	3984	
Ala	Leu	Val	Leu	Ala	Arg	Gln	Gln	Lys	Ala	Pro	Leu	Gly	Ala	Leu	Arg		
		1315				1320						1325					
gaa	atc	tgg	gag	cat	cgt	gca	gat	gcc	gct	tct	ggt	tta	ccg	ctg	ctg	4032	
Glu	Ile	Trp	Glu	His	Arg	Ala	Asp	Ala	Ala	Ser	Gly	Leu	Pro	Leu	Leu		
		1330				1335				1340							
caa	ctt	ggc	gtt	gcg	ctg	aaa	acc	atg	ggt	gat	gcg	acg	cgt	ggt	gaa	4080	
Gln	Leu	Gly	Val	Ala	Leu	Lys	Thr	Met	Gly	Asp	Ala	Thr	Arg	Gly	Glu		
		1345			1350				1355					1360			
gaa	gcg	att	gcg	ctg	gcg	ctg	aaa	acg	ccg	cgt	aat	agt	gat	gag	cgg	4128	
Glu	Ala	Ile	Ala	Leu	Ala	Leu	Lys	Thr	Pro	Arg	Asn	Ser	Asp	Glu	Arg		
			1365					1370					1375				
ata	tgg	ctg	ggt	gat	tac	ggt	agt	tca	ctg	cgc	gac	aac	gcg	tta	atg	4176	
Ile	Trp	Leu	Gly	Asp	Tyr	Gly	Ser	Ser	Leu	Arg	Asp	Asn	Ala	Leu	Met		
		1380				1385						1390					
ctc	tcc	ttg	ctg	gaa	gaa	aat	aaa	ctg	cta	ccc	gat	gag	cag	tac	act	4224	
Leu	Ser	Leu	Leu	Glu	Glu	Asn	Lys	Leu	Leu	Pro	Asp	Glu	Gln	Tyr	Thr		
		1395				1400					1405						
ttg	ctg	aac	aca	ctt	tcg	cag	cag	gcg	ttt	ggt	gaa	cgc	tgg	cta	tcg	4272	
Leu	Leu	Asn	Thr	Leu	Ser	Gln	Gln	Ala	Phe	Gly	Glu	Arg	Trp	Leu	Ser		
		1410				1415				1420							
acg	cag	gaa	agt	aac	gcg	ttg	ttc	ctg	gct	gcc	cgt	acg	att	cag	gat	4320	
Thr	Gln	Glu	Ser	Asn	Ala	Leu	Phe	Leu	Ala	Ala	Arg	Thr	Ile	Gln	Asp		
		1425			1430				1435				1440				
tta	ccc	ggt	aaa	tgg	cag	gcg	caa	acc	tct	ttc	tca	gct	gag	cag	ctg	4368	
Leu	Pro	Gly	Lys	Trp	Gln	Ala	Gln	Thr	Ser	Phe	Ser	Ala	Glu	Gln	Leu		
			1445					1450				1455					
aca	ggc	gag	aaa	gcg	caa	aac	agc	aat	ctg	aat	agc	gat	caa	ctt	gtc	4416	
Thr	Gly	Glu	Lys	Ala	Gln	Asn	Ser	Asn	Leu	Asn	Ser	Asp	Gln	Leu	Val		

1460	1465	1470	
acc ttg cag gtg agc aac agt ggc gat cag ccg tta tgg ttg cgt atg			4464
Thr Leu Gln Val Ser Asn Ser Gly Asp Gln Pro Leu Trp Leu Arg Met			
1475	1480	1485	
gat gcc agc ggt tat ccg caa tcc gca cct tta ccg gcg aac aat gtg			4512
Asp Ala Ser Gly Tyr Pro Gln Ser Ala Pro Leu Pro Ala Asn Asn Val			
1490	1495	1500	
ctg caa atc gag cgt cat att ctt ggt act gat ggt aag agc aaa tcg			4560
Leu Gln Ile Glu Arg His Ile Leu Gly Thr Asp Gly Lys Ser Lys Ser			
1505	1510	1515	1520
ctg gac tcg tta cgt agc ggc gat ctg gtg ctg gtg tgg ttg cag gta			4608
Leu Asp Ser Leu Arg Ser Gly Asp Leu Val Leu Val Trp Leu Gln Val			
1525	1530	1535	
aaa gcc agt aac agc gtg ccg gat gcg tta gtc gtg gat ctg ctg cct			4656
Lys Ala Ser Asn Ser Val Pro Asp Ala Leu Val Val Asp Leu Leu Pro			
1540	1545	1550	
gcg ggt ctg gaa ctg gaa aac cag aat ctg gcg aac ggt agc gcc agc			4704
Ala Gly Leu Glu Leu Glu Asn Gln Asn Leu Ala Asn Gly Ser Ala Ser			
1555	1560	1565	
ctg gag caa agt ggt ggc gaa gtg cag aac tta ctg aac cag atg cag			4752
Leu Glu Gln Ser Gly Gly Glu Val Gln Asn Leu Leu Asn Gln Met Gln			
1570	1575	1580	
cag gcg agc att aag cac att gag ttc cgt gac gat cgc ttt gtg gcg			4800
Gln Ala Ser Ile Lys His Ile Glu Phe Arg Asp Asp Arg Phe Val Ala			
1585	1590	1595	1600
gcg gtt gcc gtt gat gaa tac caa ccg gta acg ctg gtg tat ctg gcg			4848
Ala Val Ala Val Asp Glu Tyr Gln Pro Val Thr Leu Val Tyr Leu Ala			
1605	1610	1615	
cgg gcg gtg acg ccg gga acg tat cag gta ccg caa ccg atg gtg gaa			4896
Arg Ala Val Thr Pro Gly Thr Tyr Gln Val Pro Gln Pro Met Val Glu			
1620	1625	1630	
tca atg tat gtt ccc caa tgg cgg gcg acc ggc gcg gct gaa gat ctg			4944
Ser Met Tyr Val Pro Gln Trp Arg Ala Thr Gly Ala Ala Glu Asp Leu			
1635	1640	1645	
ctg att gtc aga ccg taa			4962
Leu Ile Val Arg Pro *			
1650			

<210> 210
 <211> 795
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS

<222> (1)...(795)

<400> 210

atg gat ctg ttg tac cgg gta aaa acg ctt tgg gcc gcg ctg cgc ggt	48
Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly	
1 5 10 15	
aat cat tac acc tgg cct gcc atc gat atc acc ctc ccc ggc aat cgc	96
Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg	
20 25 30	
cat ttt cat ctg att ggc agt att cat atg ggt agc cac gat atg gct	144
His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala	
35 40 45	
ccc ctg ccc acc cgt ttg ctc aaa aag ctc aaa aac gcc gat gcg ctg	192
Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu	
50 55 60	
atc gtc gag gcg gat gtt tcc acc agc gat acg cct ttt gct aat ttg	240
Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu	
65 70 75 80	
cct gcc tgc gag gcg ctg gaa gag cgc att agc gag gag caa ctc caa	288
Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln	
85 90 95	
aac ctg cag cac att agc cag gag atg ggc att tct ccc tca ctc ttt	336
Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe	
100 105 110	
tct acc caa ccg ctg tgg caa atc gcg atg gtt ctt cag gcg acg cag	384
Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln	
115 120 125	
gca caa aaa ctg ggg ctg cgg gca gaa tac ggt atc gat tac cag cta	432
Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu	
130 135 140	
ttg cag gcg gcg aag caa caa cat aaa ccc gtg att gaa ctg gaa ggg	480
Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly	
145 150 155 160	
gct gaa aac cag att gcc atg ttg ctc cag ctc cct gac aaa gga ctg	528
Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu	
165 170 175	
gcg ctg ctg gac gat acg ctg acc cac tgg cat acc aac gca cgg ttg	576
Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu	
180 185 190	
ctg caa caa atg atg agc tgg tgg ctg aat gca ccg ccg caa aat aat	624
Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn	
195 200 205	
gat ata acg ctg ccc aat acg ttc agt cag tcg ctg tac gat gtg ctg	672

Asp Ile Thr Leu Pro Asn Thr Phe Ser Gln Ser Leu Tyr Asp Val Leu
 210 215 220

atg cat cag cga aat ctc gcc tgg cgg gat aaa tta cgc gcc atg ccg 720
 Met His Gln Arg Asn Leu Ala Trp Arg Asp Lys Leu Arg Ala Met Pro
 225 230 235 240

ccg ggg cga tat gtg gtc gcg gtc ggt gca cta cac ctg tat gga gaa 768
 Pro Gly Arg Tyr Val Val Ala Val Gly Ala Leu His Leu Tyr Gly Glu
 245 250 255

ggg aat ttg ccg caa atg ttg cgc taa 795
 Gly Asn Leu Pro Gln Met Leu Arg *
 260

<210> 211
 <211> 969
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(969)

<400> 211

atg gat aat ttt ctt gct ctg acc tta acg ggt aaa aaa ccg gtt atc 48
 Met Asp Asn Phe Leu Ala Leu Thr Leu Thr Gly Lys Lys Pro Val Ile
 1 5 10 15

acc gag cga gaa atc aac ggc gtt cgc tgg cgc tgg ctg ggc gat ggt 96
 Thr Glu Arg Glu Ile Asn Gly Val Arg Trp Arg Trp Leu Gly Asp Gly
 20 25 30

gtg ctg gaa ctg acg cca tta acg cca ccg caa ggc gca ctg gtg att 144
 Val Leu Glu Leu Thr Pro Leu Thr Pro Pro Gln Gly Ala Leu Val Ile
 35 40 45

tca gcg gga ata cac ggt aat gag acg gca cct gtg gag atg ctg gac 192
 Ser Ala Gly Ile His Gly Asn Glu Thr Ala Pro Val Glu Met Leu Asp
 50 55 60

gcg ttg ctt ggc gcg ata tct cac ggc gag atc ccg tta cgt tgg ccg 240
 Ala Leu Leu Gly Ala Ile Ser His Gly Glu Ile Pro Leu Arg Trp Arg
 65 70 75 80

ttg ctg gtg atc ctc ggg aat cct cct gcg ctg aag caa ggg aaa cgt 288
 Leu Leu Val Ile Leu Gly Asn Pro Pro Ala Leu Lys Gln Gly Lys Arg
 85 90 95

tat tgc cat agc gat atg aat cga atg ttt ggc ggt cgt tgg cag cta 336
 Tyr Cys His Ser Asp Met Asn Arg Met Phe Gly Gly Arg Trp Gln Leu
 100 105 110

ttt gct gaa agc gga gaa acc tgt ccg gcg cgc gaa ctg gaa cag tgc 384
 Phe Ala Glu Ser Gly Glu Thr Cys Arg Ala Arg Glu Leu Glu Gln Cys
 115 120 125

ctg gaa gat ttt tat gac cag ggc aaa gaa tct gtg cgc tgg cac ctt	432
Leu Glu Asp Phe Tyr Asp Gln Gly Lys Glu Ser Val Arg Trp His Leu	
130 135 140	
gat cta cat acc gca att cgt ggc tcc ttg cat ccg cag ttc ggt gta	480
Asp Leu His Thr Ala Ile Arg Gly Ser Leu His Pro Gln Phe Gly Val	
145 150 155 160	
tta ccg caa cgc gac att ccc tgg gac gag aaa ttt ctg acg tgg ctg	528
Leu Pro Gln Arg Asp Ile Pro Trp Asp Glu Lys Phe Leu Thr Trp Leu	
165 170 175	
ggt gcg gcg ggg ctg gag gcg ctg gtg ttc cat cag gaa cct ggt ggt	576
Gly Ala Ala Gly Leu Glu Ala Leu Val Phe His Gln Glu Pro Gly Gly	
180 185 190	
acg ttt acc cat ttc agc gcc aga cat ttt ggc gcg ctg gcc tgt acg	624
Thr Phe Thr His Phe Ser Ala Arg His Phe Gly Ala Leu Ala Cys Thr	
195 200 205	
ctg gaa ctt ggc aaa gcg ttg ccc ttt ggg caa aac gat ctt cgc cag	672
Leu Glu Leu Gly Lys Ala Leu Pro Phe Gly Gln Asn Asp Leu Arg Gln	
210 215 220	
ttt gca gta act gcc agc gca att gct gcg ctg cta tct ggt gag agt	720
Phe Ala Val Thr Ala Ser Ala Ile Ala Ala Leu Leu Ser Gly Glu Ser	
225 230 235 240	
gtc ggt atc gtg aga aca ccg ccg ctc cgt tat cgg gtg gtt tcg caa	768
Val Gly Ile Val Arg Thr Pro Pro Leu Arg Tyr Arg Val Val Ser Gln	
245 250 255	
att act cgc cac tcg ccg tcc ttc gaa atg cat atg gca agt gac acg	816
Ile Thr Arg His Ser Pro Ser Phe Glu Met His Met Ala Ser Asp Thr	
260 265 270	
ctg aat ttt atg ccg ttt gag aaa gga aca ttg ctg gcg cag gac gga	864
Leu Asn Phe Met Pro Phe Glu Lys Gly Thr Leu Leu Ala Gln Asp Gly	
275 280 285	
gag gaa cgt ttt acc gta acc cat gat gta gag tat gtg tta ttc cct	912
Glu Glu Arg Phe Thr Val Thr His Asp Val Glu Tyr Val Leu Phe Pro	
290 295 300	
aat ccg ttg gta gcg ttg gga tta cgc gcg gga tta atg ctc gaa aaa	960
Asn Pro Leu Val Ala Leu Gly Leu Arg Ala Gly Leu Met Leu Glu Lys	
305 310 315 320	
ata agc taa	969
Ile Ser *	

<210> 212
 <211> 1344
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1344)

<400> 212

atg aac gcc tgg gaa gtc aat ttc gac ggg ctg gta ggg ctg acg cat	48
Met Asn Ala Trp Glu Val Asn Phe Asp Gly Leu Val Gly Leu Thr His	
1 5 10 15	
cat tac gcg ggc ctg tcg ttt ggt aat gaa gcc tct acc cgt cac cgt	96
His Tyr Ala Gly Leu Ser Phe Gly Asn Glu Ala Ser Thr Arg His Arg	
20 25 30	
ttt cag gtg tct aac ccg cga ctg gcg gcg aag cag ggc tta ctg aaa	144
Phe Gln Val Ser Asn Pro Arg Leu Ala Ala Lys Gln Gly Leu Leu Lys	
35 40 45	
atg aaa gcc ctt gcc gat gcg gga ttc ccc cag gcc gtg atc ccg ccg	192
Met Lys Ala Leu Ala Asp Ala Gly Phe Pro Gln Ala Val Ile Pro Pro	
50 55 60	
cac gag cgt ccg ttt att ccg gtg ctg cgt cag ttg gga ttc agt ggt	240
His Glu Arg Pro Phe Ile Pro Val Leu Arg Gln Leu Gly Phe Ser Gly	
65 70 75 80	
agc gat gag cag gta ctg gaa aaa gtt gca cgc cag gca ccg cac tgg	288
Ser Asp Glu Gln Val Leu Glu Lys Val Ala Arg Gln Ala Pro His Trp	
85 90 95	
ctt tcc agc gtc agt tcc gct tcg cca atg tgg gta gcc aat gcg gca	336
Leu Ser Ser Val Ser Ser Ala Ser Pro Met Trp Val Ala Asn Ala Ala	
100 105 110	
acg atc gcg cca tct gcc gat acg ctg gat ggc aaa gtg cat ctc acc	384
Thr Ile Ala Pro Ser Ala Asp Thr Leu Asp Gly Lys Val His Leu Thr	
115 120 125	
gtt gcc aac ctg aac aat aaa ttt cac cgt tcg ctg gaa gcg ccc gtc	432
Val Ala Asn Leu Asn Asn Lys Phe His Arg Ser Leu Glu Ala Pro Val	
130 135 140	
act gaa tcg ctg tta aaa gcg att ttt aac gac gaa gag aaa ttt agc	480
Thr Glu Ser Leu Leu Lys Ala Ile Phe Asn Asp Glu Glu Lys Phe Ser	
145 150 155 160	
gtc cat tcg gcg ttg cca cag gta gcg ttg ctc ggt gat gag ggg gcg	528
Val His Ser Ala Leu Pro Gln Val Ala Leu Leu Gly Asp Glu Gly Ala	
165 170 175	
gca aac cac aat cgt ctc ggc ggt cat tac ggt gaa ccg ggt atg caa	576
Ala Asn His Asn Arg Leu Gly Gly His Tyr Gly Glu Pro Gly Met Gln	
180 185 190	
ctt ttt gtc tac ggg cga gaa gaa ggc aat gat acc cgg cct tcc cgt	624
Leu Phe Val Tyr Gly Arg Glu Glu Gly Asn Asp Thr Arg Pro Ser Arg	

195	200	205	
tat ccg gcg cga cag act cgc gaa gcc agc gag gcg gtg gca agg ctg Tyr Pro Ala Arg Gln Thr Arg Glu Ala Ser Glu Ala Val Ala Arg Leu 210 215 220			672
aat cag gtg aat ccc caa cag gtg att ttc gcc cag caa aac ccg gac Asn Gln Val Asn Pro Gln Gln Val Ile Phe Ala Gln Gln Asn Pro Asp 225 230 235 240			720
gtt atc gac cag ggc gtt ttt cat aat gac gtg att gcc gtg agt aac Val Ile Asp Gln Gly Val Phe His Asn Asp Val Ile Ala Val Ser Asn 245 250 255			768
cgc cag gtg ctg ttt tgc cac caa cag gcg ttc gct cgc cag tca cag Arg Gln Val Leu Phe Cys His Gln Gln Ala Phe Ala Arg Gln Ser Gln 260 265 270			816
tta ctg gca aac ctg cgt gcg cgg gtc aat ggt ttt atg gcg ata gaa Leu Leu Ala Asn Leu Arg Ala Arg Val Asn Gly Phe Met Ala Ile Glu 275 280 285			864
gtt ccg gca act cag gtt tcc gtg tct gat acg gtg tct acc tat ctg Val Pro Ala Thr Gln Val Ser Val Ser Asp Thr Val Ser Thr Tyr Leu 290 295 300			912
ttt aac agc caa ctg ctg agc cgc gat gat ggt tcc atg atg ttg gtg Phe Asn Ser Gln Leu Ser Arg Asp Asp Gly Ser Met Met Leu Val 305 310 315 320			960
ctg cct cag gag tgt cgg gaa cac gcc gga gta tgg ggt tat ctc aat Leu Pro Gln Glu Cys Arg Glu His Ala Gly Val Trp Gly Tyr Leu Asn 325 330 335			1008
gaa ctc ctt gcc gct gac aac ccg att agc gaa cta aaa gtc ttt gat Glu Leu Leu Ala Ala Asp Asn Pro Ile Ser Glu Leu Lys Val Phe Asp 340 345 350			1056
tta cgt gaa agc atg gcg aat ggc ggc ggc ccg gcg tgc ctg cgg ttg Leu Arg Glu Ser Met Ala Asn Gly Gly Gly Pro Ala Cys Leu Arg Leu 355 360 365			1104
cgg gtg gta ttg aca gaa gaa gaa cgc cgg gcg gtg aat ccg gcg gtg Arg Val Val Leu Thr Glu Glu Glu Arg Arg Ala Val Asn Pro Ala Val 370 375 380			1152
atg atg aac gat acg ctg ttt aat gcg ctc aat gac tgg gtg gat cgt Met Met Asn Asp Thr Leu Phe Asn Ala Leu Asn Asp Trp Val Asp Arg 385 390 395 400			1200
tac tac cgc gat cgc ctt act gct gcc gat ctg gcc gac ccg caa ttg Tyr Tyr Arg Asp Arg Leu Thr Ala Ala Asp Leu Ala Asp Pro Gln Leu 405 410 415			1248
ctg cgc gaa ggg cgg gaa gca ctg gat gta ttg agc caa tta ctg aat Leu Arg Glu Gly Arg Glu Ala Leu Asp Val Leu Ser Gln Leu Leu Asn 420 425 430			1296

```

ctc ggt tgc gtt tat ccg ttc cag cgc gag gga ggg ggc aat gga taa 1344
Leu Gly Ser Val Tyr Pro Phe Gln Arg Glu Gly Gly Gly Asn Gly *
      435                440                445

```

```

<210> 213
<211> 1479
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> CDS
<222> (1)...(1479)

```

```

<400> 213
atg act tta tgg att aac ggt gac tgg ata acg ggc cag ggc gca tgc 48
Met Thr Leu Trp Ile Asn Gly Asp Trp Ile Thr Gly Gln Gly Ala Ser
  1              5              10              15

cgt gtg aag cgt aat ccg gta tgc ggc gag gtg tta tgg caa ggc aat 96
Arg Val Lys Arg Asn Pro Val Ser Gly Glu Val Leu Trp Gln Gly Asn
      20              25              30

gat gcc gat gcc gct cag gtc gag cag gct tgt cgg gca gcc cgt gcg 144
Asp Ala Asp Ala Ala Gln Val Glu Gln Ala Cys Arg Ala Ala Arg Ala
      35              40              45

gcg ttt ccg cgc tgg gcg cgg ctt tca ttt gct gaa cgt cat gcc gtt 192
Ala Phe Pro Arg Trp Ala Arg Leu Ser Phe Ala Glu Arg His Ala Val
      50              55              60

gtc gaa cgc ttt gcc gca ctg ctg gaa agc aat aaa gcc gaa tta acc 240
Val Glu Arg Phe Ala Ala Leu Leu Glu Ser Asn Lys Ala Glu Leu Thr
      65              70              75              80

gcg att att gcc aga gaa acg ggt aag ccg cgc tgg gaa gcg gca acc 288
Ala Ile Ile Ala Arg Glu Thr Gly Lys Pro Arg Trp Glu Ala Ala Thr
      85              90              95

gaa gtg acg gcg atg atc aat aaa atc gcg ata tca att aag gcg tat 336
Glu Val Thr Ala Met Ile Asn Lys Ile Ala Ile Ser Ile Lys Ala Tyr
      100             105             110

cac gtt cgt acc ggc gag cag cgt agt gaa atg ccg gac ggc gcg gcg 384
His Val Arg Thr Gly Glu Gln Arg Ser Glu Met Pro Asp Gly Ala Ala
      115             120             125

agc ctg cga cat cgc ccg cac ggc gtg ctg gcg gtg ttt ggg ccg tat 432
Ser Leu Arg His Arg Pro His Gly Val Leu Ala Val Phe Gly Pro Tyr
      130             135             140

aat ttc cct ggt cat ttg ccg aac gga cat atc gtt ccg gca ttg ctg 480
Asn Phe Pro Gly His Leu Pro Asn Gly His Ile Val Pro Ala Leu Leu
      145             150             155             160

```

gca ggt aac acc att atc ttt aaa ccc agc gaa ctg aca ccg tgg agt	528
Ala Gly Asn Thr Ile Ile Phe Lys Pro Ser Glu Leu Thr Pro Trp Ser	
165 170 175	
ggc gaa gcg gta atg cgt tta tgg cag cag gct ggc ttg ccg cca ggc	576
Gly Glu Ala Val Met Arg Leu Trp Gln Gln Ala Gly Leu Pro Pro Gly	
180 185 190	
gtg ctg aac ctg gtg cag ggc ggg cgt gaa acg ggt cag gcg ctg agt	624
Val Leu Asn Leu Val Gln Gly Gly Arg Glu Thr Gly Gln Ala Leu Ser	
195 200 205	
gcg ctg gag gat ctc gac ggt ttg ctg ttt acc ggt agc gcc aat aca	672
Ala Leu Glu Asp Leu Asp Gly Leu Leu Phe Thr Gly Ser Ala Asn Thr	
210 215 220	
ggc tac cag ttg cat cgc cag ctc tcc ggt cag ccg gag aaa att ctc	720
Gly Tyr Gln Leu His Arg Gln Leu Ser Gly Gln Pro Glu Lys Ile Leu	
225 230 235 240	
gcc ctt gag atg ggc ggt aat aat ccg cta att atc gat gag gtg gcg	768
Ala Leu Glu Met Gly Gly Asn Asn Pro Leu Ile Ile Asp Glu Val Ala	
245 250 255	
gat atc gac gcg gct gtc cat ctg acc att cag tcg gcg ttt gtc aca	816
Asp Ile Asp Ala Ala Val His Leu Thr Ile Gln Ser Ala Phe Val Thr	
260 265 270	
gcc ggt caa cgc tgc acc tgc gcc cgc cgt tta ttg ctg aaa agc ggg	864
Ala Gly Gln Arg Cys Thr Cys Ala Arg Arg Leu Leu Lys Ser Gly	
275 280 285	
gcg cag ggc gat gcg ttt ctt gct cgt ctg gtt gcc gtc agc cag cga	912
Ala Gln Gly Asp Ala Phe Leu Ala Arg Leu Val Ala Val Ser Gln Arg	
290 295 300	
tta acg ccg ggc aac tgg gat gac gaa ccg cag ccg ttt att ggc ggg	960
Leu Thr Pro Gly Asn Trp Asp Asp Glu Pro Gln Pro Phe Ile Gly Gly	
305 310 315 320	
ctg att tct gaa cag gcc gca cag cag gtg gtt act gca tgg cag caa	1008
Leu Ile Ser Glu Gln Ala Ala Gln Gln Val Val Thr Ala Trp Gln Gln	
325 330 335	
ctg gaa gcg atg ggc gga cga ccc ctg ctt gcg ccg cgc tta tta caa	1056
Leu Glu Ala Met Gly Gly Arg Pro Leu Leu Ala Pro Arg Leu Leu Gln	
340 345 350	
gca ggg aca tcg ttg ctg acg ccg ggg atc att gaa atg aca ggc gtt	1104
Ala Gly Thr Ser Leu Leu Thr Pro Gly Ile Ile Glu Met Thr Gly Val	
355 360 365	
gct ggc gta cca gat gaa gag gtg ttc gga ccg tta ttg cgc gtc tgg	1152
Ala Gly Val Pro Asp Glu Glu Val Phe Gly Pro Leu Leu Arg Val Trp	
370 375 380	
cgt tat gat act ttc gat gaa gcg att cga atg gcg aat aac act cgc	1200

Arg Tyr Asp Thr Phe Asp Glu Ala Ile Arg Met Ala Asn Asn Thr Arg
 385 390 395 400

ttc gga ctc tct tgc ggt ctg gtt tcc ccc gag cgg gaa aag ttc gat 1248
 Phe Gly Leu Ser Cys Gly Leu Val Ser Pro Glu Arg Glu Lys Phe Asp
 405 410 415

caa ctg ttg ctg gag gcg cgg gcg ggg att gtt aac tgg aac aaa ccg 1296
 Gln Leu Leu Leu Glu Ala Arg Ala Gly Ile Val Asn Trp Asn Lys Pro
 420 425 430

ctt acc ggt gct gcc agt acc gcg cca ttc ggc ggc att ggt gct tcc 1344
 Leu Thr Gly Ala Ala Ser Thr Ala Pro Phe Gly Gly Ile Gly Ala Ser
 435 440 445

ggt aac cat cgc ccc agc gcc tgg tat gcc gca gat tac tgc gca tgg 1392
 Gly Asn His Arg Pro Ser Ala Trp Tyr Ala Ala Asp Tyr Cys Ala Trp
 450 455 460

ccg atg gcg agc ctg gag tcg gac tcg tta aca ttg ccc gcc acg ctt 1440
 Pro Met Ala Ser Leu Glu Ser Asp Ser Leu Thr Leu Pro Ala Thr Leu
 465 470 475 480

aac ccc ggg ctg gat ttt tcc gat gag gtg gtg cga tga 1479
 Asn Pro Gly Leu Asp Phe Ser Asp Glu Val Val Arg *
 485 490

<210> 214
 <211> 1035
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1035)

<400> 214

atg atg gtc atc cgt ccc gtt gag cga tca gat gtc tcg gcg ctg atg 48
 Met Met Val Ile Arg Pro Val Glu Arg Ser Asp Val Ser Ala Leu Met
 1 5 10 15

cag ctt gcc agc aaa acg ggc ggc ggc ctg acg tcg ctt ccc gcc aat 96
 Gln Leu Ala Ser Lys Thr Gly Gly Gly Leu Thr Ser Leu Pro Ala Asn
 20 25 30

gaa gcc acg ctt tcg gcg cgt atc gaa agg gca atc aaa acc tgg caa 144
 Glu Ala Thr Leu Ser Ala Arg Ile Glu Arg Ala Ile Lys Thr Trp Gln
 35 40 45

ggc gaa ctg ccc aaa agt gag cag ggc tat gtg ttc gtg ctg gaa gat 192
 Gly Glu Leu Pro Lys Ser Glu Gln Gly Tyr Val Phe Val Leu Glu Asp
 50 55 60

agc gag aca ggc acc gtg gcg ggg att tgt gcc att gag gtg gcg gtt 240
 Ser Glu Thr Gly Thr Val Ala Gly Ile Cys Ala Ile Glu Val Ala Val
 65 70 75 80

ggg	ctg	aac	gat	ccc	tgg	tac	aac	tat	cgc	gtc	ggc	acg	ttg	gtt	cac	288
Gly	Leu	Asn	Asp	Pro	Trp	Tyr	Asn	Tyr	Arg	Val	Gly	Thr	Leu	Val	His	
				85					90					95		
gcc	tca	aaa	gag	ctg	aat	gtc	tat	aac	gca	ttg	ccg	acg	ctg	ttt	ctc	336
Ala	Ser	Lys	Glu	Leu	Asn	Val	Tyr	Asn	Ala	Leu	Pro	Thr	Leu	Phe	Leu	
			100					105					110			
agt	aac	gat	cac	acc	ggc	agc	agc	gag	ctg	tgc	acg	ctg	ttt	ctc	gac	384
Ser	Asn	Asp	His	Thr	Gly	Ser	Ser	Glu	Leu	Cys	Thr	Leu	Phe	Leu	Asp	
		115					120					125				
ccg	gac	tgg	cgc	aaa	gag	ggc	aac	ggc	tat	ttg	ctg	tcg	aaa	tcg	cgc	432
Pro	Asp	Trp	Arg	Lys	Glu	Gly	Asn	Gly	Tyr	Leu	Leu	Ser	Lys	Ser	Arg	
	130					135					140					
ttt	atg	ttt	atg	gcg	gct	ttt	cgc	gac	aag	ttt	aat	gac	aaa	gtg	gtt	480
Phe	Met	Phe	Met	Ala	Ala	Phe	Arg	Asp	Lys	Phe	Asn	Asp	Lys	Val	Val	
145					150				155						160	
gct	gaa	atg	cgc	ggg	gtg	att	gac	gaa	cac	ggc	tat	tca	ccg	ttc	tgg	528
Ala	Glu	Met	Arg	Gly	Val	Ile	Asp	Glu	His	Gly	Tyr	Ser	Pro	Phe	Trp	
				165					170					175		
caa	agc	ctc	ggt	aaa	cgc	ttc	ttt	tcg	atg	gat	ttt	agc	cgc	gcc	gat	576
Gln	Ser	Leu	Gly	Lys	Arg	Phe	Phe	Ser	Met	Asp	Phe	Ser	Arg	Ala	Asp	
			180					185					190			
ttt	ctc	tgc	ggc	acc	ggg	caa	aag	gca	ttt	att	gca	gaa	ctg	atg	ccg	624
Phe	Leu	Cys	Gly	Thr	Gly	Gln	Lys	Ala	Phe	Ile	Ala	Glu	Leu	Met	Pro	
		195					200					205				
aaa	cat	ccg	atc	tat	acc	cac	ttt	tta	tcc	cag	gaa	gcc	cag	gac	gtc	672
Lys	His	Pro	Ile	Tyr	Thr	His	Phe	Leu	Ser	Gln	Glu	Ala	Gln	Asp	Val	
	210					215					220					
atc	ggt	cag	gta	cat	ccg	caa	acc	gcg	cct	gcc	cgc	gcg	gtg	ctg	gag	720
Ile	Gly	Gln	Val	His	Pro	Gln	Thr	Ala	Pro	Ala	Arg	Ala	Val	Leu	Glu	
225					230				235					240		
aaa	gaa	ggt	ttt	cgc	tac	cgt	aac	tat	atc	gac	atc	ttt	gac	ggt	ggg	768
Lys	Glu	Gly	Phe	Arg	Tyr	Arg	Asn	Tyr	Ile	Asp	Ile	Phe	Asp	Gly	Gly	
				245				250					255			
ccg	acg	ctt	gag	tgt	gac	atc	gac	cgc	gtg	cgc	gcc	atc	cgt	aaa	agt	816
Pro	Thr	Leu	Glu	Cys	Asp	Ile	Asp	Arg	Val	Arg	Ala	Ile	Arg	Lys	Ser	
			260					265					270			
cgg	ctg	gtg	gaa	gtg	gca	gaa	ggg	cag	cct	gcg	cag	ggc	gat	ttc	cca	864
Arg	Leu	Val	Glu	Val	Ala	Glu	Gly	Gln	Pro	Ala	Gln	Gly	Asp	Phe	Pro	
		275					280					285				
gcc	tgc	ctg	gtc	gcc	aat	gaa	aat	tat	cac	cat	ttc	cgc	gtg	gtg	ctg	912
Ala	Cys	Leu	Val	Ala	Asn	Glu	Asn	Tyr	His	His	Phe	Arg	Val	Val	Leu	
	290					295					300					

gtg cgt acc gat ccg gca acc gag cgt ttg att tta acc gcc gca caa 960
Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln
305 310 315 320

ctg gat gcc ctc aaa tgc cac gcc ggg gat cgc gtt cgt ctg gtg cgc 1008
Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg
325 330 335

ctg tgc gca gag gag aaa aca gca tga 1035
Leu Cys Ala Glu Glu Lys Thr Ala *
340

<210> 215
<211> 1221
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1221)

<400> 215
atg tct cag cca att acg cgt gaa aac ttt gat gaa tgg atg ata cct 48
Met Ser Gln Pro Ile Thr Arg Glu Asn Phe Asp Glu Trp Met Ile Pro
1 5 10 15

gtt tac gct ccg gca ccc ttt ata ccg gta cgt ggc gaa ggt tgc cgc 96
Val Tyr Ala Pro Ala Pro Phe Ile Pro Val Arg Gly Glu Gly Ser Arg
20 25 30

ttg tgg gat cag cag ggg aaa gag tat atc gac ttc gcg ggt ggc att 144
Leu Trp Asp Gln Gln Gly Lys Glu Tyr Ile Asp Phe Ala Gly Gly Ile
35 40 45

gcg gtg aac gcg ctg ggc cat gcg cat ccg gaa ctg cgt gaa gcg ctg 192
Ala Val Asn Ala Leu Gly His Ala His Pro Glu Leu Arg Glu Ala Leu
50 55 60

aac gaa cag gcg agt aag ttc tgg cat acc ggc aac ggt tac acc aac 240
Asn Glu Gln Ala Ser Lys Phe Trp His Thr Gly Asn Gly Tyr Thr Asn
65 70 75 80

gag ccg gta ctg cga ctg gcg aaa aaa ttg atc gac gcc acg ttt gcc 288
Glu Pro Val Leu Arg Leu Ala Lys Lys Leu Ile Asp Ala Thr Phe Ala
85 90 95

gat cgc gtc ttc ttt tgt aac tcc ggt gcg gaa gcc aac gaa gcg gcg 336
Asp Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
100 105 110

cta aaa ctg gcg cgt aaa ttc gct cac gac cgc tac ggc agc cat aag 384
Leu Lys Leu Ala Arg Lys Phe Ala His Asp Arg Tyr Gly Ser His Lys
115 120 125

agc ggc atc gtg gcg ttc aaa aat gcg ttt cat ggt cgc acg ctg ttt 432
Ser Gly Ile Val Ala Phe Lys Asn Ala Phe His Gly Arg Thr Leu Phe

130	135	140	
act gtc agt gcg ggt ggg cag cca gcc tat tca cag gat ttt gcg cca			480
Thr Val Ser Ala Gly Gly Gln Pro Ala Tyr Ser Gln Asp Phe Ala Pro			
145	150	155	160
ctg ccg gcg gat att cgt cat gct gca tat aac gat att aac tct gcc			528
Leu Pro Ala Asp Ile Arg His Ala Ala Tyr Asn Asp Ile Asn Ser Ala			
	165	170	175
agc gcg ctg att gac gac tct acc tgt gcg gtg att gtc gaa ccc atc			576
Ser Ala Leu Ile Asp Asp Ser Thr Cys Ala Val Ile Val Glu Pro Ile			
	180	185	190
cag ggg gaa ggc ggt gtg gtg cca gcc agc aac gcg ttt tta caa ggt			624
Gln Gly Glu Gly Gly Val Val Pro Ala Ser Asn Ala Phe Leu Gln Gly			
	195	200	205
ctg cgt gaa ttg tgt aac cgc cac aat gcg ctg ttg att ttt gat gaa			672
Leu Arg Glu Leu Cys Asn Arg His Asn Ala Leu Leu Ile Phe Asp Glu			
	210	215	220
gta caa acc ggc gtc ggg cgc acc ggg gaa ctg tat gcc tat atg cac			720
Val Gln Thr Gly Val Gly Arg Thr Gly Glu Leu Tyr Ala Tyr Met His			
	225	230	240
tac ggc gtg acg cct gat ctg tta act acc gcc aaa gcg ctg ggc ggc			768
Tyr Gly Val Thr Pro Asp Leu Leu Thr Thr Ala Lys Ala Leu Gly Gly			
	245	250	255
ggc ttc ccg gtc ggt gcg ttg ttg gca acc gaa gag tgc gcc cgc gtg			816
Gly Phe Pro Val Gly Ala Leu Leu Ala Thr Glu Glu Cys Ala Arg Val			
	260	265	270
atg acc gtt ggc act cat ggc acc acc tat ggc ggt aat ccg ctg gcc			864
Met Thr Val Gly Thr His Gly Thr Thr Tyr Gly Gly Asn Pro Leu Ala			
	275	280	285
tcg gcg gtg gca ggc aaa gtg ctg gag ctc atc aac aca cca gag atg			912
Ser Ala Val Ala Gly Lys Val Leu Glu Leu Ile Asn Thr Pro Glu Met			
	290	295	300
ctt aat ggc gtt aaa cag cgt cac gac tgg ttt gtt gag cgt ctt aat			960
Leu Asn Gly Val Lys Gln Arg His Asp Trp Phe Val Glu Arg Leu Asn			
	305	310	320
act att aat cac cgc tat ggt ttg ttc agt gaa gtt cgc ggc tta ggt			1008
Thr Ile Asn His Arg Tyr Gly Leu Phe Ser Glu Val Arg Gly Leu Gly			
	325	330	335
ttg ctg att ggc tgt gta ctg aat gcc gat tac gcc ggg caa gcg aaa			1056
Leu Leu Ile Gly Cys Val Leu Asn Ala Asp Tyr Ala Gly Gln Ala Lys			
	340	345	350
cag atc tct cag gaa gcg gcg aaa gca ggc gtg atg gta ctg att gcg			1104
Gln Ile Ser Gln Glu Ala Ala Lys Ala Gly Val Met Val Leu Ile Ala			
	355	360	365

ggt ggc aac gtg gtg cgt ttt gcg cct gcg ctc aat gtc agc gaa gaa 1152
Gly Gly Asn Val Val Arg Phe Ala Pro Ala Leu Asn Val Ser Glu Glu
370 375 380

gag gtg acg acc gga ctg gat cgc ttt gca gct gct tgc gaa cac ttt 1200
Glu Val Thr Thr Gly Leu Asp Arg Phe Ala Ala Ala Cys Glu His Phe
385 390 395 400

gtt agc cga ggt tca tca tga 1221
Val Ser Arg Gly Ser Ser *
405

<210> 216

<211> 3147

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(3147)

<400> 216

atg aaa att ctc agc ctg cgc ctg aaa aac ctg aac tca tta aaa ggc 48
Met Lys Ile Leu Ser Leu Arg Leu Lys Asn Leu Asn Ser Leu Lys Gly
1 5 10 15

gaa tgg aag att gat ttc acc cgc gag ccg ttc gcc agc aac ggg ctg 96
Glu Trp Lys Ile Asp Phe Thr Arg Glu Pro Phe Ala Ser Asn Gly Leu
20 25 30

ttt gct att acc ggc cca aca ggt gcg ggg aaa acc acc ctg ctg gac 144
Phe Ala Ile Thr Gly Pro Thr Gly Ala Gly Lys Thr Thr Leu Leu Asp
35 40 45

gcc att tgt ctg gcg ctg tat cac gaa act ccg cgt ctc tct aac gtt 192
Ala Ile Cys Leu Ala Leu Tyr His Glu Thr Pro Arg Leu Ser Asn Val
50 55 60

tca caa tcg caa aat gat ctc atg acc cgc gat acc gcc gaa tgt ctg 240
Ser Gln Ser Gln Asn Asp Leu Met Thr Arg Asp Thr Ala Glu Cys Leu
65 70 75 80

gcg gag gtg gag ttt gaa gtg aaa ggt gaa gcg tac cgt gca ttc tgg 288
Ala Glu Val Glu Phe Glu Val Lys Gly Glu Ala Tyr Arg Ala Phe Trp
85 90 95

agc cag aat cgg gcg cgt aac caa ccc gac ggt aat ttg cag gtg cca 336
Ser Gln Asn Arg Ala Arg Asn Gln Pro Asp Gly Asn Leu Gln Val Pro
100 105 110

cgc gta gag ctg gcg cgc tgc gcc gac ggc aaa att ctc gcc gac aaa 384
Arg Val Glu Leu Ala Arg Cys Ala Asp Gly Lys Ile Leu Ala Asp Lys
115 120 125

gtg aaa gat aag ctg gaa ctg aca gcg acg tta acc ggg ctg gat tac 432

Val	Lys	Asp	Lys	Leu	Glu	Leu	Thr	Ala	Thr	Leu	Thr	Gly	Leu	Asp	Tyr		
130						135						140					
ggg	cgc	ttc	acc	cgt	tcg	atg	ctg	ctt	tcg	cag	ggg	caa	ttt	gct	gcc	480	
Gly	Arg	Phe	Thr	Arg	Ser	Met	Leu	Leu	Ser	Gln	Gly	Gln	Phe	Ala	Ala		
145					150					155					160		
ttc	ctg	aat	gcc	aaa	ccc	aaa	gaa	cgc	gcg	gaa	ttg	ctc	gag	gag	tta	528	
Phe	Leu	Asn	Ala	Lys	Pro	Lys	Glu	Arg	Ala	Glu	Leu	Leu	Glu	Glu	Leu		
				165					170						175		
acc	ggc	act	gaa	atc	tac	ggg	caa	atc	tcg	gcg	atg	gtt	ttt	gag	cag	576	
Thr	Gly	Thr	Glu	Ile	Tyr	Gly	Gln	Ile	Ser	Ala	Met	Val	Phe	Glu	Gln		
			180					185						190			
cac	aaa	tcg	gcc	cgc	aca	gag	ctg	gag	aag	ctg	caa	gcg	cag	gcc	agc	624	
His	Lys	Ser	Ala	Arg	Thr	Glu	Leu	Glu	Lys	Leu	Gln	Ala	Gln	Ala	Ser		
		195					200						205				
ggc	gtc	acg	ttg	ctc	acg	ccg	gaa	caa	gtg	caa	tcg	ctg	aca	gcg	agt	672	
Gly	Val	Thr	Leu	Leu	Thr	Pro	Glu	Gln	Val	Gln	Ser	Leu	Thr	Ala	Ser		
	210					215						220					
ttg	cag	gta	ctt	act	gac	gaa	gaa	aaa	cag	tta	att	acc	gcg	cag	cag	720	
Leu	Gln	Val	Leu	Thr	Asp	Glu	Glu	Lys	Gln	Leu	Ile	Thr	Ala	Gln	Gln		
225					230					235					240		
caa	gaa	caa	caa	tcg	cta	aac	tgg	tta	acg	cgt	cag	gac	gaa	ttg	cag	768	
Gln	Glu	Gln	Gln	Ser	Leu	Asn	Trp	Leu	Thr	Arg	Gln	Asp	Glu	Leu	Gln		
				245					250					255			
caa	gaa	gcc	agc	cgc	cgt	cag	cag	gcc	ttg	caa	cag	gcg	tta	gcc	gaa	816	
Gln	Glu	Ala	Ser	Arg	Arg	Gln	Gln	Ala	Leu	Gln	Gln	Ala	Leu	Ala	Glu		
			260					265						270			
gaa	gaa	aaa	gcg	caa	cct	caa	ctg	gcg	gcg	ctt	agt	ctg	gca	caa	ccg	864	
Glu	Glu	Lys	Ala	Gln	Pro	Gln	Leu	Ala	Ala	Leu	Ser	Leu	Ala	Gln	Pro		
		275					280					285					
gca	cga	aat	ctt	cgt	cca	cac	tgg	gaa	cgc	atc	gca	gaa	cac	agc	gcg	912	
Ala	Arg	Asn	Leu	Arg	Pro	His	Trp	Glu	Arg	Ile	Ala	Glu	His	Ser	Ala		
		290				295					300						
gcg	ctg	gcg	cat	att	cgc	cag	cag	att	gaa	gaa	gta	aat	act	cgc	tta	960	
Ala	Leu	Ala	His	Ile	Arg	Gln	Gln	Ile	Glu	Glu	Val	Asn	Thr	Arg	Leu		
305					310					315					320		
cag	agc	aca	atg	gcg	ctt	cgc	gcg	agc	att	cgc	cac	cac	gcg	gcg	aag	1008	
Gln	Ser	Thr	Met	Ala	Leu	Arg	Ala	Ser	Ile	Arg	His	His	Ala	Ala	Lys		
				325					330					335			
cag	tca	gca	gaa	tta	cag	cag	cag	caa	caa	agc	ctg	aat	acc	tgg	tta	1056	
Gln	Ser	Ala	Glu	Leu	Gln	Gln	Gln	Gln	Gln	Ser	Leu	Asn	Thr	Trp	Leu		
			340					345						350			
cag	gaa	cac	gac	cgc	ttc	cgt	cag	tgg	aac	aac	gaa	ccg	gcg	ggt	tgg	1104	
Gln	Glu	His	Asp	Arg	Phe	Arg	Gln	Trp	Asn	Asn	Glu	Pro	Ala	Gly	Trp		

355	360	365	
cgt gcg cag ttc tcc caa caa acc agc gat cgc gag cat ctg cgg caa Arg Ala Gln Phe Ser Gln Gln Thr Ser Asp Arg Glu His Leu Arg Gln 370 375 380			1152
tgg cag caa cag tta acc cat gct gag caa aaa ctt aat gcg ctt gcg Trp Gln Gln Gln Leu Thr His Ala Glu Gln Lys Leu Asn Ala Leu Ala 385 390 395 400			1200
gcg atc acg ttg acg tta acc gcc gat gaa gtt gct acc gcc ctg gcg Ala Ile Thr Leu Thr Leu Thr Ala Asp Glu Val Ala Thr Ala Leu Ala 405 410 415			1248
caa cat gct gag caa cgc cca ctg cgt cag cac ctg gtc gcg ctg cat Gln His Ala Glu Gln Arg Pro Leu Arg Gln His Leu Val Ala Leu His 420 425 430			1296
gga cag att gtt ccc caa caa aaa cgt ctg gcg cag tta cag gtc gct Gly Gln Ile Val Pro Gln Gln Lys Arg Leu Ala Gln Leu Gln Val Ala 435 440 445			1344
atc cag aat gtc acg caa gaa cag acg caa cgt aac gcc gca ctt aac Ile Gln Asn Val Thr Gln Glu Gln Thr Gln Arg Asn Ala Ala Leu Asn 450 455 460			1392
gaa atg cgc cag cgt tat aaa gaa aag acg cag caa ctt gcc gat gtg Glu Met Arg Gln Arg Tyr Lys Glu Lys Thr Gln Gln Leu Ala Asp Val 465 470 475 480			1440
aaa acc att tgc gag cag gaa gcg cgc atc aaa acg ctg gaa gct caa Lys Thr Ile Cys Glu Gln Glu Ala Arg Ile Lys Thr Leu Glu Ala Gln 485 490 495			1488
cgt gca cag tta cag gcg ggt cag cct tgc cca ctt tgt ggt tcc acc Arg Ala Gln Leu Gln Ala Gly Gln Pro Cys Pro Leu Cys Gly Ser Thr 500 505 510			1536
agc cac ccg gcg gtc gag gcg tat cag gcg ctg gag cct ggc gtt aat Ser His Pro Ala Val Glu Ala Tyr Gln Ala Leu Glu Pro Gly Val Asn 515 520 525			1584
cag tct cga tta ctg gcg ctg gaa aac gaa gtt aaa aag ctc ggt gaa Gln Ser Arg Leu Leu Ala Leu Glu Asn Glu Val Lys Lys Leu Gly Glu 530 535 540			1632
gaa ggt gcg acg cta cgt ggg caa ctg gac gcc ata aca aag cag ctt Glu Gly Ala Thr Leu Arg Gly Gln Leu Asp Ala Ile Thr Lys Gln Leu 545 550 555 560			1680
cag cgt gat gaa aac gaa gcg caa agc ctc cga caa gat gag caa gca Gln Arg Asp Glu Asn Glu Ala Gln Ser Leu Arg Gln Asp Glu Gln Ala 565 570 575			1728
ctt act caa caa tgg caa gcc gtc acg gcc agc ctc aat atc acc ttg Leu Thr Gln Gln Trp Gln Ala Val Thr Ala Ser Leu Asn Ile Thr Leu 580 585 590			1776

cag cca ctg gac gat att caa ccg tgg ctg gat gca caa gat gag cac Gln Pro Leu Asp Asp Ile Gln Pro Trp Leu Asp Ala Gln Asp Glu His 595 600 605	1824
gaa cgc cag ctg cgg tta ctc agc caa cgg cat gaa tta caa ggg cag Glu Arg Gln Leu Arg Leu Leu Ser Gln Arg His Glu Leu Gln Gly Gln 610 615 620	1872
att gcc gcg cat aat cag caa att atc cag tat caa cag caa att gaa Ile Ala Ala His Asn Gln Gln Ile Ile Gln Tyr Gln Gln Gln Ile Glu 625 630 635 640	1920
caa cgc cag caa cta ctt tta acg aca ttg acg ggt tat gca ctg aca Gln Arg Gln Gln Leu Leu Leu Thr Thr Leu Thr Gly Tyr Ala Leu Thr 645 650 655	1968
ttg cca cag gaa gat gaa gaa gag agc tgg ttg gcg aca cgt cag caa Leu Pro Gln Glu Asp Glu Glu Glu Ser Trp Leu Ala Thr Arg Gln Gln 660 665 670	2016
gaa gcg cag agc tgg cag caa cgc cag aac gaa tta acc gcg ctg caa Glu Ala Gln Ser Trp Gln Gln Arg Gln Asn Glu Leu Thr Ala Leu Gln 675 680 685	2064
aac cgt att cag cag ctg acg ccg att ctg gaa acg ttg ccg caa agt Asn Arg Ile Gln Gln Leu Thr Pro Ile Leu Glu Thr Leu Pro Gln Ser 690 695 700	2112
gat gaa ctc ccg cac tgc gaa gaa act gtg gta ttg gaa aac tgg cgg Asp Glu Leu Pro His Cys Glu Glu Thr Val Val Leu Glu Asn Trp Arg 705 710 715 720	2160
cag gta cat gaa caa tgt ctc gca tta cac agc cag cag cag acg tta Gln Val His Glu Gln Cys Leu Ala Leu His Ser Gln Gln Gln Thr Leu 725 730 735	2208
cag caa cag gat gtt ctg gcg gcg caa agt ctg caa aaa gcc cag gcg Gln Gln Gln Asp Val Leu Ala Ala Gln Ser Leu Gln Lys Ala Gln Ala 740 745 750	2256
cag ttt gac acc gcg cta cag gcc agc gtc ttt gac gat cag cag gcg Gln Phe Asp Thr Ala Leu Gln Ala Ser Val Phe Asp Asp Gln Gln Ala 755 760 765	2304
ttc ctt gcg gcg cta atg gat gaa caa aca cta acg cag ctg gaa cag Phe Leu Ala Ala Leu Met Asp Glu Gln Thr Leu Thr Gln Leu Glu Gln 770 775 780	2352
ctc aag cag aat ctg gaa aac cag cgc cgt cag gcg caa act ctg gtc Leu Lys Gln Asn Leu Glu Asn Gln Arg Arg Gln Ala Gln Thr Leu Val 785 790 795 800	2400
act cag aca gca gaa acg ctg gca cag cat caa caa cac cga cct gac Thr Gln Thr Ala Glu Thr Leu Ala Gln His Gln Gln His Arg Pro Asp 805 810 815	2448

gac ggg ttg gct ctc act gtg acg gtg gag cag att cag caa gag tta	2496
Asp Gly Leu Ala Leu Thr Val Thr Val Glu Gln Ile Gln Gln Glu Leu	
820 825 830	
gcg caa act cac caa aag ttg cgt gaa aac acc acg agt caa ggc gag	2544
Ala Gln Thr His Gln Lys Leu Arg Glu Asn Thr Thr Ser Gln Gly Glu	
835 840 845	
att cgc cag cag ctg aag cag gat gca gat aac cgt cag caa caa caa	2592
Ile Arg Gln Gln Leu Lys Gln Asp Ala Asp Asn Arg Gln Gln Gln Gln	
850 855 860	
acc tta atg cag caa att gct caa atg acg cag cag gtt gag gac tgg	2640
Thr Leu Met Gln Gln Ile Ala Gln Met Thr Gln Gln Val Glu Asp Trp	
865 870 875 880	
gga tat ctg aat tcg cta ata ggt tcc aaa gag ggc gat aaa ttc cgc	2688
Gly Tyr Leu Asn Ser Leu Ile Gly Ser Lys Glu Gly Asp Lys Phe Arg	
885 890 895	
aag ttt gcc cag ggg ctg acg ctg gat aat tta gtc cat ctc gct aat	2736
Lys Phe Ala Gln Gly Leu Thr Leu Asp Asn Leu Val His Leu Ala Asn	
900 905 910	
cag caa ctt acc cgg ctg cac ggg cgc tat ctg tta cag cgc aaa gcc	2784
Gln Gln Leu Thr Arg Leu His Gly Arg Tyr Leu Leu Gln Arg Lys Ala	
915 920 925	
agc gag gcg ctg gaa gtc gag gtt gtt gat acc tgg cag gca gat gcg	2832
Ser Glu Ala Leu Glu Val Glu Val Val Asp Thr Trp Gln Ala Asp Ala	
930 935 940	
gta cgc gat acc cgt acc ctt tcc ggc ggc gaa agt ttc ctc gtt agt	2880
Val Arg Asp Thr Arg Thr Leu Ser Gly Gly Glu Ser Phe Leu Val Ser	
945 950 955 960	
ctg gcg ctg gcg ctg gcg ctt tcg gat ctg gtc agc cat aaa aca cgt	2928
Leu Ala Leu Ala Leu Ala Leu Ser Asp Leu Val Ser His Lys Thr Arg	
965 970 975	
att gac tcg ctg ttc ctt gat gaa ggt ttt ggc acg ctg gat agc gaa	2976
Ile Asp Ser Leu Phe Leu Asp Glu Gly Phe Gly Thr Leu Asp Ser Glu	
980 985 990	
acg ctg gat acc gcc ctt gat gcg ctg gat gcc ctg aac gcc agt ggc	3024
Thr Leu Asp Thr Ala Leu Asp Ala Leu Asp Ala Leu Asn Ala Ser Gly	
995 1000 1005	
aaa acc atc ggt gtg att agc cac gta gaa gcg atg aaa gag cgt att	3072
Lys Thr Ile Gly Val Ile Ser His Val Glu Ala Met Lys Glu Arg Ile	
1010 1015 1020	
ccg gtg cag atc aaa gtg aaa aag atc aac ggc ctg ggc tac agc aaa	3120
Pro Val Gln Ile Lys Val Lys Lys Ile Asn Gly Leu Gly Tyr Ser Lys	
1025 1030 1035 1040	
ctg gaa agt acg ttt gca gtg aaa taa	3147

Leu Glu Ser Thr Phe Ala Val Lys *
1045

<210> 217
<211> 1203
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1203)

<400> 217
atg cgc atc ctt cac acc tca gac tgg cat ctc ggc cag aac ttc tac 48
Met Arg Ile Leu His Thr Ser Asp Trp His Leu Gly Gln Asn Phe Tyr
1 5 10 15

agt aaa agc cgc gaa gct gaa cat cag gct ttt ctt gac tgg ctg ctg 96
Ser Lys Ser Arg Glu Ala Glu His Gln Ala Phe Leu Asp Trp Leu Leu
20 25 30

gag aca gca caa acc cat cag gtg gat gcg att att gtt gcc ggt gat 144
Glu Thr Ala Gln Thr His Gln Val Asp Ala Ile Ile Val Ala Gly Asp
35 40 45

gtt ttc gat acc ggc tcg ccg ccc agt tac gcc cgc acg tta tac aac 192
Val Phe Asp Thr Gly Ser Pro Pro Ser Tyr Ala Arg Thr Leu Tyr Asn
50 55 60

cgt ttt gtt gtc aat tta cag caa act ggc tgt cat ctg gtg gta ctg 240
Arg Phe Val Val Asn Leu Gln Gln Thr Gly Cys His Leu Val Val Leu
65 70 75 80

gca gga aac cat gac tcg gtc gcc acg ctg aat gaa tcg cgc gat atc 288
Ala Gly Asn His Asp Ser Val Ala Thr Leu Asn Glu Ser Arg Asp Ile
85 90 95

atg gcg ttc ctc aat act acc gtg gtc gcc agc gcc gga cat gcg ccg 336
Met Ala Phe Leu Asn Thr Thr Val Val Ala Ser Ala Gly His Ala Pro
100 105 110

caa atc ttg cct cgt cgc gac ggg acg cca ggc gca gtg ctg tgc ccc 384
Gln Ile Leu Pro Arg Arg Asp Gly Thr Pro Gly Ala Val Leu Cys Pro
115 120 125

att ccg ttt tta cgt ccg cgt gac att att acc agc cag gcg ggg ctt 432
Ile Pro Phe Leu Arg Pro Arg Asp Ile Ile Thr Ser Gln Ala Gly Leu
130 135 140

aac ggt att gaa aaa cag cag cat tta ctg gca gcg att acc gat tat 480
Asn Gly Ile Glu Lys Gln Gln His Leu Leu Ala Ala Ile Thr Asp Tyr
145 150 155 160

tac caa caa cac tat gcc gat gcc tgc aaa ctg cgc ggc gat cag cct 528
Tyr Gln Gln His Tyr Ala Asp Ala Cys Lys Leu Arg Gly Asp Gln Pro
165 170 175

ctg	ccc	atc	atc	gcc	acg	gga	cat	tta	acg	acc	gtg	ggg	gcc	agt	aaa	576
Leu	Pro	Ile	Ile	Ala	Thr	Gly	His	Leu	Thr	Thr	Val	Gly	Ala	Ser	Lys	
180						185			190							
agt	gac	gcc	gtg	cgt	gac	att	tat	att	ggc	acg	ctg	gac	gcg	ttt	ccg	624
Ser	Asp	Ala	Val	Arg	Asp	Ile	Tyr	Ile	Gly	Thr	Leu	Asp	Ala	Phe	Pro	
195						200			205							
gca	caa	aac	ttt	cca	cca	gcc	gac	tac	atc	gcg	ctc	ggg	cat	att	cac	672
Ala	Gln	Asn	Phe	Pro	Pro	Ala	Asp	Tyr	Ile	Ala	Leu	Gly	His	Ile	His	
210						215			220							
cgc	gca	cag	att	att	ggc	ggc	atg	gaa	cat	gtt	cgc	tat	tgc	ggc	tcc	720
Arg	Ala	Gln	Ile	Ile	Gly	Gly	Met	Glu	His	Val	Arg	Tyr	Cys	Gly	Ser	
225						230			235			240				
ccc	att	cca	ctg	agt	ttt	gat	gaa	tgc	ggt	aag	agt	aaa	tat	gtc	cat	768
Pro	Ile	Pro	Leu	Ser	Phe	Asp	Glu	Cys	Gly	Lys	Ser	Lys	Tyr	Val	His	
245						250			255							
ctg	gtg	aca	ttt	tca	aac	ggc	aaa	tta	gag	agc	gtg	gaa	aac	ctg	aac	816
Leu	Val	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Glu	Ser	Val	Glu	Asn	Leu	Asn	
260						265			270							
gta	ccg	gta	acg	caa	ccc	atg	gca	gtg	ctg	aaa	ggc	gat	ctg	gcg	tcg	864
Val	Pro	Val	Thr	Gln	Pro	Met	Ala	Val	Leu	Lys	Gly	Asp	Leu	Ala	Ser	
275						280			285							
att	acc	gca	cag	ctg	gaa	cag	tgg	cgc	gat	gta	tcg	cag	gag	cca	cct	912
Ile	Thr	Ala	Gln	Leu	Glu	Gln	Trp	Arg	Asp	Val	Ser	Gln	Glu	Pro	Pro	
290						295			300							
gtc	tgg	ctg	gat	atc	gaa	atc	act	act	gat	gag	tat	ctg	cat	gat	att	960
Val	Trp	Leu	Asp	Ile	Glu	Ile	Thr	Thr	Asp	Glu	Tyr	Leu	His	Asp	Ile	
305						310			315			320				
cag	cgc	aaa	atc	cag	gca	tta	acc	gaa	tca	ttg	cct	gtc	gaa	gta	ttg	1008
Gln	Arg	Lys	Ile	Gln	Ala	Leu	Thr	Glu	Ser	Leu	Pro	Val	Glu	Val	Leu	
325						330			335							
ctg	gta	cgt	cgg	agt	cgt	gaa	cag	cgc	gag	cgt	gtg	tta	gcc	agc	caa	1056
Leu	Val	Arg	Arg	Ser	Arg	Glu	Gln	Arg	Glu	Arg	Val	Leu	Ala	Ser	Gln	
340						345			350							
cag	cgt	gaa	acc	ctc	agc	gaa	ctc	agc	gtc	gaa	gag	gtg	ttc	aat	cgc	1104
Gln	Arg	Glu	Thr	Leu	Ser	Glu	Leu	Ser	Val	Glu	Glu	Val	Phe	Asn	Arg	
355						360			365							
cgt	ctg	gca	ctg	gaa	gaa	ctg	gat	gaa	tcg	cag	cag	caa	cgt	ctg	cag	1152
Arg	Leu	Ala	Leu	Glu	Glu	Leu	Asp	Glu	Ser	Gln	Gln	Gln	Arg	Leu	Gln	
370						375			380							
cat	ctt	ttc	acc	acg	acg	ttg	cat	acc	ctc	gcc	gga	gaa	cac	gaa	gca	1200
His	Leu	Phe	Thr	Thr	Thr	Leu	His	Thr	Leu	Ala	Gly	Glu	His	Glu	Ala	
385						390			395			400				

tga
*

1203

<210> 218

<211> 765

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(765)

<400> 218

atg aac gat cta ttt tca ctg gca gga aaa aat atc ttg att acc ggt	48
Met Asn Asp Leu Phe Ser Leu Ala Gly Lys Asn Ile Leu Ile Thr Gly	
1 5 10 15	
tca gca cag ggc att ggc ttt tta ctg gca acc ggc ctg ggt aaa tat	96
Ser Ala Gln Gly Ile Gly Phe Leu Leu Ala Thr Gly Leu Gly Lys Tyr	
20 25 30	
ggc gca caa ata att att aat gat att act gcc gaa cgc gca gaa ctt	144
Gly Ala Gln Ile Ile Ile Asn Asp Ile Thr Ala Glu Arg Ala Glu Leu	
35 40 45	
gct gta gaa aaa ctc cac cag gag ggt att cag gcc gtt gcc gca cct	192
Ala Val Glu Lys Leu His Gln Glu Gly Ile Gln Ala Val Ala Ala Pro	
50 55 60	
ttt aat gtt act cat aaa cat gaa att gat gcc gcc gtt gaa cat atc	240
Phe Asn Val Thr His Lys His Glu Ile Asp Ala Ala Val Glu His Ile	
65 70 75 80	
gaa aag gac atc ggc ccc att gat gtg ctg gtg aat aac gcc ggt atc	288
Glu Lys Asp Ile Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile	
85 90 95	
cag cgc cgt cat cct ttt act gag ttc cct gaa caa gag tgg aat gat	336
Gln Arg Arg His Pro Phe Thr Glu Phe Pro Glu Gln Glu Trp Asn Asp	
100 105 110	
gtg atc gca gta aac cag acc gcc gtg ttc ctg gta tcg caa gcg gta	384
Val Ile Ala Val Asn Gln Thr Ala Val Phe Leu Val Ser Gln Ala Val	
115 120 125	
act cgt cac atg gtt gaa cgc aag gca ggt aaa gtt att aat att tgc	432
Thr Arg His Met Val Glu Arg Lys Ala Gly Lys Val Ile Asn Ile Cys	
130 135 140	
tcg atg caa agc gaa ctg gga cgt gac acc atc acc cct tat gcc gca	480
Ser Met Gln Ser Glu Leu Gly Arg Asp Thr Ile Thr Pro Tyr Ala Ala	
145 150 155 160	
tcg aaa ggg gcg gta aaa atg ctc acc cgc ggc atg tgc gtc gag ctg	528
Ser Lys Gly Ala Val Lys Met Leu Thr Arg Gly Met Cys Val Glu Leu	

165	170	175	
gcg cgc cac aat att cag gtc aac ggt att gcg ccg ggc tat ttc aaa			576
Ala Arg His Asn Ile Gln Val Asn Gly Ile Ala Pro Gly Tyr Phe Lys			
180	185	190	
aca gaa atg act aaa gca ctg gtt gag gac gaa gcc ttc acc gcc tgg			624
Thr Glu Met Thr Lys Ala Leu Val Glu Asp Glu Ala Phe Thr Ala Trp			
195	200	205	
ttg tgc aaa cgg acc ccc gcc gca cgc tgg gga gat ccg cag gaa ctg			672
Leu Cys Lys Arg Thr Pro Ala Ala Arg Trp Gly Asp Pro Gln Glu Leu			
210	215	220	
att ggt gct gcg gtg ttc ctt tct tca aaa gcc tct gat ttc gta aac			720
Ile Gly Ala Ala Val Phe Leu Ser Ser Lys Ala Ser Asp Phe Val Asn			
225	230	235	240
ggc cac ctg ttg ttt gtt gat ggc ggc atg tta gtg gct gtt taa			765
Gly His Leu Leu Phe Val Asp Gly Gly Met Leu Val Ala Val *			
245	250		

<210> 219

<211> 1032

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1032)

<400> 219

atg caa gtg aaa aca cag tcc tgc gtt gtt gcg ggc aag aaa act gtt	48
Met Gln Val Lys Thr Gln Ser Cys Val Val Ala Gly Lys Lys Thr Val	
1 5 10 15	

gcc gtt acc gag cag acg ata gat tgg aat aat aat gga aca tta gta	96
Ala Val Thr Glu Gln Thr Ile Asp Trp Asn Asn Asn Gly Thr Leu Val	
20 25 30	

caa ata acc cga ggt gga att tgc ggt tcc gat tta cat tat tat cag	144
Gln Ile Thr Arg Gly Gly Ile Cys Gly Ser Asp Leu His Tyr Tyr Gln	
35 40 45	

gaa gga aaa gta ggt aat ttc atg ata aag gca ccg atg gtg tta ggt	192
Glu Gly Lys Val Gly Asn Phe Met Ile Lys Ala Pro Met Val Leu Gly	
50 55 60	

cat gaa gtt atc ggt aaa gtt att cat agc gac tca tca gaa tta cat	240
His Glu Val Ile Gly Lys Val Ile His Ser Asp Ser Ser Glu Leu His	
65 70 75 80	

gaa ggg caa acg gta gcc att aat ccg tct aaa ccg tgc ggt cac tgc	288
Glu Gly Gln Thr Val Ala Ile Asn Pro Ser Lys Pro Cys Gly His Cys	
85 90 95	

aaa tac tgc att gaa cat aac gag aat cag tgt aca gat atg cgt ttt	336
Lys Tyr Cys Ile Glu His Asn Glu Asn Gln Cys Thr Asp Met Arg Phe	
100 105 110	
ttt ggc agt gcc atg tat ttc cct cat gtt gat ggt ggt ttt acc cgt	384
Phe Gly Ser Ala Met Tyr Phe Pro His Val Asp Gly Gly Phe Thr Arg	
115 120 125	
tat aaa atg gtc gaa acg tcg caa tgt gtc cct tat ccg gcc aaa gct	432
Tyr Lys Met Val Glu Thr Ser Gln Cys Val Pro Tyr Pro Ala Lys Ala	
130 135 140	
gac gaa aag gtt atg gct ttt gcc gaa cct tta gcc gtc gcg att cat	480
Asp Glu Lys Val Met Ala Phe Ala Glu Pro Leu Ala Val Ala Ile His	
145 150 155 160	
gcc gca cat cag gcc ggc gag tta cag ggc aag cga gta ttt att tcc	528
Ala Ala His Gln Ala Gly Glu Leu Gln Gly Lys Arg Val Phe Ile Ser	
165 170 175	
ggt gtt gga ccc att ggc tgc ctg att gtc agt gca gtg aaa aca ctg	576
Gly Val Gly Pro Ile Gly Cys Leu Ile Val Ser Ala Val Lys Thr Leu	
180 185 190	
ggg gcc gcg gaa att gtc tgt gct gat gtg agt ccc cgt tcc ctt tcg	624
Gly Ala Ala Glu Ile Val Cys Ala Asp Val Ser Pro Arg Ser Leu Ser	
195 200 205	
ctg ggc aaa gag atg ggg gcg gat gtg ctc gta aac cca caa aac gac	672
Leu Gly Lys Glu Met Gly Ala Asp Val Leu Val Asn Pro Gln Asn Asp	
210 215 220	
gac atg gat cac tgg aaa gcg gaa aaa ggc tat ttc gat gtc agc ttt	720
Asp Met Asp His Trp Lys Ala Glu Lys Gly Tyr Phe Asp Val Ser Phe	
225 230 235 240	
gaa gtg tcc ggt cat cct tca tca gtg aat acc tgt ctg gag gtc act	768
Glu Val Ser Gly His Pro Ser Ser Val Asn Thr Cys Leu Glu Val Thr	
245 250 255	
cgt gca cgc ggc gta atg gtg cag gta ggt atg gga ggc gcg atg gca	816
Arg Ala Arg Gly Val Met Val Gln Val Gly Met Gly Gly Ala Met Ala	
260 265 270	
gaa ttc cca atg atg acg ttg att ggt aag gag att tca ctc aga ggc	864
Glu Phe Pro Met Met Thr Leu Ile Gly Lys Glu Ile Ser Leu Arg Gly	
275 280 285	
tct ttc cgt ttt acc agc gaa ttt aat acc gca gtg tca tgg ctg gcg	912
Ser Phe Arg Phe Thr Ser Glu Phe Asn Thr Ala Val Ser Trp Leu Ala	
290 295 300	
aat ggc gtt atc aat cca ctg cct tta ctg agt gct gaa tat ccc ttc	960
Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe	
305 310 315 320	

act gac ctg gaa gag gcg cta cgt ttc gcc ggt gat aaa acc cag gca 1008
 Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala
 325 330 335

gca aaa gtc cag ctt gtt ttc taa 1032
 Ala Lys Val Gln Leu Val Phe *
 340

<210> 220
 <211> 1647
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1647)

<400> 220

atg gat tcg caa cgc aat ctt tta gtc atc gct ttg ctg ttc gtg tct 48
 Met Asp Ser Gln Arg Asn Leu Leu Val Ile Ala Leu Leu Phe Val Ser
 1 5 10 15

ttc atg atc tgg caa gcc tgg gag cag gat aaa aac ccg caa cct cag 96
 Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln
 20 25 30

gcc caa cag acc acg cag aca acg acc acc gca gcg ggt agc gcc gcc 144
 Ala Gln Gln Thr Thr Gln Thr Thr Thr Ala Ala Gly Ser Ala Ala
 35 40 45

gac cag ggc gta ccg gcc agt ggc cag ggg aaa ctg atc tcg gtt aag 192
 Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys
 50 55 60

acc gac gtg ctt gat ctg acc atc aac acc cgt ggt ggt gat gtt gag 240
 Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu
 65 70 75 80

caa gct ctg ctg cct gct tac ccg aaa gag ctg aac tct acc cag ccg 288
 Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro
 85 90 95

ttc cag ctg ttg gaa act tca ccg cag ttt att tat cag gca cag agc 336
 Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser
 100 105 110

ggt ctg acc ggt cgt gat ggc ccg gat aac ccg gct aac ggc ccg cgt 384
 Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg
 115 120 125

ccg ctg tat aac gtt gaa aaa gac gct tat gtg ctg gct gaa ggt caa 432
 Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln
 130 135 140

aac gaa ctg cag gtg ccg atg acg tat acc gac gcg gca ggc aac acg 480
 Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr

145				150				155				160					
ttt	acc	aaa	acg	ttt	gtc	ctg	aaa	cgt	ggg	gat	tac	gct	gtc	aac	gtc	528	
Phe	Thr	Lys	Thr	Phe	Val	Leu	Lys	Arg	Gly	Asp	Tyr	Ala	Val	Asn	Val		
				165				170				175					
aac	tac	aac	gtg	cag	aac	gct	ggc	gag	aaa	ccg	ctg	gaa	atc	tcc	tcg	576	
Asn	Tyr	Asn	Val	Gln	Asn	Ala	Gly	Glu	Lys	Pro	Leu	Glu	Ile	Ser	Ser		
				180				185				190					
ttt	ggg	cag	ttg	aag	caa	tcc	atc	act	ctg	cca	ccg	cat	ctc	gat	acc	624	
Phe	Gly	Gln	Leu	Lys	Gln	Ser	Ile	Thr	Leu	Pro	Pro	His	Leu	Asp	Thr		
				195				200				205					
gga	agc	agc	aac	ttc	gca	ctg	cac	acc	ttc	cgt	ggc	gcg	gcg	tac	tcc	672	
Gly	Ser	Ser	Asn	Phe	Ala	Leu	His	Thr	Phe	Arg	Gly	Ala	Ala	Tyr	Ser		
				210				215				220					
acg	cct	gac	gag	aag	tat	gag	aaa	tac	aag	ttc	gat	acc	att	gcc	gat	720	
Thr	Pro	Asp	Glu	Lys	Tyr	Glu	Lys	Tyr	Lys	Phe	Asp	Thr	Ile	Ala	Asp		
				225				230				235				240	
aac	gaa	aac	ctg	aac	atc	tct	tcg	aaa	ggg	ggg	tgg	gtg	gcg	atg	ctg	768	
Asn	Glu	Asn	Leu	Asn	Ile	Ser	Ser	Lys	Gly	Gly	Trp	Val	Ala	Met	Leu		
				245				250				255					
caa	cag	tat	ttc	gcg	acg	gcg	tgg	atc	ccg	cat	aac	gac	ggg	acc	aac	816	
Gln	Gln	Tyr	Phe	Ala	Thr	Ala	Trp	Ile	Pro	His	Asn	Asp	Gly	Thr	Asn		
				260				265				270					
aac	ttc	tat	acc	gct	aat	ctg	ggg	aac	ggc	atc	gcc	gct	atc	ggc	tat	864	
Asn	Phe	Tyr	Thr	Ala	Asn	Leu	Gly	Asn	Gly	Ile	Ala	Ala	Ile	Gly	Tyr		
				275				280				285					
aaa	tct	cag	ccg	gta	ctg	gtt	cag	cct	ggg	cag	act	ggc	gcg	atg	aac	912	
Lys	Ser	Gln	Pro	Val	Leu	Val	Gln	Pro	Gly	Gln	Thr	Gly	Ala	Met	Asn		
				290				295				300					
agc	acc	ctg	tgg	gtt	ggc	ccg	gaa	atc	cag	gac	aaa	atg	gca	gct	gtt	960	
Ser	Thr	Leu	Trp	Val	Gly	Pro	Glu	Ile	Gln	Asp	Lys	Met	Ala	Ala	Val		
				305				310				315				320	
gct	ccg	cac	ctg	gat	ctg	acc	gtt	gat	tac	ggg	tgg	ttg	tgg	ttc	atc	1008	
Ala	Pro	His	Leu	Asp	Leu	Thr	Val	Asp	Tyr	Gly	Trp	Leu	Trp	Phe	Ile		
				325				330				335					
tct	cag	ccg	ctg	ttc	aaa	ctg	ctg	aaa	tgg	atc	cat	agc	ttt	gtg	ggg	1056	
Ser	Gln	Pro	Leu	Phe	Lys	Leu	Leu	Lys	Trp	Ile	His	Ser	Phe	Val	Gly		
				340				345				350					
aac	tgg	ggc	ttc	tcc	att	atc	atc	atc	acc	ttt	atc	gtt	cgt	ggc	atc	1104	
Asn	Trp	Gly	Phe	Ser	Ile	Ile	Ile	Ile	Thr	Phe	Ile	Val	Arg	Gly	Ile		
				355				360				365					
atg	tac	ccg	ctg	acc	aaa	gcg	cag	tac	acc	tcc	atg	gcg	aag	atg	cgt	1152	
Met	Tyr	Pro	Leu	Thr	Lys	Ala	Gln	Tyr	Thr	Ser	Met	Ala	Lys	Met	Arg		
				370				375				380					

atg ttg cag ccg aag att cag gca atg cgt gag cgt ctg ggc gat gac 1200
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp
385 390 395 400

aaa cag cgt atc agc cag gaa atg atg gcg ctg tac aaa gct gag aag 1248
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys
405 410 415

gtt aac ccg ctg ggc ggc tgc ttc ccg ctg ctg atc cag atg cca atc 1296
Val Asn Pro Leu Gly Gly Cys Phe Pro Leu Leu Ile Gln Met Pro Ile
420 425 430

ttc ctg gcg ttg tac tac atg ctg atg ggt tcc gtt gaa ctg cgt cag 1344
Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln
435 440 445

gca ccg ttt gca ctg tgg atc cac gac ctg tcg gca cag gac ccg tac 1392
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr
450 455 460

tac atc ctg ccg atc ctg atg ggc gta acg atg ttc ttc att cag aag 1440
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys
465 470 475 480

atg tcg ccg acc aca gtg acc gac ccg atg cag cag aag atc atg acc 1488
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr
485 490 495

ttt atg ccg gtc atc ttc acc gtg ttc ttc ctg tgg ttc ccg tca ggt 1536
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly
500 505 510

ctg gtg ctg tac tat atc gtc agc aac ctg gta acc att att cag cag 1584
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln
515 520 525

cag ctg att tac cgt ggt ctg gaa aaa cgt ggc ctg cat agc cgc gag 1632
Gln Leu Ile Tyr Arg Gly Leu Glu Lys Arg Gly Leu His Ser Arg Glu
530 535 540

aag aaa aaa tcc tga 1647
Lys Lys Lys Ser *
545

<210> 221
<211> 1629
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1629)

<400> 221
atg aaa act cgc gac tcg caa tca agt gac gtg att atc att ggc ggc 48

Met	Lys	Thr	Arg	Asp	Ser	Gln	Ser	Ser	Asp	Val	Ile	Ile	Ile	Gly	Gly		
1				5					10					15			
ggc	gca	acg	gga	gcc	ggg	att	gcc	cgc	gac	tgt	gcc	ctg	cgc	ggg	ctg	96	
Gly	Ala	Thr	Gly	Ala	Gly	Ile	Ala	Arg	Asp	Cys	Ala	Leu	Arg	Gly	Leu		
			20					25				30					
cgc	gtg	att	ttg	gtt	gag	cgc	cac	gac	atc	gca	acc	ggt	gcc	acc	ggg	144	
Arg	Val	Ile	Leu	Val	Glu	Arg	His	Asp	Ile	Ala	Thr	Gly	Ala	Thr	Gly		
		35					40					45					
cgt	aac	cac	ggc	ctg	ctg	cac	agc	ggt	gcg	cgc	tat	gcg	gta	acc	gat	192	
Arg	Asn	His	Gly	Leu	Leu	His	Ser	Gly	Ala	Arg	Tyr	Ala	Val	Thr	Asp		
	50					55					60						
gcg	gaa	tcg	gcc	cgc	gaa	tgc	att	agt	gaa	aac	cag	atc	ctg	aaa	cgc	240	
Ala	Glu	Ser	Ala	Arg	Glu	Cys	Ile	Ser	Glu	Asn	Gln	Ile	Leu	Lys	Arg		
65					70				75					80			
att	gca	cgt	cac	tgc	gtt	gaa	cca	acc	aac	ggc	ctg	ttt	atc	acc	ctg	288	
Ile	Ala	Arg	His	Cys	Val	Glu	Pro	Thr	Asn	Gly	Leu	Phe	Ile	Thr	Leu		
				85					90				95				
ccg	gaa	gat	gac	ctc	tcc	ttc	cag	gcc	act	ttt	att	cgc	gcc	tgc	gaa	336	
Pro	Glu	Asp	Asp	Leu	Ser	Phe	Gln	Ala	Thr	Phe	Ile	Arg	Ala	Cys	Glu		
			100					105					110				
gaa	gca	ggg	atc	agc	gca	gaa	gct	ata	gac	ccg	cag	caa	gcg	cgc	att	384	
Glu	Ala	Gly	Ile	Ser	Ala	Glu	Ala	Ile	Asp	Pro	Gln	Gln	Ala	Arg	Ile		
		115					120					125					
atc	gaa	cct	gcc	gtt	aac	ccg	gca	ctg	att	ggc	gcg	gtg	aaa	gtt	ccg	432	
Ile	Glu	Pro	Ala	Val	Asn	Pro	Ala	Leu	Ile	Gly	Ala	Val	Lys	Val	Pro		
	130					135					140						
gat	ggc	acc	gtt	gat	cca	ttt	cgt	ctg	acc	gca	gca	aac	atg	ctg	gat	480	
Asp	Gly	Thr	Val	Asp	Pro	Phe	Arg	Leu	Thr	Ala	Ala	Asn	Met	Leu	Asp		
145					150					155				160			
gcc	aaa	gaa	cac	ggt	gcc	gtt	atc	ctt	acc	gct	cat	gaa	gtc	acg	ggg	528	
Ala	Lys	Glu	His	Gly	Ala	Val	Ile	Leu	Thr	Ala	His	Glu	Val	Thr	Gly		
			165					170					175				
ctg	att	cgt	gaa	ggc	gcg	acg	gtg	tgc	ggt	gtt	cgt	gta	cgt	aac	cat	576	
Leu	Ile	Arg	Glu	Gly	Ala	Thr	Val	Cys	Gly	Val	Arg	Val	Arg	Asn	His		
		180						185					190				
ctc	acc	ggc	gaa	act	cag	gcc	ctt	cat	gca	cct	gtc	gtg	gtt	aat	gcc	624	
Leu	Thr	Gly	Glu	Thr	Gln	Ala	Leu	His	Ala	Pro	Val	Val	Val	Val	Asn	Ala	
		195					200					205					
gct	ggg	atc	tgg	ggg	caa	cac	att	gcc	gaa	tat	gcc	gat	ctg	cgc	att	672	
Ala	Gly	Ile	Trp	Gly	Gln	His	Ile	Ala	Glu	Tyr	Ala	Asp	Leu	Arg	Ile		
	210					215					220						
cgc	atg	ttc	ccg	gcg	aaa	gga	tcg	ctg	ctg	atc	atg	gat	cac	cgc	att	720	
Arg	Met	Phe	Pro	Ala	Lys	Gly	Ser	Leu	Leu	Ile	Met	Asp	His	Arg	Ile		

gaa agc ggt gcg caa ttg cag ggc agc gta gaa ctt gct cac cag cgg	336
Glu Ser Gly Ala Gln Leu Gln Gly Ser Val Glu Leu Ala His Gln Arg	
100 105 110	
ggt acg ccg ctc ggc act ctg cgc tct acc tgg cta agt tcg cca gaa	384
Val Thr Pro Leu Gly Thr Leu Arg Ser Thr Trp Leu Ser Ser Pro Glu	
115 120 125	
gtc ccc gtc tgg ccg ctg ccc gcg aag aaa ata tgt gta gtg gga att	432
Val Pro Val Trp Pro Leu Pro Ala Lys Lys Ile Cys Val Val Gly Ile	
130 135 140	
agc ggc ctg atg gat ttt cag gcg cac ctt gcg gca gct tcg ttg cgt	480
Ser Gly Leu Met Asp Phe Gln Ala His Leu Ala Ala Ala Ser Leu Arg	
145 150 155 160	
gaa ctc ggc ctt gcc gtt gaa acc gca gaa ata gag ctg ccg gaa ctg	528
Glu Leu Gly Leu Ala Val Glu Thr Ala Glu Ile Glu Leu Pro Glu Leu	
165 170 175	
gat gtg ctg cgc aat aac gcc acc gaa ttt cgc gcg gtg aat atc gcc	576
Asp Val Leu Arg Asn Asn Ala Thr Glu Phe Arg Ala Val Asn Ile Ala	
180 185 190	
cgt ttc ctt gat aat gaa gaa aac tgg ccg ctg tta ctt gat gcg ctt	624
Arg Phe Leu Asp Asn Glu Glu Asn Trp Pro Leu Leu Leu Asp Ala Leu	
195 200 205	
att cct gtc gcc aat acc tgc gaa atg atc ctg atg ccc gcc tgc ttc	672
Ile Pro Val Ala Asn Thr Cys Glu Met Ile Leu Met Pro Ala Cys Phe	
210 215 220	
ggt ctg gcc gat gac aaa ctg tgg cgt tgg ttg aat gaa aaa cta cct	720
Gly Leu Ala Asp Asp Lys Leu Trp Arg Trp Leu Asn Glu Lys Leu Pro	
225 230 235 240	
tgt tca ctg atg ctt ttg cca acg ctg ccg cct tcc gtg ctg ggc att	768
Cys Ser Leu Met Leu Leu Pro Thr Leu Pro Pro Ser Val Leu Gly Ile	
245 250 255	
cgt ctg caa aac cag tta cag cgc cag ttt gtg cgc cag ggt ggc gtg	816
Arg Leu Gln Asn Gln Leu Gln Arg Gln Phe Val Arg Gln Gly Gly Val	
260 265 270	
tgg atg ccg ggc gat gaa gtg aaa aaa gtg acc tgt aaa aat ggc gta	864
Trp Met Pro Gly Asp Glu Val Lys Lys Val Thr Cys Lys Asn Gly Val	
275 280 285	
gtg aac gaa atc tgg acc cgc aat cac gcc gat att ccg cta cgt cca	912
Val Asn Glu Ile Trp Thr Arg Asn His Ala Asp Ile Pro Leu Arg Pro	
290 295 300	
cgt ttc gcg gtt ctc gcc agc ggc agt ttc ttt agt ggc gga ctg gta	960
Arg Phe Ala Val Leu Ala Ser Gly Ser Phe Phe Ser Gly Gly Leu Val	
305 310 315 320	
gcg gaa cgt aac ggc att cga gag ccg att ctc ggc ctt gat gtg cta	1008

Ala Glu Arg Asn Gly Ile Arg Glu Pro Ile Leu Gly Leu Asp Val Leu	
325 330 335	
caa acc gcc acg cgg ggt gaa tgg tat aag gga gat ttt ttt gcg ccg	1056
Gln Thr Ala Thr Arg Gly Glu Trp Tyr Lys Gly Asp Phe Phe Ala Pro	
340 345 350	
caa ccg tgg cag cag ttc ggt gta acc act gat gag acg cta cgc ccg	1104
Gln Pro Trp Gln Gln Phe Gly Val Thr Thr Asp Glu Thr Leu Arg Pro	
355 360 365	
tca cag gca ggg caa acc att gaa aac ctg ttt gcc atc ggt tcg gtg	1152
Ser Gln Ala Gly Gln Thr Ile Glu Asn Leu Phe Ala Ile Gly Ser Val	
370 375 380	
ctg ggc gga ttt gat ccc atc gcc cag gga tgc ggc ggc ggt gtt tgt	1200
Leu Gly Gly Phe Asp Pro Ile Ala Gln Gly Cys Gly Gly Gly Val Cys	
385 390 395 400	
gcc gtc agt gct tta cat gcc gct caa cag att gcc caa cgc gca gga	1248
Ala Val Ser Ala Leu His Ala Ala Gln Gln Ile Ala Gln Arg Ala Gly	
405 410 415	
ggc caa caa tga	1260
Gly Gln Gln *	
<210> 223	
<211> 1191	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(1191)	
<400> 223	
atg aat gac acc agc ttc gaa aac tgc att aag tgc acc gtc tgc acc	48
Met Asn Asp Thr Ser Phe Glu Asn Cys Ile Lys Cys Thr Val Cys Thr	
1 5 10 15	
acc gcc tgc ccg gtg agc cgg gtg aat ccc ggt tat cca ggg cca aaa	96
Thr Ala Cys Pro Val Ser Arg Val Asn Pro Gly Tyr Pro Gly Pro Lys	
20 25 30	
caa gcc ggg ccg gat ggc gag cgt ctg cgt ttg aaa gat ggc gca ctg	144
Gln Ala Gly Pro Asp Gly Glu Arg Leu Arg Leu Lys Asp Gly Ala Leu	
35 40 45	
tat gac gag gcg ctg aaa tat tgc atc aac tgc aaa cgt tgt gaa gtc	192
Tyr Asp Glu Ala Leu Lys Tyr Cys Ile Asn Cys Lys Arg Cys Glu Val	
50 55 60	
gcc tgc ccg tcc gat gtg aag att ggc gat att atc cag cgc gcg ccg	240
Ala Cys Pro Ser Asp Val Lys Ile Gly Asp Ile Ile Gln Arg Ala Arg	
65 70 75 80	

gcg aaa tat gac acc acg cgc ccg tcg ctg cgt aat ttt gtg ttg agt	288
Ala Lys Tyr Asp Thr Thr Arg Pro Ser Leu Arg Asn Phe Val Leu Ser	
85 90 95	
cat acc gac ctg atg ggt agc gtt tcc acg ccg ttc gca cca atc gtc	336
His Thr Asp Leu Met Gly Ser Val Ser Thr Pro Phe Ala Pro Ile Val	
100 105 110	
aac acc gct acc tcg ctg aaa ccg gtg cgg cag ctg ctt gat gcg gcg	384
Asn Thr Ala Thr Ser Leu Lys Pro Val Arg Gln Leu Leu Asp Ala Ala	
115 120 125	
tta aaa atc gat cat cgc cgc acg cta ccg aaa tac tcc ttc ggc acg	432
Leu Lys Ile Asp His Arg Arg Thr Leu Pro Lys Tyr Ser Phe Gly Thr	
130 135 140	
ttc cgt cgc tgg tat cgc agc gtg gcg gct cag caa gca caa tat aaa	480
Phe Arg Arg Trp Tyr Arg Ser Val Ala Ala Gln Gln Ala Gln Tyr Lys	
145 150 155 160	
gac cag gtc gct ttc ttt cac ggc tgc ttc gtt aac tac aac cat ccg	528
Asp Gln Val Ala Phe Phe His Gly Cys Phe Val Asn Tyr Asn His Pro	
165 170 175	
cag tta ggt aaa gat tta att aaa gtg ctc aac gca atg ggt acc ggt	576
Gln Leu Gly Lys Asp Leu Ile Lys Val Leu Asn Ala Met Gly Thr Gly	
180 185 190	
gta caa ctg ctc agc aaa gaa aaa tgc tgc ggc gta ccg cta atc gcc	624
Val Gln Leu Leu Ser Lys Glu Lys Cys Cys Gly Val Pro Leu Ile Ala	
195 200 205	
aac ggc ttt acc gat aaa gca cgc aaa cag gca att acg aat gta gag	672
Asn Gly Phe Thr Asp Lys Ala Arg Lys Gln Ala Ile Thr Asn Val Glu	
210 215 220	
tcg atc cgc gaa gct gtg gga gta aaa ggc att ccg gtg att gcc acc	720
Ser Ile Arg Glu Ala Val Gly Val Lys Gly Ile Pro Val Ile Ala Thr	
225 230 235 240	
tcc tca acc tgt aca ttt gcc ctg cgc gac gaa tac ccg gaa gtg ctg	768
Ser Ser Thr Cys Thr Phe Ala Leu Arg Asp Glu Tyr Pro Glu Val Leu	
245 250 255	
aat gtc gac aac aaa ggc ttg cgc gat cat atc gaa ctg gca acc cgc	816
Asn Val Asp Asn Lys Gly Leu Arg Asp His Ile Glu Leu Ala Thr Arg	
260 265 270	
tgg ctg tgg cgc aag ctg gac gaa ggc aaa acg tta ccg ctg aaa ccg	864
Trp Leu Trp Arg Lys Leu Asp Glu Gly Lys Thr Leu Pro Leu Lys Pro	
275 280 285	
ctg ccg ctg aaa gtg gtt tat cac act ccg tgc cat atg gaa aaa atg	912
Leu Pro Leu Lys Val Val Tyr His Thr Pro Cys His Met Glu Lys Met	
290 295 300	

ggc tgg acg ctc tac acc ctg gag ctg ttg cgt aac atc ccg ggg ctt 960
 Gly Trp Thr Leu Tyr Thr Leu Glu Leu Leu Arg Asn Ile Pro Gly Leu
 305 310 315 320

gag tta acg gtg ctg gat tcc cag tgc tgc ggt att gcg ggt act tac 1008
 Glu Leu Thr Val Leu Asp Ser Gln Cys Cys Gly Ile Ala Gly Thr Tyr
 325 330 335

ggt ttc aaa aaa gag aac tac ccc acc tca caa gcc atc ggc gca cca 1056
 Gly Phe Lys Lys Glu Asn Tyr Pro Thr Ser Gln Ala Ile Gly Ala Pro
 340 345 350

ctg ttc cgc cag ata gaa gaa agc ggc gca gat ctg gtg gtc acc gac 1104
 Leu Phe Arg Gln Ile Glu Glu Ser Gly Ala Asp Leu Val Val Thr Asp
 355 360 365

tgc gaa acc tgt aaa tgg cag att gag atg tcc aca agt ctt cgc tgc 1152
 Cys Glu Thr Cys Lys Trp Gln Ile Glu Met Ser Thr Ser Leu Arg Cys
 370 375 380

gaa cat ccg att acg cta ctg gcc cag gcg ctg gct taa 1191
 Glu His Pro Ile Thr Leu Leu Ala Gln Ala Leu Ala *
 385 390 395

<210> 224
 <211> 909
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(909)

<400> 224

atg caa tta cgt aaa cct gcc aca gca atc ctc gcc ctg gcg ctt tcc 48
 Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
 1 5 10 15

gca gga ctg gca cag gca gat gac gcc gcc ccg gca gcg ggc agt act 96
 Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
 20 25 30

ctg gac aaa atc gcc aaa aac ggt gtg att gtc gtc ggt cac cgt gaa 144
 Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
 35 40 45

tct tca gtg cct ttc tct tat tac gac aat cag caa aaa gtg gtg ggt 192
 Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
 50 55 60

tac tcg cag gat tac tcc aac gcc att gtt gaa gca gtg aaa aag aaa 240
 Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
 65 70 75 80

ctc aac aaa ccg gac ttg cag gta aaa ctg att ccg att acc tca caa 288
 Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln

110
 115
 120
 125
 130
 135
 140
 145
 150
 155
 160
 165
 170
 175
 180
 185
 190
 195
 200
 205
 210
 215
 220
 225
 230
 235
 240
 245
 250
 255
 260
 265
 270
 275
 280
 285
 290
 295
 300

	85	90	95	
aac cgt att cca ctg ctg caa aac ggc act ttc gat ttt gaa tgt ggt				336
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly	100	105	110	
tct acc acc aac aac gtc gaa cgc caa aaa cag gcg gct ttc tct gac				384
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp	115	120	125	
act att ttc gtg gtc ggt acg cgc ctg ttg acc aaa aag ggt ggc gat				432
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp	130	135	140	
atc aaa gat ttt gcc aac ctg aaa gac aaa gcc gta gtc gtc act tcc				480
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser	145	150	155	160
ggc act acc tct gaa gtt ttg ctc aac aaa ctg aat gaa gag caa aaa				528
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys	165	170	175	
atg aat atg cgc atc atc agc gcc aaa gat cac ggt gac tct ttc cgc				576
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg	180	185	190	
acc ctg gaa agc ggt cgt gcc gtt gcc ttt atg atg gat gac gct ctg				624
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu	195	200	205	
ctg gcc ggt gaa cgt gcg aaa gcg aag aaa cca gac aac tgg gaa atc				672
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile	210	215	220	
gtc ggc aag ccg cag tct cag gag gcc tac ggt tgt atg ttg cgt aaa				720
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys	225	230	235	240
gat gat ccg cag ttc aaa aag ctg atg gat gac acc atc gct cag gtg				768
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val	245	250	255	
cag acc tcc ggt gaa gcg gaa aaa tgg ttt gat aag tgg ttc aaa aat				816
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn	260	265	270	
cca att ccg ccg aaa aac ctg aac atg aat ttc gaa ctg tca gac gaa				864
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu	275	280	285	
atg aaa gca ctg ttc aaa gaa ccg aat gac aag gca ctg aac taa				909
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn *	290	295	300	

<210> 225

<211> 987
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(987)

<400> 225

atg aat aac agc gct ttt act ttc cag aca cta cac ccg gat acc atc	48
Met Asn Asn Ser Ala Phe Thr Phe Gln Thr Leu His Pro Asp Thr Ile	
1 5 10 15	
atg gac gct ctg ttt gag cat ggg atc cgg gtg gat tcc ggt ctt acc	96
Met Asp Ala Leu Phe Glu His Gly Ile Arg Val Asp Ser Gly Leu Thr	
20 25 30	
ccg ctt aac agc tat gaa aac cgt gtc tat caa ttt cag gac gaa gat	144
Pro Leu Asn Ser Tyr Glu Asn Arg Val Tyr Gln Phe Gln Asp Glu Asp	
35 40 45	
cgt cga cgt ttt gtc gtc aaa ttt tat cgc cct gaa cgt tgg aca gcc	192
Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala	
50 55 60	
gat caa atc ctc gaa gaa cat caa ttt gcg ttg cag ctg gta aat gat	240
Asp Gln Ile Leu Glu Glu His Gln Phe Ala Leu Gln Leu Val Asn Asp	
65 70 75 80	
gaa gtt ccg gtc gca gca cct gtg gcc ttt aac ggt cag act tta ttg	288
Glu Val Pro Val Ala Ala Pro Val Ala Phe Asn Gly Gln Thr Leu Leu	
85 90 95	
aat cat cag gga ttt tat ttc gct gtt ttt cca agc gtc ggt ggt cgc	336
Asn His Gln Gly Phe Tyr Phe Ala Val Phe Pro Ser Val Gly Gly Arg	
100 105 110	
cag ttc gaa gct gat aat atc gat cag atg gaa gcg gtt ggg cgt tat	384
Gln Phe Glu Ala Asp Asn Ile Asp Gln Met Glu Ala Val Gly Arg Tyr	
115 120 125	
tta ggg cgt atg cac cag acg ggg cgc aaa cag ctt ttt atc cat cgc	432
Leu Gly Arg Met His Gln Thr Gly Arg Lys Gln Leu Phe Ile His Arg	
130 135 140	
ccg acc atc ggt ttg aac gaa tat ctc att gag cca cgc aag ctg ttt	480
Pro Thr Ile Gly Leu Asn Glu Tyr Leu Ile Glu Pro Arg Lys Leu Phe	
145 150 155 160	
gag gac gct aca ctg ata cct tcc ggg ttg aaa gcg gca ttc ctg aaa	528
Glu Asp Ala Thr Leu Ile Pro Ser Gly Leu Lys Ala Ala Phe Leu Lys	
165 170 175	
gcg aca gat gag ctg att gcc gcc gtt aca gca cac tgg cgg gaa gat	576
Ala Thr Asp Glu Leu Ile Ala Ala Val Thr Ala His Trp Arg Glu Asp	
180 185 190	


```

ttc acc gtt ctg cgg cta cat gga gac tgc cac gcc ggg aat att ctc 624
Phe Thr Val Leu Arg Leu His Gly Asp Cys His Ala Gly Asn Ile Leu
      195                      200                      205

tgg cgc gat ggt cca atg ttt gtt gat ctg gat gat gca cgt aat ggt 672
Trp Arg Asp Gly Pro Met Phe Val Asp Leu Asp Asp Ala Arg Asn Gly
      210                      215                      220

cca gcc gtt cag gat ttg tgg atg ttg ctc aat ggc gat aaa gcc gag 720
Pro Ala Val Gln Asp Leu Trp Met Leu Leu Asn Gly Asp Lys Ala Glu
      225                      230                      235                      240

cag cgg atg caa ctg gaa act att att gaa gct tat gaa gaa ttt agc 768
Gln Arg Met Gln Leu Glu Thr Ile Ile Glu Ala Tyr Glu Glu Phe Ser
      245                      250                      255

gag ttc gac acc gct gaa atc gga ctg att gaa cct tta cgc gcc atg 816
Glu Phe Asp Thr Ala Glu Ile Gly Leu Ile Glu Pro Leu Arg Ala Met
      260                      265                      270

cgt ttg gtt tat tat ctt gcc tgg cta atg cgg cgt tgg gct gat ccc 864
Arg Leu Val Tyr Tyr Leu Ala Trp Leu Met Arg Arg Trp Ala Asp Pro
      275                      280                      285

gcg ttc ccg aaa aat ttc ccg tgg tta acc ggg gaa gat tac tgg ctg 912
Ala Phe Pro Lys Asn Phe Pro Trp Leu Thr Gly Glu Asp Tyr Trp Leu
      290                      295                      300

cga cag acg gcg act ttt ata gaa cag gca aaa gtt cta caa gaa ccc 960
Arg Gln Thr Ala Thr Phe Ile Glu Gln Ala Lys Val Leu Gln Glu Pro
      305                      310                      315                      320

cct ttg caa tta aca cct atg tat taa 987
Pro Leu Gln Leu Thr Pro Met Tyr *
      325

<210> 226
<211> 627
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(627)

<400> 226
atg aaa aag att tgg ctg gcg ctg gct ggt tta gtt tta gcg ttt agc 48
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
      1                      5                      10                      15

gca tcg gcg gcg cag tat gaa gat ggt aaa cag tac act acc ctg gaa 96
Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu
      20                      25                      30

aaa ccg gta gct ggc gcg ccg caa gtg ctg gag ttt ttc tct ttc ttc 144
Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe

```

35	40	45	
tgc ccg cac tgc tat cag ttt gaa gaa gtt ctg cat att tct gat aat			192
Cys Pro His Cys Tyr Gln Phe Glu Glu Val Leu His Ile Ser Asp Asn			
50	55	60	
gtg aag aaa aaa ctg ccg gaa ggc gtg aag atg act aaa tac cac gtc			240
Val Lys Lys Lys Leu Pro Glu Gly Val Lys Met Thr Lys Tyr His Val			
65	70	75	80
aac ttc atg ggt ggt gac ctg ggc aaa gat ctg act cag gca tgg gct			288
Asn Phe Met Gly Gly Asp Leu Gly Lys Asp Leu Thr Gln Ala Trp Ala			
	85	90	95
gtg gcg atg gcg ctg ggc gtg gaa gac aaa gtg act gtt ccg ctg ttt			336
Val Ala Met Ala Leu Gly Val Glu Asp Lys Val Thr Val Pro Leu Phe			
	100	105	110
gaa ggc gta cag aaa acc cag acc att cgt tct gct tct gat atc cgc			384
Glu Gly Val Gln Lys Thr Gln Thr Ile Arg Ser Ala Ser Asp Ile Arg			
	115	120	125
gat gta ttt atc aac gca ggt att aaa ggt gaa gag tac gac gcg gcg			432
Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala			
	130	135	140
tgg aac agc ttc gtg gtg aaa tct ctg gtc gct cag cag gaa aaa gct			480
Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala			
	145	150	155
gca gct gac gtg caa ttg cgt ggc gtt ccg gcg atg ttt gtt aac ggt			528
Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly			
	165	170	175
aaa tat cag ctg aat ccg cag ggt atg gat acc agc aat atg gat gtt			576
Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val			
	180	185	190
ttt gtt cag cag tat gct gat aca gtg aaa tat ctg tcc gag aaa aaa			624
Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys			
	195	200	205
taa			627
*			

<210> 227
 <211> 339
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(339)

<400> 227

```

atg acg atg aat tca ttc gag cga agg aat aag atc atc caa tta gtg 48
Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
1 5 10 15

aat gaa cag gga acc gtg ctt gtt cag gat ctg gcg gga gta ttt gct 96
Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
20 25 30

gcc tcg gaa gcg aca atc cgt gcc gat ttg cgc ttt ctc gaa caa aaa 144
Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
35 40 45

ggc gtg gtt acg cgc ttt cat ggc ggt gcg gcg aaa ata atg tct ggt 192
Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
50 55 60

aat agt gaa acc gag acc cag gaa gtc ggg ttt aaa gag cga ttt cag 240
Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
65 70 75 80

ctc gcc agc gcg cca aaa aac aga ata gcg cag gcg gca gtc aaa atg 288
Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
85 90 95

atc cac gaa ggg atg act gat cct acc cac gta ata tgg aca cag gcc 336
Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
100 105 110

taa
* 339

<210> 228
<211> 1041
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1041)

<400> 228
atg aaa tca gtg gtg aat gat act gat ggt atc gtg cgc gtt gca gaa 48
Met Lys Ser Val Val Asn Asp Thr Asp Gly Ile Val Arg Val Ala Glu
1 5 10 15

agc gtc att cct gaa att aaa cat cag gat gag gtg cgg gta aaa att 96
Ser Val Ile Pro Glu Ile Lys His Gln Asp Glu Val Arg Val Lys Ile
20 25 30

gcc agc tcg gcc tta tgt ggt tcc gat tta ccc agg ata ttt aaa aat 144
Ala Ser Ser Gly Leu Cys Gly Ser Asp Leu Pro Arg Ile Phe Lys Asn
35 40 45

ggt gca cat tat tat cca ata acg tta ggc cat gaa ttt agc ggc tat 192
Gly Ala His Tyr Tyr Pro Ile Thr Leu Gly His Glu Phe Ser Gly Tyr

```

239

```

aac tac tcc agc cct tgg ccg ggg cag gag tgg gaa acg gcg agc cgg 912
Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
290 295 300

ttg ctg aca gaa cgt aag tta agc ctg gag cca tta atc gct cac cgt 960
Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
305 310 315 320

gga agc ttt gaa agc ttc gcc cag gcg gtg cgt gac atc gct cgt aat 1008
Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
325 330 335

gct atg ccg ggc aaa gtg ttg ctc att ccc tga 1041
Ala Met Pro Gly Lys Val Leu Leu Ile Pro *
340 345

<210> 229
<211> 1356
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1356)

<400> 229
atg ttt tca gaa gtc atg cgt tat att ctc gac ctc ggc cct acg gtg 48
Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
1 5 10 15

atg ctg ccg att gtc atc att att ttt tct aaa ata tta ggc atg aag 96
Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
20 25 30

gca ggc gat tgc ttt aaa gcg ggt ctg cat atc ggg att ggc ttt gtt 144
Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
35 40 45

ggc att ggc ctt gtg att ggc tta atg ctg gat tcc att ggc ccg gcg 192
Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
50 55 60

gcg aaa gcg atg gcg gaa aat ttc gac ctg aat ctg cat gtg gtc gat 240
Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
65 70 75 80

gtt ggc tgg ccg ggc tct tca cca atg acc tgg gcg tcg caa att gcg 288
Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
85 90 95

ctg gtg gcg att ccg att gcg att ctg gtt aac gtg gcg atg tta ctg 336
Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
100 105 110

acc cgt atg acg cgg gtg gta aat gtt gat atc tgg aat atc tgg cat 384

```

Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His	
115 120 125	
atg acc ttc acc ggc gcg ttg ctg cat ctg gca acc ggt tca tgg atg	432
Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met	
130 135 140	
ata ggg atg gca ggt gtg gta att cac gcg gcg ttt gtt tat aag ctc	480
Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu	
145 150 155 160	
ggc gac tgg ttt gcc cgc gat acc cga aat ttc ttt gag ctg gaa ggt	528
Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly	
165 170 175	
att gct att ccg cac ggt acg tcg gcg tat atg ggg ccg att gcg gtg	576
Ile Ala Ile Pro His Gly Thr Ser Ala Tyr Met Gly Pro Ile Ala Val	
180 185 190	
ctg gtc gat gct atc atc gag aaa atc cca ggc gtt aac cga att aaa	624
Leu Val Asp Ala Ile Ile Glu Lys Ile Pro Gly Val Asn Arg Ile Lys	
195 200 205	
ttt agc gcc gac gat att cag cgc aaa ttt ggt cca ttt ggc gag cct	672
Phe Ser Ala Asp Asp Ile Gln Arg Lys Phe Gly Pro Phe Gly Glu Pro	
210 215 220	
gtc acc gtg ggt ttt gtg atg ggg ctg att atc ggc atc ctc gcg ggt	720
Val Thr Val Gly Phe Val Met Gly Leu Ile Ile Gly Ile Leu Ala Gly	
225 230 235 240	
tac gat gtc aaa ggt gta ttg cag ctg gcg gta aaa acg gcg gca gtg	768
Tyr Asp Val Lys Gly Val Leu Gln Leu Ala Val Lys Thr Ala Ala Val	
245 250 255	
atg ctg cta atg cca cgg gtg att aaa ccc atc atg gat ggt tta acg	816
Met Leu Leu Met Pro Arg Val Ile Lys Pro Ile Met Asp Gly Leu Thr	
260 265 270	
ccc atc gct aag cag gct cgt agt cgt tta cag gcg aag ttc ggc ggt	864
Pro Ile Ala Lys Gln Ala Arg Ser Arg Leu Gln Ala Lys Phe Gly Gly	
275 280 285	
cag gag ttc ctg att ggc ctt gat ccg gcg ttg ctg ctg gga cat acg	912
Gln Glu Phe Leu Ile Gly Leu Asp Pro Ala Leu Leu Gly His Thr	
290 295 300	
gcg gtg gta tcg gca agc ctg att ttt atc cca ctc acc att tta att	960
Ala Val Val Ser Ala Ser Leu Ile Phe Ile Pro Leu Thr Ile Leu Ile	
305 310 315 320	
gct gtt tgt gtg ccg ggt aat cag gtg ctg ccg ttt ggc gat ctt gcc	1008
Ala Val Cys Val Pro Gly Asn Gln Val Leu Pro Phe Gly Asp Leu Ala	
325 330 335	
acc atc ggc ttc ttc gtg gcg atg gcg gtc gcc gtg cat cgt gga aat	1056
Thr Ile Gly Phe Phe Val Ala Met Ala Val Ala Val His Arg Gly Asn	

340	345	350	
ctg ttc cgc acc tta atc tcg ggt gtc atc att atg agc atc acc ctg			1104
Leu Phe Arg Thr Leu Ile Ser Gly Val Ile Ile Met Ser Ile Thr Leu			
355	360	365	
tgg atc gcg acg caa act att ggt ttg cac acc caa ctg gcg gct aat			1152
Trp Ile Ala Thr Gln Thr Ile Gly Leu His Thr Gln Leu Ala Ala Asn			
370	375	380	
gct ggg gcg tta aaa gcc ggg ggt atg gtg gct tca atg gat cag ggc			1200
Ala Gly Ala Leu Lys Ala Gly Gly Met Val Ala Ser Met Asp Gln Gly			
385	390	395	400
ggt tct ccc att acc tgg tta ctg att cag gtt ttc tcc ccg caa aat			1248
Gly Ser Pro Ile Thr Trp Leu Leu Ile Gln Val Phe Ser Pro Gln Asn			
405	410	415	
att ccc ggt ttc att att atc ggt gca att tat ctg acc ggt att ttc			1296
Ile Pro Gly Phe Ile Ile Ile Gly Ala Ile Tyr Leu Thr Gly Ile Phe			
420	425	430	
atg acc tgg cgt aga gcg cgt ggc ttt att aaa caa gag aaa gtc gtt			1344
Met Thr Trp Arg Arg Ala Arg Gly Phe Ile Lys Gln Glu Lys Val Val			
435	440	445	
ctc gca gaa taa			1356
Leu Ala Glu *			
450			
<210> 230			
<211> 285			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(285)			
<400> 230			
atg aaa cgc aag att att gtc gct tgc gga ggc gcg gtt gcg acc tct			48
Met Lys Arg Lys Ile Ile Val Ala Cys Gly Gly Ala Val Ala Thr Ser			
1	5	10	15
acg atg gcg gcg gaa gaa att aaa gag ttg tgt cag aat cat aat att			96
Thr Met Ala Ala Glu Glu Ile Lys Glu Leu Cys Gln Asn His Asn Ile			
20	25	30	
cct gtt gaa tta atc cag tgt cgg gtt aat gaa ata gaa acc tat atg			144
Pro Val Glu Leu Ile Gln Cys Arg Val Asn Glu Ile Glu Thr Tyr Met			
35	40	45	
gat ggt gtg cat ttg ata tgc acc act gcc aaa gtg gat cgt agt ttt			192
Asp Gly Val His Leu Ile Cys Thr Thr Ala Lys Val Asp Arg Ser Phe			
50	55	60	

Val Leu Asp Ser Asp Glu *
145 150

<210> 232
<211> 1263
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1263)

<400> 232
atg aaa acg tta att gcc cgg cat aaa gct ggt gaa cat atc ggc ata 48
Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
1 5 10 15
tgt tca gtc tgt tct gcc cat cgg ttg gtt atc gaa gcg gcg ctg gca 96
Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
20 25 30
ttt gat cgc aac agc acg cgc aaa gtg ctg att gaa gca acg tca aac 144
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
35 40 45
cag gtc aat caa ttt ggc ggt tat acc gga atg aca ccg gca gac ttt 192
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
50 55 60
cgc gaa ttt gtt ttt acg att gcc gat aaa gtt ggg ttt gca cgc gaa 240
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
65 70 75 80
cgc att att ctc ggc ggc gat cat ctg ggg cca aac tgc tgg cag caa 288
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
85 90 95
gaa aat gcg gat gcg gcg atg gaa aaa tcc gtc gag ctg gta aag gaa 336
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
100 105 110
tat gtt cgt gcc ggc ttc agt aaa att cat ctt gat gcg tca atg tcc 384
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
115 120 125
tgc gcg ggg gat ccc ata ccg tta gca cca gaa acg gtt gcg gaa cga 432
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
130 135 140
gct gct gtg ctt tgc ttt gct gcg gaa agt gtg gcg aca gat tgc cag 480
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
145 150 155 160
cgt gag caa ctg agc tat gtc att ggc acc gaa gtt ccg gtt ccg ggc 528
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly
165 170 175

ggg Gly	gag Glu	gcc Ala	agc Ser 180	gcc Ala	att Ile	cag Gln	tca Ser	gta Val 185	cac His	atc Ile	acc Thr	cat His	gtt Val 190	gaa Glu	gat Asp	576
gcc Ala	gcc Ala	aat Asn 195	act Thr	tta Leu	cgt Arg	acg Thr	cat His 200	caa Gln	aag Lys	gcc Ala	ttt Phe 205	att Ile	gcc Ala	cgt Arg	ggg Gly	624
ctg Leu	aca Thr 210	gag Glu	gcg Ala	tta Leu	aca Thr	cgt Arg 215	gtg Val	att Ile	gcc Ala	atc Ile	gtg Val 220	gtg Val	cag Gln	ccg Pro	ggg Gly	672
gtg Val 225	gaa Glu	ttt Phe	gat Asp	cac His	agc Ser 230	aat Asn	att Ile	atc Ile	cat His	tat Tyr 235	cag Gln	ccg Pro	cag Gln	gaa Glu	gcg Ala 240	720
cag Gln	ccg Pro	ctg Leu	gcg Ala	caa Gln 245	tgg Trp	ata Ile	gaa Glu	aac Asn 250	acc Thr	cga Arg	atg Met	gtt Val	tat Tyr	gaa Glu 255	gca Ala	768
cat His	tct Ser	acc Thr	gat Asp 260	tac Tyr	cag Gln	acc Thr	cgg Arg	acg Thr 265	gct Ala	tat Tyr	tgg Trp	gaa Glu	tta Leu 270	gtc Val	cgc Arg	816
gat Asp	cac His	ttt Phe 275	gca Ala	ata Ile	ttg Leu	aaa Lys	gtc Val 280	ggg Gly	ccc Pro	gca Ala	tta Leu	acc Thr 285	ttt Phe	gct Ala	tta Leu	864
cgc Arg 290	gag Glu	gcg Ala	ata Ile	ttt Phe	gca Ala	ctg Leu 295	gca Ala	caa Gln	att Ile	gag Glu	cag Gln 300	gaa Glu	ctt Leu	atc Ile	gcc Ala	912
cct Pro 305	gaa Glu	aat Asn	cgc Arg	agc Ser	ggg Gly 310	tgc Cys	ctg Leu	gcg Ala	gta Val	att Ile 315	gaa Glu	gaa Glu	gtg Val	atg Met	ctc Leu 320	960
gac Asp	gaa Glu	ccg Pro	caa Gln	tac Tyr 325	tgg Trp	aaa Lys	aaa Lys	tat Tyr 330	tat Tyr	cgt Arg	acg Thr	ggg Gly	ttt Phe	aac Asn 335	gat Asp	1008
tca Ser	tta Leu	ctg Leu	gat Asp 340	att Ile	cgt Arg	tac Tyr	agc Ser	ctg Leu 345	tcg Ser	gat Asp	cgt Arg	att Ile	cgt Arg 350	tat Tyr	tac Tyr	1056
tgg Trp	ccg Pro	cat His 355	agt Ser	cgg Arg	att Ile	aaa Lys	aat Asn 360	agc Ser	gtc Val	gaa Glu	acg Thr 365	atg Met	atg Met	gtg Val	aat Asn	1104
ctt Leu	gaa Glu 370	ggc Gly	gtg Val	gac Asp	atc Ile	cca Pro 375	ctg Leu	ggc Gly	atg Met	att Ile	agt Ser 380	cag Gln	tat Tyr	ctt Leu	ccc Pro	1152
aaa Lys 385	caa Gln	ttt Phe	gaa Glu	cgc Arg	att Ile 390	cag Gln	tcc Ser	ggg Gly	gaa Glu	tta Leu 395	tca Ser	gca Ala	ata Ile	ccg Pro	cat His 400	1200

cag	ctg	att	atg	gat	aaa	att	tat	gat	gtt	ttg	cgc	gcc	tat	cgc	tac	1248
Gln	Leu	Ile	Met	Asp	Lys	Ile	Tyr	Asp	Val	Leu	Arg	Ala	Tyr	Arg	Tyr	
				405					410					415		

ggc	tgt	gcg	gaa	taa												1263
Gly	Cys	Ala	Glu	*												
			420													

<210> 233
 <211> 861
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(861)

<400> 233																
atg	aaa	atg	tac	gtg	gta	tcg	aca	aag	cag	atg	ctg	aac	aac	gca	cag	48
Met	Lys	Met	Tyr	Val	Val	Ser	Thr	Lys	Gln	Met	Leu	Asn	Asn	Ala	Gln	
1				5					10					15		
cgc	ggc	ggt	tat	gcg	gtt	ccg	gca	ttc	aat	att	cac	aat	ctc	gaa	acg	96
Arg	Gly	Gly	Tyr	Ala	Val	Pro	Ala	Phe	Asn	Ile	His	Asn	Leu	Glu	Thr	
			20					25					30			
atg	caa	gtg	gtg	gta	gaa	acc	gct	gcc	aac	ctg	cat	gcg	ccg	gtc	atc	144
Met	Gln	Val	Val	Val	Glu	Thr	Ala	Ala	Asn	Leu	His	Ala	Pro	Val	Ile	
		35					40					45				
atc	gcc	gga	acg	cct	ggc	aca	ttt	act	cat	gct	ggt	aca	gaa	aat	ctg	192
Ile	Ala	Gly	Thr	Pro	Gly	Thr	Phe	Thr	His	Ala	Gly	Thr	Glu	Asn	Leu	
	50					55					60					
ttg	gcg	ctg	gtc	agc	gcg	atg	gcg	aag	caa	tat	cac	cat	cca	ctg	gca	240
Leu	Ala	Leu	Val	Ser	Ala	Met	Ala	Lys	Gln	Tyr	His	His	Pro	Leu	Ala	
65					70				75					80		
att	cat	ctc	gac	cat	cac	acg	aaa	ttt	gac	gat	atc	gct	cag	aag	gtt	288
Ile	His	Leu	Asp	His	His	Thr	Lys	Phe	Asp	Asp	Ile	Ala	Gln	Lys	Val	
			85						90					95		
cgt	tct	ggc	gtg	cgc	tca	gtc	atg	att	gac	gcc	tcg	cat	ttg	cct	ttt	336
Arg	Ser	Gly	Val	Arg	Ser	Val	Met	Ile	Asp	Ala	Ser	His	Leu	Pro	Phe	
			100					105					110			
gcg	caa	aat	att	tca	cgg	gtc	aaa	gag	gtg	gtg	gat	ttt	tgc	cat	cgc	384
Ala	Gln	Asn	Ile	Ser	Arg	Val	Lys	Glu	Val	Val	Asp	Phe	Cys	His	Arg	
		115					120					125				
ttt	gat	gtc	agc	gtc	gag	gcg	gag	ctg	ggg	caa	ctt	ggc	ggc	cag	gaa	432
Phe	Asp	Val	Ser	Val	Glu	Ala	Glu	Leu	Gly	Gln	Leu	Gly	Gly	Gln	Glu	
	130					135					140					
gat	gat	gtg	caa	gtc	aat	gaa	gcc	gat	gcg	ttg	tac	acc	aac	ccc	gct	480
Asp	Asp	Val	Gln	Val	Asn	Glu	Ala	Asp	Ala	Leu	Tyr	Thr	Asn	Pro	Ala	

145	150	155	160	
cag gcg cgt gaa ttt gcc gag gca acc gga att gat tcc ctg gcg gtc				528
Gln Ala Arg Glu Phe Ala Glu Ala Thr Gly Ile Asp Ser Leu Ala Val	165	170	175	
gcc atc ggc acg gct cat ggg atg tat gcc agc gca ccg gcg ctt gat				576
Ala Ile Gly Thr Ala His Gly Met Tyr Ala Ser Ala Pro Ala Leu Asp	180	185	190	
ttt tct aga ctg gag aac att cgc cag tgg gtg aac tta ccg ctg gtg				624
Phe Ser Arg Leu Glu Asn Ile Arg Gln Trp Val Asn Leu Pro Leu Val	195	200	205	
ctg cat ggc gcg tca ggg tta tcg act aag gat att cag caa acc atc				672
Leu His Gly Ala Ser Gly Leu Ser Thr Lys Asp Ile Gln Gln Thr Ile	210	215	220	
aaa ctg ggg ata tgc aaa atc aac gtt gca acg gag ctg aaa aat gcc				720
Lys Leu Gly Ile Cys Lys Ile Asn Val Ala Thr Glu Leu Lys Asn Ala	225	230	235	240
ttc tcg cag gcg tta aaa aat tac ctg acc gag cac cct gaa gcg acc				768
Phe Ser Gln Ala Leu Lys Asn Tyr Leu Thr Glu His Pro Glu Ala Thr	245	250	255	
gat ccc cgg gat tat ttg cag tcg gct aaa tcc gca atg cgc gat gtg				816
Asp Pro Arg Asp Tyr Leu Gln Ser Ala Lys Ser Ala Met Arg Asp Val	260	265	270	
gtg agc aaa gtg att gcc gat tgt ggc tgc gag ggc agg gca taa				861
Val Ser Lys Val Ile Ala Asp Cys Gly Cys Glu Gly Arg Ala *	275	280	285	

<210> 234
 <211> 474
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(474)

<400> 234	
atg agt caa aac gat atc att atc aga act cat tat aag tct cct cat	48
Met Ser Gln Asn Asp Ile Ile Ile Arg Thr His Tyr Lys Ser Pro His	
1 5 10 15	
aga ttg cac atc gat agc gac ata cca aca cct tca tca gag cct att	96
Arg Leu His Ile Asp Ser Asp Ile Pro Thr Pro Ser Ser Glu Pro Ile	
20 25 30	
aat caa ttt gcg cgc cag ctc atc acc cta ctt gat acc tct gac tta	144
Asn Gln Phe Ala Arg Gln Leu Ile Thr Leu Leu Asp Thr Ser Asp Leu	
35 40 45	

```

    agt tcg atg ctg tca tac tgt gtt act cag gaa ttt acc gca aac tgt 192
    Ser Ser Met Leu Ser Tyr Cys Val Thr Gln Glu Phe Thr Ala Asn Cys
        50                55                60

    cga aaa ata tca caa aat tgt tat tcc act gcc ctt ttt acc att aac 240
    Arg Lys Ile Ser Gln Asn Cys Tyr Ser Thr Ala Leu Phe Thr Ile Asn
        65                70                75                80

    ttt gcc act tca ccc atc cat aca gaa aat ata ctc att aca tta cac 288
    Phe Ala Thr Ser Pro Ile His Thr Glu Asn Ile Leu Ile Thr Leu His
        85                90                95

    tat aaa aaa gaa atc att tcc tta tta ctg gaa acc acg cct att aaa 336
    Tyr Lys Lys Glu Ile Ile Ser Leu Leu Leu Glu Thr Thr Pro Ile Lys
        100                105                110

    gct aac cat ttg cga agc ata ctg gat tat att gaa cag gaa cag tta 384
    Ala Asn His Leu Arg Ser Ile Leu Asp Tyr Ile Glu Gln Glu Gln Leu
        115                120                125

    act gct gaa gat cgt aac cat tgt atg aaa ctg tct aaa aaa atc cat 432
    Thr Ala Glu Asp Arg Asn His Cys Met Lys Leu Ser Lys Lys Ile His
        130                135                140

    aga gaa aaa aac tat aca ccc aac agt aaa tct caa tgg tag 474
    Arg Glu Lys Asn Tyr Thr Pro Asn Ser Lys Ser Gln Trp *
        145                150                155

    <210> 235
    <211> 1416
    <212> DNA
    <213> Escherichia coli

    <220>
    <221> CDS
    <222> (1)...(1416)

    <400> 235
    ttg caa tct cct tct gac gct att ttt tgt cgc cat ctg tca ttg caa 48
    Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln
        1                5                10                15

    tac gcc ctt gat tca ttg aga aat gga aaa ggc aaa gtc aac ctg att 96
    Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile
        20                25                30

    aaa cat tac tcc tcc gtt gaa tcc ata cag cag cat gtc ccc tta gtc 144
    Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val
        35                40                45

    cgg gac gcg gag ttc aga gca tta ctt cgc cat cct cct gca ggg agt 192
    Arg Asp Ala Glu Phe Arg Ala Leu Leu Arg His Pro Pro Ala Gly Ser
        50                55                60

```

cgc gtt atc gcg agt aag gat ttt ggc ttc gct tta gat att ttc ttt	240
Arg Val Ile Ala Ser Lys Asp Phe Gly Phe Ala Leu Asp Ile Phe Phe	
65 70 75 80	
tgt cga atg atg gca aac aat gtc agt cat atg tcc gcg att tta tat	288
Cys Arg Met Met Ala Asn Asn Val Ser His Met Ser Ala Ile Leu Tyr	
85 90 95	
ata gac aat cat act ttg tca gta agg cta cga ata aag cag tca gtg	336
Ile Asp Asn His Thr Leu Ser Val Arg Leu Arg Ile Lys Gln Ser Val	
100 105 110	
tat gga caa tta aat tat gtt gtg tcc gtt tac gac ccg aac gat acc	384
Tyr Gly Gln Leu Asn Tyr Val Val Ser Val Tyr Asp Pro Asn Asp Thr	
115 120 125	
aac gtt gcc gtc aga gac acc cac agg aca gca cgg ggc ttt ctt tcg	432
Asn Val Ala Val Arg Asp Thr His Arg Thr Ala Arg Gly Phe Leu Ser	
130 135 140	
ctt gat aag ttc atc agt tca ggt ccc gat gct cag acc tgg gct gat	480
Leu Asp Lys Phe Ile Ser Ser Gly Pro Asp Ala Gln Thr Trp Ala Asp	
145 150 155 160	
aga tat gtt cgc aac tgt gca att gct att ctg ccc cta tta cct gtg	528
Arg Tyr Val Arg Asn Cys Ala Ile Ala Ile Leu Pro Leu Leu Pro Val	
165 170 175	
gga gtt cca ggg gct att ttc gcg ggt att gca tca cga atg cca ttt	576
Gly Val Pro Gly Ala Ile Phe Ala Gly Ile Ala Ser Arg Met Pro Phe	
180 185 190	
gcc cct ata cat cca tcg gca atg ttg tta ata atg gct aca ggc cag	624
Ala Pro Ile His Pro Ser Ala Met Leu Leu Ile Met Ala Thr Gly Gln	
195 200 205	
tct caa cag ctt att aca tta ttc aaa cag ttg ccc ata ctc cct gaa	672
Ser Gln Gln Leu Ile Thr Leu Phe Lys Gln Leu Pro Ile Leu Pro Glu	
210 215 220	
aaa gaa atc att gaa ata ata act gcg cag aat agc gtt ggt aca cct	720
Lys Glu Ile Ile Glu Ile Ile Thr Ala Gln Asn Ser Val Gly Thr Pro	
225 230 235 240	
gct tta ttt ttg gct atg atg aac gga cat act gac aac gtg aaa ata	768
Ala Leu Phe Leu Ala Met Met Asn Gly His Thr Asp Asn Val Lys Ile	
245 250 255	
ttt atg caa gaa att cag tca ctg gta gat aat cac atc att cat gaa	816
Phe Met Gln Glu Ile Gln Ser Leu Val Asp Asn His Ile Ile His Glu	
260 265 270	
gat aat ctg gtt aaa tta ctg caa act aaa agt gct aac gaa aca cct	864
Asp Asn Leu Val Lys Leu Leu Gln Thr Lys Ser Ala Asn Glu Thr Pro	
275 280 285	
gga ctt tat atc tcc atg ttg tat gga ttc gat gaa ata atc gat atc	912

Gly Leu Tyr Ile Ser Met Leu Tyr Gly Phe Asp Glu Ile Ile Asp Ile	
290 295 300	
ttt ctg aat gca tta acc act cca ata gca caa gag ctt tta aac aaa	960
Phe Leu Asn Ala Leu Thr Thr Pro Ile Ala Gln Glu Leu Leu Asn Lys	
305 310 315 320	
aaa ctg gtg atg agt att tta gcc atg aaa ata cat gat ggt gag cca	1008
Lys Leu Val Met Ser Ile Leu Ala Met Lys Ile His Asp Gly Glu Pro	
325 330 335	
gga tta tac gcc gca atg gaa aat aat cac cct ttg tgt gtc aca cgg	1056
Gly Leu Tyr Ala Ala Met Glu Asn Asn His Pro Leu Cys Val Thr Arg	
340 345 350	
ttc ctc tct aaa att aat ggc atc gcc ttt aaa tac aag ttg agc aaa	1104
Phe Leu Ser Lys Ile Asn Gly Ile Ala Phe Lys Tyr Lys Leu Ser Lys	
355 360 365	
gct aac atc atg gat tta tta aaa gga gct aca gca cag gga acc cct	1152
Ala Asn Ile Met Asp Leu Leu Lys Gly Ala Thr Ala Gln Gly Thr Pro	
370 375 380	
gca tta tac atc gcc atg agc aag ggt aat gaa gac gtc gtg tta tct	1200
Ala Leu Tyr Ile Ala Met Ser Lys Gly Asn Glu Asp Val Val Leu Ser	
385 390 395 400	
tat ata tcg acg ctg ggt gct ttt gca aaa aaa cat tct ttt agt caa	1248
Tyr Ile Ser Thr Leu Gly Ala Phe Ala Lys Lys His Ser Phe Ser Gln	
405 410 415	
cat cag tta ttt aca cta ttg gcc gct aaa aat cat gac aac atg tca	1296
His Gln Leu Phe Thr Leu Leu Ala Ala Lys Asn His Asp Asn Met Ser	
420 425 430	
gct gtt cat ata gcc att cat cat aag cat tat aaa act gta gaa aca	1344
Ala Val His Ile Ala Ile His His Lys His Tyr Lys Thr Val Glu Thr	
435 440 445	
tat tat gct gct att aat gca atc agc caa agc ctg agt ttt agt gct	1392
Tyr Tyr Ala Ala Ile Asn Ala Ile Ser Gln Ser Leu Ser Phe Ser Ala	
450 455 460	
gat gaa ata aag acg tat tta taa	1416
Asp Glu Ile Lys Thr Tyr Leu *	
465 470	

<210> 236
 <211> 387
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(387)

<400> 236

atg cca tct gga tta ttt atg gac tta ttg cct ttt tta ctg gac gcg 48
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15

aac ctc agc gcg aca aac cca ccc gct att ccg cac tgg tgg aag cgt 96
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30

caa ccg ctt att ccc aac ctt ctg tca cag gaa ctg aaa aac tat ctg 144
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45

aag ctt aat gtt aaa gag aaa aat att cag att gca gac cag gta att 192
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60

att gat gaa act gca ggt gaa gtt gtt atc ggc gcg aat acc cgt att 240
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80

tgt cat ggt gcc gtt att cag ggt ccg gta gtg att ggc gca aac tgc 288
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95

ctg ata ggt aat tgg att tgc ccc tat att tcc aga cat ctg tta tca 336
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110

ctt aac cca tta caa gcc cgc tgc cgc aga tat tcc cgt ggc gag cga 384
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

taa 387
*

<210> 237

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1197)

<400> 237

atg aaa acc tgg ata ttt atc tgt atg tcc ata gca atg ttg cta tgg 48
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15

ttt tta agt acg cta aga cgt aaa ccc agt caa aag aaa ggc tgt att 96
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30

gac gcc att ata cct gcg tat aac gaa ggc ccg tgt ctg gcg cag tca 144

Asp	Ala	Ile	Ile	Pro	Ala	Tyr	Asn	Glu	Gly	Pro	Cys	Leu	Ala	Gln	Ser		
	35						40					45					
ctg	gat	aat	cta	ctg	cgt	aac	cct	tat	ttt	tgc	cgg	gta	att	tgc	gtt	192	
Leu	Asp	Asn	Leu	Leu	Arg	Asn	Pro	Tyr	Phe	Cys	Arg	Val	Ile	Cys	Val		
	50					55					60						
aac	gac	ggc	tcc	acg	gac	aat	acc	gaa	gcg	gtc	atg	gcg	gaa	gtc	aaa	240	
Asn	Asp	Gly	Ser	Thr	Asp	Asn	Thr	Glu	Ala	Val	Met	Ala	Glu	Val	Lys		
	65				70					75					80		
cgc	aaa	tgg	ggc	gac	cgc	ttt	gtt	gcc	gtc	acg	caa	aaa	aat	acc	ggc	288	
Arg	Lys	Trp	Gly	Asp	Arg	Phe	Val	Ala	Val	Thr	Gln	Lys	Asn	Thr	Gly		
				85					90					95			
aaa	ggc	ggc	gac	ctg	atg	aat	ggc	ctc	aat	tac	gcc	acc	tgc	gac	cag	336	
Lys	Gly	Gly	Ala	Leu	Met	Asn	Gly	Leu	Asn	Tyr	Ala	Thr	Cys	Asp	Gln		
			100					105					110				
gtt	ttt	tta	agt	gat	gcc	gac	acc	tat	gtt	ccg	ccc	gat	caa	gac	gga	384	
Val	Phe	Leu	Ser	Asp	Ala	Asp	Thr	Tyr	Val	Pro	Pro	Asp	Gln	Asp	Gly		
		115					120					125					
atg	ggc	tat	atg	ctg	gca	gaa	att	gag	cgc	ggc	gcc	gat	gcc	gta	ggc	432	
Met	Gly	Tyr	Met	Leu	Ala	Glu	Ile	Glu	Arg	Gly	Ala	Asp	Ala	Val	Gly		
	130					135					140						
ggc	att	ccc	tct	act	gag	ttg	aaa	ggc	gag	ggc	ctg	tta	ccg	cac	atc	480	
Gly	Ile	Pro	Ser	Thr	Ala	Leu	Lys	Gly	Ala	Gly	Leu	Leu	Pro	His	Ile		
	145				150					155					160		
cgc	gag	acc	gta	aag	ttg	ccg	atg	att	gtt	atg	aag	cgc	acg	cta	cag	528	
Arg	Ala	Thr	Val	Lys	Leu	Pro	Met	Ile	Val	Met	Lys	Arg	Thr	Leu	Gln		
				165					170					175			
cag	ctc	ctg	ggc	gca	ccg	ttt	att	atc	agc	ggc	gcc	tgc	ggg	atg		576	
Gln	Leu	Leu	Gly	Gly	Ala	Pro	Phe	Ile	Ile	Ser	Gly	Ala	Cys	Gly	Met		
			180					185					190				
ttc	cgt	act	gat	gta	ttg	cgt	aag	ttc	ggc	ttc	tgc	gat	cgt	act	aaa	624	
Phe	Arg	Thr	Asp	Val	Leu	Arg	Lys	Phe	Gly	Phe	Ser	Asp	Arg	Thr	Lys		
		195					200					205					
gtc	gaa	gac	ctt	gat	ctc	acc	tgg	aca	ttg	gtg	gca	aac	ggc	tac	cgt	672	
Val	Glu	Asp	Leu	Asp	Leu	Thr	Trp	Thr	Leu	Val	Ala	Asn	Gly	Tyr	Arg		
	210					215					220						
att	cgg	cag	gag	aat	cgc	tgc	atc	gta	tac	cca	cag	gaa	tgc	aac	agc	720	
Ile	Arg	Gln	Ala	Asn	Arg	Cys	Ile	Val	Tyr	Pro	Gln	Glu	Cys	Asn	Ser		
	225				230					235					240		
ccg	cgt	gag	gag	tgg	cgt	cgc	tgg	cgg	cgt	tgg	att	gtg	gga	tac	gag	768	
Pro	Arg	Glu	Glu	Trp	Arg	Arg	Trp	Arg	Arg	Trp	Ile	Val	Gly	Tyr	Ala		
				245					250					255			
gtc	tgt	atg	cgc	ctg	cat	aaa	aga	ctt	tta	ttt	agc	cgc	ttc	ggc	atc	816	
Val	Cys	Met	Arg	Leu	His	Lys	Arg	Leu	Leu	Phe	Ser	Arg	Phe	Gly	Ile		

260	265	270	
ttc agt ata ttt cct atg ctg ttg gtt gtg ctt tat ggc gtt ggg att			864
Phe Ser Ile Phe Pro Met Leu Leu Val Val Leu Tyr Gly Val Gly Ile			
275	280	285	
tat ctc act acc tgg ttt aat gaa ttc atc acc acc ggg ccg cat gga			912
Tyr Leu Thr Thr Trp Phe Asn Glu Phe Ile Thr Thr Gly Pro His Gly			
290	295	300	
gtg gtg ttg gca atg ttt ccg ctt atc tgg gtc ggc gta gtt tgt gtt			960
Val Val Leu Ala Met Phe Pro Leu Ile Trp Val Gly Val Val Cys Val			
305	310	315	320
att ggt gct ttt agc gcc tgg ttt cat cgt tgc tgg ttg ttg gtg cct			1008
Ile Gly Ala Phe Ser Ala Trp Phe His Arg Cys Trp Leu Leu Val Pro			
325	330	335	
tta gcg ccg ctt tcc gtt gtg tat gta tta tta gct tat gcc atc tgg			1056
Leu Ala Pro Leu Ser Val Val Tyr Val Leu Leu Ala Tyr Ala Ile Trp			
340	345	350	
att att tat gga ctt att gcc ttt ttt act gga cgc gaa cct cag cgc			1104
Ile Ile Tyr Gly Leu Ile Ala Phe Phe Thr Gly Arg Glu Pro Gln Arg			
355	360	365	
gac aaa ccc acc cgc tat tcc gca ctg gtg gaa gcg tca acc gct tat			1152
Asp Lys Pro Thr Arg Tyr Ser Ala Leu Val Glu Ala Ser Thr Ala Tyr			
370	375	380	
tcc caa cct tct gtc aca gga act gaa aaa cta tct gaa gct taa			1197
Ser Gln Pro Ser Val Thr Gly Thr Glu Lys Leu Ser Glu Ala *			
385	390	395	
<210> 238			
<211> 1659			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(1659)			
<400> 238			
atg att ctt gag cgc gtt gaa att gtg ggt ttt cgc ggt atc aac cgt			48
Met Ile Leu Glu Arg Val Glu Ile Val Gly Phe Arg Gly Ile Asn Arg			
1	5	10	15
ttg tcg ttg atg ctg gaa caa aac aac gtc ctg att ggg gag aac gcg			96
Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala			
20	25	30	
tgg ggt aaa tcc agc ttg ctg gac gcc tta act ctg ctg cta tcg cca			144
Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Leu Ser Pro			
35	40	45	

gaa tca gat ctc tac cat ttt gag cgc gac gat ttc tgg ttc ccg ccg																192	
Glu	Ser	Asp	Leu	Tyr	His	Phe	Glu	Arg	Asp	Asp	Phe	Trp	Phe	Pro	Pro		
50							55		60								
gga gat atc aac ggg cga gaa cat cat ctg cat att att ttg acc ttc																240	
Gly	Asp	Ile	Asn	Gly	Arg	Glu	His	His	Leu	His	Ile	Ile	Leu	Thr	Phe		
65							70		75					80			
cgc gaa tcg ctg cca ggc cga cat cgg gtt cgc cgt tat cgg ccg ctg																288	
Arg	Glu	Ser	Leu	Pro	Gly	Arg	His	Arg	Val	Arg	Arg	Tyr	Arg	Pro	Leu		
				85		90					95						
gaa gcg tgc tgg acg cca tgc acc gat ggc tat cac cgt att ttt tat																336	
Glu	Ala	Cys	Trp	Thr	Pro	Cys	Thr	Asp	Gly	Tyr	His	Arg	Ile	Phe	Tyr		
			100		105					110							
cgt ctg gaa ggg gag agt gcg gaa gac ggc agc gtg atg aca ctg cgc																384	
Arg	Leu	Glu	Gly	Glu	Ser	Ala	Glu	Asp	Gly	Ser	Val	Met	Thr	Leu	Arg		
		115		120					125								
agt ttt ctc gat aaa gac gga cat ccg att gat gtc gag gat att aac																432	
Ser	Phe	Leu	Asp	Lys	Asp	Gly	His	Pro	Ile	Asp	Val	Glu	Asp	Ile	Asn		
130		135					140										
gat cag gca cgc cat ctg gtg cgt tta atg ccg gtg ctg cgc ttg cgt																480	
Asp	Gln	Ala	Arg	His	Leu	Val	Arg	Leu	Met	Pro	Val	Leu	Arg	Leu	Arg		
145		150					155					160					
gat gcc cgt ttt atg cgc cgt att cgt aac ggc acg gtg cca aat gtc																528	
Asp	Ala	Arg	Phe	Met	Arg	Arg	Ile	Arg	Asn	Gly	Thr	Val	Pro	Asn	Val		
				165		170					175						
cct aat gtg gaa gtc acc gcg cgc cag ctc gat ttc ctc gcc cgt gag																576	
Pro	Asn	Val	Glu	Val	Thr	Ala	Arg	Gln	Leu	Asp	Phe	Leu	Ala	Arg	Glu		
			180		185					190							
tta tcc tca cat ccg caa aat ctc tct gat ggg cag att cgt cag gga																624	
Leu	Ser	Ser	His	Pro	Gln	Asn	Leu	Ser	Asp	Gly	Gln	Ile	Arg	Gln	Gly		
195		200					205										
ctt tcc gca atg gta cag ctg ctt gag cat tat ttc tct gag cag ggg																672	
Leu	Ser	Ala	Met	Val	Gln	Leu	Leu	Glu	His	Tyr	Phe	Ser	Glu	Gln	Gly		
210		215					220										
gcc gga cag gcg cga tat cgt tta atg cgg cgg cga gcc agc aat gag																720	
Ala	Gly	Gln	Ala	Arg	Tyr	Arg	Leu	Met	Arg	Arg	Arg	Ala	Ser	Asn	Glu		
225		230					235					240					
caa cga agc tgg cgc tat ctg gat atc atc aac cgg atg att gac cga																768	
Gln	Arg	Ser	Trp	Arg	Tyr	Leu	Asp	Ile	Ile	Asn	Arg	Met	Ile	Asp	Arg		
				245		250					255						
cct ggt ggg cgc tcg tat cgg gtt att ttg ctc ggc cta ttt gct act																816	
Pro	Gly	Gly	Arg	Ser	Tyr	Arg	Val	Ile	Leu	Leu	Gly	Leu	Phe	Ala	Thr		
			260		265					270							

ttg ttg cag gca aaa ggc aca ttg cga ctg gat aaa gac gcc cgt cca	864
Leu Leu Gln Ala Lys Gly Thr Leu Arg Leu Asp Lys Asp Ala Arg Pro	
275 280 285	
ttg ttg ctg atc gaa gat cca gaa acc cgt tta cac ccc att atg ctt	912
Leu Leu Leu Ile Glu Asp Pro Glu Thr Arg Leu His Pro Ile Met Leu	
290 295 300	
tca gtt gcc tgg cat ctg ttg aat ctt ctg cca ttg cag cgc att gcc	960
Ser Val Ala Trp His Leu Leu Asn Leu Leu Pro Leu Gln Arg Ile Ala	
305 310 315 320	
acc acc aac tcg ggt gag ttg ctt tcg tta acg ccg gta gag cat gtt	1008
Thr Thr Asn Ser Gly Glu Leu Leu Ser Leu Thr Pro Val Glu His Val	
325 330 335	
tgc cga ctg gta cgt gag tcc tcg cgc gtt gcc gcc tgg cgt ctg ggg	1056
Cys Arg Leu Val Arg Glu Ser Ser Arg Val Ala Ala Trp Arg Leu Gly	
340 345 350	
ccg agt ggc ttg agt acc gaa gat agc cga cgc ata tcc ttt cac att	1104
Pro Ser Gly Leu Ser Thr Glu Asp Ser Arg Arg Ile Ser Phe His Ile	
355 360 365	
cgt ttt aac cgt ccg tca tcg ctg ttt gca cgc tgc tgg ttg ctg gtg	1152
Arg Phe Asn Arg Pro Ser Ser Leu Phe Ala Arg Cys Trp Leu Leu Val	
370 375 380	
gaa ggg gaa acg gaa acc tgg gtt atc aat gaa ctg gcg cgt cag tgc	1200
Glu Gly Glu Thr Glu Thr Trp Val Ile Asn Glu Leu Ala Arg Gln Cys	
385 390 395 400	
gga cat cat ttt gat gcc gaa ggg atc aag gtc att gag ttt gcc cag	1248
Gly His His Phe Asp Ala Glu Gly Ile Lys Val Ile Glu Phe Ala Gln	
405 410 415	
tcc ggg cta aag cca ctg gtt aaa ttt gcc cgc cga atg ggg att gaa	1296
Ser Gly Leu Lys Pro Leu Val Lys Phe Ala Arg Arg Met Gly Ile Glu	
420 425 430	
tgg cat gta ctg gtc gat ggc gat gaa gca ggg aag aaa tat gcc gct	1344
Trp His Val Leu Val Asp Gly Asp Glu Ala Gly Lys Lys Tyr Ala Ala	
435 440 445	
acg gta cgc agc ctg ttg aat aac gat cgg gaa gcc gaa cga gaa cat	1392
Thr Val Arg Ser Leu Leu Asn Asn Asp Arg Glu Ala Glu Arg Glu His	
450 455 460	
tta acg gcg tta ccg gcg ctg gat atg gaa cat ttt atg tat cgc cag	1440
Leu Thr Ala Leu Pro Ala Leu Asp Met Glu His Phe Met Tyr Arg Gln	
465 470 475 480	
gga ttt tcc gat gtg ttc cac cgc atg gcg caa atc ccg gaa aat gta	1488
Gly Phe Ser Asp Val Phe His Arg Met Ala Gln Ile Pro Glu Asn Val	
485 490 495	
ccg atg aat cta cgc aaa att atc tcg aaa gcg atc cat cgc tct tcc	1536

Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser
500 505 510

aaa ccc gat ctt gcc att gaa gtg gca atg gag gca gga cgt cgt ggt 1584
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly
515 520 525

gtg gac tcc gta ccg acg ctg ctg aaa aaa atg ttc tca cgc gtg ctg 1632
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu
530 535 540

tgg ctg gcg cgc ggt cgc gcg gat taa 1659
Trp Leu Ala Arg Gly Arg Ala Asp *
545 550

<210> 239

<211> 1059

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1059)

<400> 239

atg cta cca tct att tca atc aac aat acc agc gca gct tac cca gaa 48
Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu
1 5 10 15

tcc atc aat gaa aat aac aat gat gaa gtt aat gga tta gta caa gag 96
Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu
20 25 30

ttc aaa aac ctt ttt aat ggt aag gaa gga ata agc acc tgt att aaa 144
Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys
35 40 45

cat cta ctt gag ctt ata aaa aac gcc ata cga gta aac gac gat cct 192
His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro
50 55 60

tat aga ttt aat att aat aat tcc tca gtt act tat att gat att gac 240
Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp
65 70 75 80

tcc aat gat aca gac cat att act att ggt atc gac aac caa gaa cca 288
Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro
85 90 95

ata gaa tta cct gcg aac tat aaa gac aaa gaa ctc gtc cgt act atc 336
Ile Glu Leu Pro Ala Asn Tyr Lys Asp Lys Glu Leu Val Arg Thr Ile
100 105 110

att aat gac aac ata gtt gag aag act cat gat atc aat aac aag gaa 384
Ile Asn Asp Asn Ile Val Glu Lys Thr His Asp Ile Asn Asn Lys Glu
115 120 125

atg atc ttc agc gca tta aaa gaa ata tat gat gga gat cct ggt ttt	432
Met Ile Phe Ser Ala Leu Lys Glu Ile Tyr Asp Gly Asp Pro Gly Phe	
130 135 140	
atc ttc gat aag ata tca cac aaa ctc aga cat acg gta acg gaa ttt	480
Ile Phe Asp Lys Ile Ser His Lys Leu Arg His Thr Val Thr Glu Phe	
145 150 155 160	
gat gag agc ggg aaa agc gaa cca acg gac tta ttt acc tgg tac ggt	528
Asp Glu Ser Gly Lys Ser Glu Pro Thr Asp Leu Phe Thr Trp Tyr Gly	
165 170 175	
aaa gat aaa aaa ggc gac tct ctc gct att gta att aaa aat aaa aac	576
Lys Asp Lys Lys Gly Asp Ser Leu Ala Ile Val Ile Lys Asn Lys Asn	
180 185 190	
gga aat gat tac tta tct ctc ggt tac tac gat cag gac gac tac cac	624
Gly Asn Asp Tyr Leu Ser Leu Gly Tyr Tyr Asp Gln Asp Asp Tyr His	
195 200 205	
att caa aga gga att cgt att aat ggt gat agt ctc acc caa tat tgt	672
Ile Gln Arg Gly Ile Arg Ile Asn Gly Asp Ser Leu Thr Gln Tyr Cys	
210 215 220	
agt gaa aac gcc agg agt gct tca gcg tgg ttt gaa agc agt aaa gct	720
Ser Glu Asn Ala Arg Ser Ala Ser Ala Trp Phe Glu Ser Ser Lys Ala	
225 230 235 240	
atc atg gca gaa tca ttt gca act ggt tcc gat cat cag gtt gta aac	768
Ile Met Ala Glu Ser Phe Ala Thr Gly Ser Asp His Gln Val Val Asn	
245 250 255	
gag ctc aac ggg gaa aga ctg aga gaa cca aac gac gtt ttt aaa cgt	816
Glu Leu Asn Gly Glu Arg Leu Arg Glu Pro Asn Asp Val Phe Lys Arg	
260 265 270	
tat ggt cga gca ata aga tat gat ttt caa gtg gac gat gca aaa tat	864
Tyr Gly Arg Ala Ile Arg Tyr Asp Phe Gln Val Asp Asp Ala Lys Tyr	
275 280 285	
aaa tgc gac cat cta aaa gaa ata gtt tct act tta gtc ggt aac aaa	912
Lys Cys Asp His Leu Lys Glu Ile Val Ser Thr Leu Val Gly Asn Lys	
290 295 300	
att aac gtt ggc cat tct caa aaa ata tat aag cat ttt aag gat ctc	960
Ile Asn Val Gly His Ser Gln Lys Ile Tyr Lys His Phe Lys Asp Leu	
305 310 315 320	
gaa ggt aaa att gaa gaa agg ctt caa aat cgc cag gct gaa tat caa	1008
Glu Gly Lys Ile Glu Glu Arg Leu Gln Asn Arg Gln Ala Glu Tyr Gln	
325 330 335	
aat gaa att aat caa cca tct gcg cca ggt gtt aat ttt gat gat att	1056
Asn Glu Ile Asn Gln Pro Ser Ala Pro Gly Val Asn Phe Asp Asp Ile	
340 345 350	

taa
*

1059

<210> 240
<211> 1128
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1128)

<400> 240

atg atg cgc cat tta cgc aat att ttt aat ctg ggt atc aaa gag ttg	48
Met Met Arg His Leu Arg Asn Ile Phe Asn Leu Gly Ile Lys Glu Leu	
1 5 10 15	
cgc agt ctg ctc ggt gat aaa gcg atg ctg acg ctg att gtc ttc tcg	96
Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser	
20 25 30	
ttt acg gtg tcg gtg tat tcg tca gcg acc gtt acg cca gga tcg ttg	144
Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu	
35 40 45	
aac ctc gcg ccg atc gcc att gcc gat atg gat caa tcg cag tta tcg	192
Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser	
50 55 60	
aac cgg atc gtt aac agc ttc tat cgt ccg tgg ttt ttg cca ccg gag	240
Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu	
65 70 75 80	
atg atc acc gcc gat gag atg gat gcc gga ctg gac gcc gga cgc tat	288
Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr	
85 90 95	
acc ttc gcg ata aat att ccg cct aat ttt cag cgt gat gtc ctc gcc	336
Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala	
100 105 110	
gga cgc cag ccg gat att cag gtg aac gtc gat gcc acg cgc atg agc	384
Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser	
115 120 125	
cag gca ttt acc ggc aat ggg tat atc cag aat att atc aac ggt gaa	432
Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu	
130 135 140	
gtg aac agc ttt gtc gcg cgc tac cgt gat aac agc gaa ccg ttg gta	480
Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val	
145 150 155 160	
tcg ctg gaa acc cgg atg cgc ttt aac ccg aac ctc gat ccc gcg tgg	528
Ser Leu Glu Thr Arg Met Arg Phe Asn Pro Asn Leu Asp Pro Ala Trp	

	165	170	175	
ttt ggc ggg gtg atg gcg atc atc aac aac att acc atg ctg gcg att				576
Phe Gly Gly Val Met Ala Ile Ile Asn Asn Ile Thr Met Leu Ala Ile	180	185	190	
gta ttg acc gga tcg gcg ctg atc cgc gag cgt gaa cac ggc acg gtg				624
Val Leu Thr Gly Ser Ala Leu Ile Arg Glu Arg Glu His Gly Thr Val	195	200	205	
gaa cac tta ctg gtg atg ccg ata acg ccg ttt gag atc atg atg gcg				672
Glu His Leu Leu Val Met Pro Ile Thr Pro Phe Glu Ile Met Met Ala	210	215	220	
aag atc tgg tcg atg ggg ctg gtg gtg ctg gtg gta tcg gga tta tcg				720
Lys Ile Trp Ser Met Gly Leu Val Val Leu Val Val Ser Gly Leu Ser	225	230	235	240
ctg gtg ctg atg gtg aaa ggt gta ctg ggc gta ccg att gaa ggc tcg				768
Leu Val Leu Met Val Lys Gly Val Leu Gly Val Pro Ile Glu Gly Ser	245	250	255	
atc ccg ctg ttt atg ctg ggc gtg gcg ctc agt ctg ttt gcc acc acg				816
Ile Pro Leu Phe Met Leu Gly Val Ala Leu Ser Leu Phe Ala Thr Thr	260	265	270	
tca atc ggc att ttt atg ggg acg ata gcg cgt tca atg ccg caa ctg				864
Ser Ile Gly Ile Phe Met Gly Thr Ile Ala Arg Ser Met Pro Gln Leu	275	280	285	
ggg ctg ctg gtg att ctg gtg ctg ctg ccg ctg caa atg ctt tcc ggt				912
Gly Leu Leu Val Ile Leu Val Leu Leu Pro Leu Gln Met Leu Ser Gly	290	295	300	
ggt tcc acg ccg cgc gaa agt atg ccg cag atg gtg cag gac att atg				960
Gly Ser Thr Pro Arg Glu Ser Met Pro Gln Met Val Gln Asp Ile Met	305	310	315	320
ctg acc atg ccg acg aca cac ttt gtt agc ctc gcg cag gcc atc ctc				1008
Leu Thr Met Pro Thr Thr His Phe Val Ser Leu Ala Gln Ala Ile Leu	325	330	335	
tac cgg ggt gcc gga ttc gaa atc gtc tgg ccg cag ttt ctg acg ctg				1056
Tyr Arg Gly Ala Gly Phe Glu Ile Val Trp Pro Gln Phe Leu Thr Leu	340	345	350	
atg gca att ggc ggc gca ttt ttc acc att gcg ctg ctg cga ttc agg				1104
Met Ala Ile Gly Gly Ala Phe Phe Thr Ile Ala Leu Leu Arg Phe Arg	355	360	365	
aag acg att ggg aca atg gcg taa				1128
Lys Thr Ile Gly Thr Met Ala *	370	375		

<210> 241
<211> 2685

<212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2685)

<400> 241

gtg agc cag cat tat gga aaa acc gtt gcg ctg aac aat atc act ctc	48
Met Ser Gln His Tyr Gly Lys Thr Val Ala Leu Asn Asn Ile Thr Leu	
1 5 10 15	
gat att ccg gcc cgc tgt atg gtc ggg ctg att ggc ccg gac ggc gtc	96
Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val	
20 25 30	
ggg aag tcg agc ttg ttg tcg ttg att tcc ggt gcc cgc gtc att gaa	144
Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu	
35 40 45	
cag ggc aat gtg atg gtg ctg ggc ggc gat atg cgc gac ccg aag cat	192
Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His	
50 55 60	
cgc cgc gac gtc tgc ccg cgc atc gcc tgg atg ccg cag ggg ctg ggc	240
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly	
65 70 75 80	
aaa aac ctc tac cac acc ttg tcg gtg tat gaa aac gtc gat ttt ttc	288
Lys Asn Leu Tyr His Thr Leu Ser Val Tyr Glu Asn Val Asp Phe Phe	
85 90 95	
gct cgc ctg ttc ggt cac gac aaa gcg gag cgg gaa gtg cga atc aat	336
Ala Arg Leu Phe Gly His Asp Lys Ala Glu Arg Glu Val Arg Ile Asn	
100 105 110	
gag ctg ctg acc agc acc ggg tta gca ccg ttt cgc gat cgt ccg gca	384
Glu Leu Leu Thr Ser Thr Gly Leu Ala Pro Phe Arg Asp Arg Pro Ala	
115 120 125	
ggg aaa ctc tcc ggc ggg atg aag caa aaa ctt ggg ctg tgc tgc gcg	432
Gly Lys Leu Ser Gly Gly Met Lys Gln Lys Leu Gly Leu Cys Cys Ala	
130 135 140	
tta atc cac gac ccg gaa ctg ttg atc ctt gat gag cca aca acg ggg	480
Leu Ile His Asp Pro Glu Leu Leu Ile Leu Asp Glu Pro Thr Thr Gly	
145 150 155 160	
gtt gac ccg ctc tcc cgc tcc cag ttc tgg gat ctg atc gac agt att	528
Val Asp Pro Leu Ser Arg Ser Gln Phe Trp Asp Leu Ile Asp Ser Ile	
165 170 175	
cgc cag cgg cag agc aat atg agc gtg ctg gtc gcc acc gcc tat atg	576
Arg Gln Arg Gln Ser Asn Met Ser Val Leu Val Ala Thr Ala Tyr Met	
180 185 190	
gaa gag gcc gaa cgc ttc gac tgg ctg gta gcg atg aat gcc gga gaa	624

Glu	Glu	Ala	Glu	Arg	Phe	Asp	Trp	Leu	Val	Ala	Met	Asn	Ala	Gly	Glu		
		195					200					205					
gtg	ctg	gca	act	ggc	agc	gcc	gaa	gag	cta	cgg	cag	caa	acg	caa	agc	672	
Val	Leu	Ala	Thr	Gly	Ser	Ala	Glu	Glu	Leu	Arg	Gln	Gln	Thr	Gln	Ser		
		210				215					220						
gct	acg	ctg	gaa	gaa	gca	ttt	ata	aat	ctg	tta	cgg	caa	gcg	caa	cgc	720	
Ala	Thr	Leu	Glu	Glu	Ala	Phe	Ile	Asn	Leu	Leu	Pro	Gln	Ala	Gln	Arg		
225					230					235					240		
cag	gcg	cat	cag	gcg	gta	gtg	atc	cca	cgg	tat	caa	cct	gaa	aac	gca	768	
Gln	Ala	His	Gln	Ala	Val	Val	Ile	Pro	Pro	Tyr	Gln	Pro	Glu	Asn	Ala		
				245					250						255		
gag	att	gcc	atc	gaa	gcg	cgc	gat	ctg	acc	atg	cgt	ttt	ggg	tcc	ttc	816	
Glu	Ile	Ala	Ile	Glu	Ala	Arg	Asp	Leu	Thr	Met	Arg	Phe	Gly	Ser	Phe		
			260					265						270			
gtt	gcc	gtt	gat	cac	gtt	aat	ttc	cgc	att	cca	cgc	ggg	gag	att	ttt	864	
Val	Ala	Val	Asp	His	Val	Asn	Phe	Arg	Ile	Pro	Arg	Gly	Glu	Ile	Phe		
		275					280						285				
ggg	ttt	ctt	ggg	tcg	aac	ggc	tgc	ggg	aaa	tcc	acc	acc	atg	aaa	atg	912	
Gly	Phe	Leu	Gly	Ser	Asn	Gly	Cys	Gly	Lys	Ser	Thr	Thr	Met	Lys	Met		
		290				295					300						
ctc	acc	gga	ctg	ctg	ccc	gcc	agc	gaa	ggg	gag	gcg	tgg	ctg	ttc	ggg	960	
Leu	Thr	Gly	Leu	Leu	Pro	Ala	Ser	Glu	Gly	Glu	Ala	Trp	Leu	Phe	Gly		
305					310					315					320		
caa	cgg	gtt	gat	cca	aaa	gat	atc	gat	acc	cgc	cgt	cgg	gtg	ggc	tat	1008	
Gln	Pro	Val	Asp	Pro	Lys	Asp	Ile	Asp	Thr	Arg	Arg	Arg	Val	Gly	Tyr		
				325					330					335			
atg	tcg	cag	gcg	ttt	tcg	ctc	tat	aac	gaa	ctc	acc	gtg	cgg	caa	aac	1056	
Met	Ser	Gln	Ala	Phe	Ser	Leu	Tyr	Asn	Glu	Leu	Thr	Val	Arg	Gln	Asn		
			340				345						350				
ctt	gag	tta	cat	gcc	cgt	ttg	ttt	cac	atc	cgg	gaa	gcg	gaa	att	ccc	1104	
Leu	Glu	Leu	His	Ala	Arg	Leu	Phe	His	Ile	Pro	Glu	Ala	Glu	Ile	Pro		
		355					360					365					
gca	aga	gtg	gct	gaa	atg	agc	gag	cgt	ttt	aag	ctc	aac	gac	gtt	gaa	1152	
Ala	Arg	Val	Ala	Glu	Met	Ser	Glu	Arg	Phe	Lys	Leu	Asn	Asp	Val	Glu		
		370				375					380						
gat	att	ctg	cgg	gag	tca	ttg	cgg	ctc	ggc	att	cgc	cag	cgg	ctt	tcg	1200	
Asp	Ile	Leu	Pro	Glu	Ser	Leu	Pro	Leu	Gly	Ile	Arg	Gln	Arg	Leu	Ser		
385					390					395					400		
ctg	gcg	gtg	gcg	gtg	att	cat	cgc	cgg	gag	atg	tta	atc	ctc	gat	gag	1248	
Leu	Ala	Val	Ala	Val	Ile	His	Arg	Pro	Glu	Met	Leu	Ile	Leu	Asp	Glu		
				405					410					415			
cct	act	tct	ggg	gtc	gat	cgg	gtg	gcg	agg	gat	atg	ttc	tgg	cag	ttg	1296	
Pro	Thr	Ser	Gly	Val	Asp	Pro	Val	Ala	Arg	Asp	Met	Phe	Trp	Gln	Leu		

				420				425				430							
atg	gtc	gat	ctc	tgc	cgc	cag	gac	aaa	gtg	act	atc	ttc	atc	tcc	acc	1344			
Met	Val	Asp	Leu	Ser	Arg	Gln	Asp	Lys	Val	Thr	Ile	Phe	Ile	Ser	Thr				
		435				440						445							
cac	ttt	atg	aac	gaa	gcg	gaa	cgt	tgc	gac	cgc	atc	tca	ctg	atg	cac	1392			
His	Phe	Met	Asn	Glu	Ala	Glu	Arg	Cys	Asp	Arg	Ile	Ser	Leu	Met	His				
		450				455						460							
gcc	gga	aaa	gtg	ctt	gcc	agc	ggc	aca	ccg	cag	gaa	ctg	ggt	gag	aaa	1440			
Ala	Gly	Lys	Val	Leu	Ala	Ser	Gly	Thr	Pro	Gln	Glu	Leu	Val	Glu	Lys				
465						470						475				480			
cgc	gga	gcc	gcc	agt	ctg	gaa	gag	gca	ttt	atc	gcc	tat	ttg	cag	gaa	1488			
Arg	Gly	Ala	Ala	Ser	Leu	Glu	Glu	Ala	Phe	Ile	Ala	Tyr	Leu	Gln	Glu				
				485						490						495			
gcg	gca	ggg	cag	agc	aac	gaa	gcc	gaa	gcg	ccg	ccc	gtg	gta	cac	gac	1536			
Ala	Ala	Gly	Gln	Ser	Asn	Glu	Ala	Glu	Ala	Pro	Pro	Val	Val	His	Asp				
		500						505						510					
acc	acc	cac	gcg	ccg	cgt	cag	gga	ttt	agc	ctg	cgc	cgt	ctg	ttt	agc	1584			
Thr	Thr	His	Ala	Pro	Arg	Gln	Gly	Phe	Ser	Leu	Arg	Arg	Leu	Phe	Ser				
		515				520						525							
tac	agc	cgc	cgc	gaa	gcg	ctg	gaa	ctg	cga	cgc	gat	cca	gta	cgt	tcg	1632			
Tyr	Ser	Arg	Arg	Glu	Ala	Leu	Glu	Leu	Arg	Arg	Asp	Pro	Val	Arg	Ser				
		530				535						540							
acg	ctg	gcg	ctg	atg	gga	acg	gtg	atc	ctg	atg	ctg	ata	atg	ggt	tac	1680			
Thr	Leu	Ala	Leu	Met	Gly	Thr	Val	Ile	Leu	Met	Leu	Ile	Met	Gly	Tyr				
545						550						555				560			
ggc	atc	agt	atg	gat	gtg	gaa	aac	ctg	cgc	ttt	gcg	gtg	ctc	gac	cgc	1728			
Gly	Ile	Ser	Met	Asp	Val	Glu	Asn	Leu	Arg	Phe	Ala	Val	Leu	Asp	Arg				
				565						570				575					
gac	cag	acc	gtc	agt	agc	cag	gcg	tgg	aca	ctc	aac	ctc	tcc	ggt	tcc	1776			
Asp	Gln	Thr	Val	Ser	Ser	Gln	Ala	Trp	Thr	Leu	Asn	Leu	Ser	Gly	Ser				
		580						585						590					
cgt	tac	ttt	atc	gaa	cag	ccg	ccg	ctc	acc	agt	tat	gac	gag	ctt	gat	1824			
Arg	Tyr	Phe	Ile	Glu	Gln	Pro	Pro	Leu	Thr	Ser	Tyr	Asp	Glu	Leu	Asp				
		595				600						605							
cgt	cgg	atg	cgt	gcg	ggc	gat	atc	acg	gtg	gcg	att	gag	atc	ccg	ccc	1872			
Arg	Arg	Met	Arg	Ala	Gly	Asp	Ile	Thr	Val	Ala	Ile	Glu	Ile	Pro	Pro				
610						615						620							
aat	ttc	ggg	cgc	gat	atc	gcg	cgt	ggc	acg	cct	gtg	gaa	ctc	ggc	gtc	1920			
Asn	Phe	Gly	Arg	Asp	Ile	Ala	Arg	Gly	Thr	Pro	Val	Glu	Leu	Gly	Val				
625						630				635						640			
tgg	atc	gac	gga	gcg	atg	ccg	agc	cgt	gct	gaa	acg	gta	aaa	ggt	tac	1968			
Trp	Ile	Asp	Gly	Ala	Met	Pro	Ser	Arg	Ala	Glu	Thr	Val	Lys	Gly	Tyr				
				645						650				655					

gtg Val	cag Gln	gcc Ala	atg Met 660	cac His	cag Gln	agc Ser	tgg Trp 665	tta Leu 665	cag Gln	gat Asp	gtg Val	gcg Ala	agc Ser 670	cga Arg	caa Gln	2016
tcg Ser	aca Thr 675	ccc Pro	gcc Ala	agc Ser	caa Gln	agc Ser	ggg Gly 680	ctg Leu	atg Met	aat Asn	att Ile	gag Glu 685	acg Thr	cgc Arg	tat Tyr	2064
cgc Arg	tat Tyr 690	aac Asn	ccg Pro	gac Asp	gta Val	aaa Lys 695	agc Ser	ctg Leu	cca Pro	gcg Ala	att Ile 700	gtt Val	ccg Pro	gcg Ala	gtg Val	2112
atc Ile 705	ccg Pro	ctt Leu	ctg Leu	ctg Leu	atg Met 710	atg Met	atc Ile	ccg Pro	tca Ser	atg Met 715	cta Leu	agc Ser	gcc Ala	ctt Leu	agc Ser 720	2160
gtg Val	gtg Val	cgg Arg	gaa Glu 725	aaa Lys	gag Glu	ctt Leu	ggg Gly	tcg Ser 730	att Ile	atc Ile	aac Asn	ctt Leu	tac Tyr	gtg Val 735	acc Thr	2208
ccc Pro	acc Thr	acg Thr	cgt Arg 740	agt Ser	gaa Glu	ttt Phe	ttg Leu	ctt Leu 745	ggt Gly	aaa Lys	cag Gln	ttg Leu	cca Pro	tac Tyr	atc Ile	2256
gcg Ala	ctg Leu	ggg Gly 755	atg Met	ctg Leu	aac Asn	ttt Phe	ttc Phe 760	ctg Leu	ctc Leu	tgc Cys	ggc Gly	ctg Leu 765	tcg Ser	gtg Val	ttt Phe	2304
gtg Val	ttt Phe 770	ggc Gly	gta Val	ccg Pro	cat His	aaa Lys 775	ggc Gly	agt Ser	ttc Phe	ctg Leu	acg Thr 780	ctc Leu	acc Thr	ctg Leu	gcg Ala	2352
gcg Ala 785	ctg Leu	ctg Leu	tat Tyr	atc Ile	atc Ile	att Ile	gcc Ala	acc Thr	gga Gly	atg Met 795	ggg Gly	ctg Leu	ctg Leu	atc Ile	tcc Ser 800	2400
acc Thr	ttt Phe	atg Met	aaa Lys 805	agc Ser	cag Gln	att Ile	gcc Ala	gcc Ala	att Ile 810	ttc Phe	gga Gly	acg Thr	gcg Ala	att Ile 815	atc Ile	2448
acg Thr	ttg Leu	atc Ile	ccg Pro 820	gcg Ala	aca Thr	cag Gln	ttt Phe	tcc Ser 825	ggg Gly	atg Met	atc Ile	gat Asp	ccg Pro 830	gta Val	gct Ala	2496
tcg Ser	ctg Leu	gaa Glu 835	ggg Gly	cct Pro	gga Gly	cgt Arg	tgg Trp 840	atc Ile	ggc Gly	gag Glu	gtt Val	tac Tyr 845	ccg Pro	acc Thr	agt Ser	2544
cat His	ttt Phe 850	ctg Leu	act Thr	atc Ile	gcc Ala	cgc Arg	ggg Gly 855	acg Thr	ttc Phe	tgc Ser	aaa Lys 860	gcg Ala	ctg Leu	gat Asp	ctg Leu	2592
act Thr 865	gat Asp	ttg Leu	tgg Trp	caa Gln	ctt Leu 870	ttt Phe	atc Ile	ccg Pro	tta Leu	ctg Leu 875	ata Ile	gcc Ala	atc Ile	ccg Pro	ctg Leu 880	2640

gtg atg ggc tta agt atc ctg ctg ctg aaa aaa cag gag gga tga 2685
 Val Met Gly Leu Ser Ile Leu Leu Leu Lys Lys Gln Glu Gly *
 885 890

<210> 242
 <211> 1068
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1068)

<400> 242
 atg gat aag agt aag cgc cat ctg gcg tgg tgg gtt gtc ggg tta ctg 48
 Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu
 1 5 10 15
 gcg gtg gcg gct atc gtg gcg tgg tgg ctg ttg cgc ccg gca ggt gtg 96
 Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val
 20 25 30
 ccg gaa ggc ttt gct gtc agt aat ggg cgc att gaa gcg acg gaa gtg 144
 Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val
 35 40 45
 gat att gcc agc aaa att gcc ggg cgt atc gac acc att ctg gtg aaa 192
 Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys
 50 55 60
 gaa ggc aag ttt gtt cgc gaa ggt gaa gtg ctg gcg aag atg gat act 240
 Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr
 65 70 75 80
 cgc gtg ttg cag gaa cag cga ctg gaa gcc atc gcg caa atc aaa gag 288
 Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu
 85 90 95
 gca caa agc gcc gtt gct gcc gcg cag gct ttg ctg gag caa cga caa 336
 Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln
 100 105 110
 agc gaa act cgt gcc gca cag tcg ctg gtt aat caa cgc cag gca gaa 384
 Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu
 115 120 125
 ctg gac tcc gta gca aaa cgt cat acg cgt tcc cgt tca ctg gcc caa 432
 Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln
 130 135 140
 cga ggg gct att tct gcg caa cag ctg gat gac gat cgc gcc gcc gct 480
 Arg Gly Ala Ile Ser Ala Gln Gln Leu Asp Asp Asp Arg Ala Ala Ala
 145 150 155 160
 gag agc gcc cga gct gcg ctg gaa tcg gcg aaa gct cag gta tcg gct 528

Glu Ser Ala Arg Ala Ala Leu Glu Ser Ala Lys Ala Gln Val Ser Ala	
165 170 175	
tct aaa gcg gct ata gaa gcg gca cgc acc aat atc att cag gcg caa	576
Ser Lys Ala Ala Ile Glu Ala Ala Arg Thr Asn Ile Ile Gln Ala Gln	
180 185 190	
acc cgc gtc gaa gcg gca caa gcc act gaa cgg cgc att gcc gca gat	624
Thr Arg Val Glu Ala Ala Gln Ala Thr Glu Arg Arg Ile Ala Ala Asp	
195 200 205	
atc gat gac agc gaa ctg aaa gcc ccg cgt gac gga cgc gtg cag tat	672
Ile Asp Asp Ser Glu Leu Lys Ala Pro Arg Asp Gly Arg Val Gln Tyr	
210 215 220	
cgg gtt gcc gag cca ggc gaa gtg ctg gcg gca ggc ggt cgg gtg ctg	720
Arg Val Ala Glu Pro Gly Glu Val Leu Ala Ala Gly Gly Arg Val Leu	
225 230 235 240	
aat atg gtc gat ctc agc gac gtc tat atg act ttc ttc ctg cca acc	768
Asn Met Val Asp Leu Ser Asp Val Tyr Met Thr Phe Phe Leu Pro Thr	
245 250 255	
gaa cag gcg ggc acg ctg aaa ctg ggc ggt gaa gcc cgg ctg atc ctc	816
Glu Gln Ala Gly Thr Leu Lys Leu Gly Gly Glu Ala Arg Leu Ile Leu	
260 265 270	
gat gcc gcg cca gat ctg cgt att cct gca acc atc agt ttt gtc gcc	864
Asp Ala Ala Pro Asp Leu Arg Ile Pro Ala Thr Ile Ser Phe Val Ala	
275 280 285	
agt gtc gcc cag ttc acg cca aaa acc gtc gaa acc agc gat gaa cgg	912
Ser Val Ala Gln Phe Thr Pro Lys Thr Val Glu Thr Ser Asp Glu Arg	
290 295 300	
ctg aaa ctg atg ttc cgc gtc aaa gcg cgt atc cca ccg gaa tta ctc	960
Leu Lys Leu Met Phe Arg Val Lys Ala Arg Ile Pro Pro Glu Leu Leu	
305 310 315 320	
cag cag cat ctg gaa tat gtc aaa acc ggt ttg ccg ggc gta gcg tgg	1008
Gln Gln His Leu Glu Tyr Val Lys Thr Gly Leu Pro Gly Val Ala Trp	
325 330 335	
gtg cgg gtg aat gaa gaa ctt ccg tgg cct gac gac ctc gtg gtg agg	1056
Val Arg Val Asn Glu Glu Leu Pro Trp Pro Asp Asp Leu Val Val Arg	
340 345 350	
ttg ccg caa tga	1068
Leu Pro Gln *	
355	

<210> 243
 <211> 708
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(708)

<400> 243

atg tac cgt tat ttg tct att gct gcg gtg gta ctg agc gca gca ttt	48
Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe	
1 5 10 15	
tcc ggc ccg gcg ttg gcc gaa ggt atc aat agt ttt tct cag gcg aaa	96
Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys	
20 25 30	
gcc gcg gcg gta aaa gtc cac gct gac gcg ccc ggt acg ttt tat tgc	144
Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys	
35 40 45	
gga tgt aaa att aac tgg cag ggc aaa aaa ggc gtt gtt gat ctg caa	192
Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln	
50 55 60	
tcg tgc ggc tat cag gtg cgc aaa aat gaa aac cgc gcc agc cgc gta	240
Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val	
65 70 75 80	
gag tgg gaa cat gtc gtt ccc gcc tgg cag ttc ggt cac cag cgc cag	288
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln	
85 90 95	
tgc tgg cag gac ggt gga cgt aaa aac tgc gct aaa gat ccg gtc tat	336
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr	
100 105 110	
cgc aag atg gaa agc gat atg cat aac ctg cag ccg tca gtc ggt gag	384
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu	
115 120 125	
gtg aat ggc gat cgc ggc aac ttt atg tac agc cag tgg aat ggc ggt	432
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly	
130 135 140	
gaa ggc cag tac ggt caa tgc gcc atg aag gtc gat ttc aaa gaa aaa	480
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys	
145 150 155 160	
gct gcc gaa cca cca gcg cgt gca cgc ggt gcc att gcg cgc acc tac	528
Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr	
165 170 175	
ttc tat atg cgc gac caa tac aac ctg aca ctc tct cgc cag caa acg	576
Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr	
180 185 190	
cag ctg ttc aac gca tgg aac aag atg tat ccg gtt acc gac tgg gag	624
Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu	
195 200 205	

tgc gag cgc gat gaa cgc atc gcg aag gtg cag ggc aat cat aac ccg 672
 Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
 210 215 220

tat gtg caa cgc gct tgc cag gcg cga aag agc taa 708
 Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser *
 225 230 235

<210> 244
 <211> 1443
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1443)

<400> 244
 atg tcc aga agg ctt cgc aga aca aaa atc gtt acc acg tta ggc cca 48
 Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro
 1 5 10 15

gca aca gat cgc gat aat aat ctt gaa aaa gtt atc gcg gcg ggt gcc 96
 Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala
 20 25 30

aac gtt gta cgt atg aac ttt tct cac ggc tcg cct gaa gat cac aaa 144
 Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys
 35 40 45

atg cgc gcg gat aaa gtt cgt gag att gcc gca aaa ctg ggg cgt cat 192
 Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His
 50 55 60

gtg gct att ctg ggt gac ctc cag ggg ccc aaa atc cgt gta tcc acc 240
 Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr
 65 70 75 80

ttt aaa gaa ggc aaa gtt ttc ctc aat att ggg gat aaa ttc ctg ctc 288
 Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu
 85 90 95

gac gcc aac ctg ggt aaa ggt gaa ggc gac aaa gaa aaa gtc ggt atc 336
 Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile
 100 105 110

gac tac aaa ggc ctg cct gct gac gtc gtg cct ggt gac atc ctg ctg 384
 Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu
 115 120 125

ctg gac gat ggt cgc gtc cag tta aaa gta ctg gaa gtt cag ggc atg 432
 Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met
 130 135 140

aaa gtg ttc acc gaa gtc acc gtc ggt ggt ccc ctc tcc aac aat aaa 480
 Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys

145	150	155	160	
ggt atc aac aaa ctt ggc ggc ggt ttg tgc gct gaa gcg ctg acc gaa				528
Gly Ile Asn Lys Leu Gly Gly Gly Leu Ser Ala Glu Ala Leu Thr Glu	165	170	175	
aaa gac aaa gca gac att aag act gcg gcg ttg att ggc gta gat tac				576
Lys Asp Lys Ala Asp Ile Lys Thr Ala Ala Leu Ile Gly Val Asp Tyr	180	185	190	
ctg gct gtc tcc ttc cca cgc tgt ggc gaa gat ctg aac tat gcc cgt				624
Leu Ala Val Ser Phe Pro Arg Cys Gly Glu Asp Leu Asn Tyr Ala Arg	195	200	205	
cgc ctg gca cgc gat gca gga tgt gat gcg aaa att gtt gcc aag gtt				672
Arg Leu Ala Arg Asp Ala Gly Cys Asp Ala Lys Ile Val Ala Lys Val	210	215	220	
gaa cgt gcg gaa gcc gtt tgc agc cag gat gca atg gat gac atc atc				720
Glu Arg Ala Glu Ala Val Cys Ser Gln Asp Ala Met Asp Asp Ile Ile	225	230	235	240
ctc gcc tct gac gtg gta atg gtt gca cgt ggc gac ctc ggt gtg gaa				768
Leu Ala Ser Asp Val Val Met Val Ala Arg Gly Asp Leu Gly Val Glu	245	250	255	
att ggc gac ccg gaa ctg gtc ggc att cag aaa gcg ttg atc cgt cgt				816
Ile Gly Asp Pro Glu Leu Val Gly Ile Gln Lys Ala Leu Ile Arg Arg	260	265	270	
gcg cgt cag cta aac cga gcg gta atc acg gcg acc cag atg atg gag				864
Ala Arg Gln Leu Asn Arg Ala Val Ile Thr Ala Thr Gln Met Met Glu	275	280	285	
tca atg att act aac ccg atg ccg acg cgt gca gaa gtc atg gac gta				912
Ser Met Ile Thr Asn Pro Met Pro Thr Arg Ala Glu Val Met Asp Val	290	295	300	
gca aac gcc gtt ctg gat ggt act gac gct gtg atg ctg tct gca gaa				960
Ala Asn Ala Val Leu Asp Gly Thr Asp Ala Val Met Leu Ser Ala Glu	305	310	315	320
act gcc gct ggg cag tat ccg tca gaa acc gtt gca gcc atg gcg cgc				1008
Thr Ala Ala Gly Gln Tyr Pro Ser Glu Thr Val Ala Ala Met Ala Arg	325	330	335	
gtt tgc ctg ggt gcg gaa aaa atc ccg agc atc aac gtt tct aaa cac				1056
Val Cys Leu Gly Ala Glu Lys Ile Pro Ser Ile Asn Val Ser Lys His	340	345	350	
cgt ctg gac gtt cag ttc gac aat gtg gaa gaa gct att gcc atg tca				1104
Arg Leu Asp Val Gln Phe Asp Asn Val Glu Glu Ala Ile Ala Met Ser	355	360	365	
gca atg tac gca gct aac cac ctg aaa ggc gtt acg gcg atc atc acc				1152
Ala Met Tyr Ala Ala Asn His Leu Lys Gly Val Thr Ala Ile Ile Thr	370	375	380	

```

atg acc gaa tcg ggt cgt acc gcg ctg atg acc tcc cgt atc agc tct 1200
Met Thr Glu Ser Gly Arg Thr Ala Leu Met Thr Ser Arg Ile Ser Ser
385          390          395          400

ggt ctg cca att ttc gcc atg tcg cgc cat gaa cgt acg ctg aac ctg 1248
Gly Leu Pro Ile Phe Ala Met Ser Arg His Glu Arg Thr Leu Asn Leu
          405          410          415

act gct ctc tat cgt ggc gtt acg ccg gtg cac ttt gat agc gct aat 1296
Thr Ala Leu Tyr Arg Gly Val Thr Pro Val His Phe Asp Ser Ala Asn
          420          425          430

gac ggc gta gca gct gcc agc gaa gcg gtt aat ctg ctg cgc gat aaa 1344
Asp Gly Val Ala Ala Ala Ser Glu Ala Val Asn Leu Leu Arg Asp Lys
          435          440          445

ggt tac ttg atg tct ggt gac ctg gtg att gtc acc cag ggc gac gtg 1392
Gly Tyr Leu Met Ser Gly Asp Leu Val Ile Val Thr Gln Gly Asp Val
          450          455          460

atg agt acc gtg ggt tct act aat acc acg cgt att tta acg gta gag 1440
Met Ser Thr Val Gly Ser Thr Asn Thr Thr Arg Ile Leu Thr Val Glu
465          470          475          480

taa
*
1443

```

```

<210> 245
<211> 720
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(720)

```

```

<400> 245
atg atc aat gta tta att atc gat gac gac gca atg gtc gcg gag ctg 48
Met Ile Asn Val Leu Ile Ile Asp Asp Asp Ala Met Val Ala Glu Leu
1          5          10          15

aat cgc cga tac gta gca caa atc cca ggc ttt caa tgc tgt gga aca 96
Asn Arg Arg Tyr Val Ala Gln Ile Pro Gly Phe Gln Cys Cys Gly Thr
          20          25          30

gcc tcg acg ctg gag aaa gcc aaa gag att atc ttc aat agc gat acg 144
Ala Ser Thr Leu Glu Lys Ala Lys Glu Ile Ile Phe Asn Ser Asp Thr
          35          40          45

cct atc gac ctg ata ttg ctc gat atc tat atg caa aaa gag aac ggg 192
Pro Ile Asp Leu Ile Leu Leu Asp Ile Tyr Met Gln Lys Glu Asn Gly
          50          55          60

ctc gat tta ctg cct gtc ctg cat aac gcg cgt tgc aaa agt gat gtg 240

```

Leu	Asp	Leu	Leu	Pro	Val	Leu	His	Asn	Ala	Arg	Cys	Lys	Ser	Asp	Val	
65					70					75					80	
att	gtc	atc	tcc	tcc	gca	gcc	gat	gcg	gca	acc	att	aaa	gat	tcg	ctg	288
Ile	Val	Ile	Ser	Ser	Ala	Ala	Asp	Ala	Ala	Thr	Ile	Lys	Asp	Ser	Leu	
			85					90						95		
cat	tac	ggg	gtc	gtg	gat	tac	ctg	atc	aaa	ccc	ttc	cag	gct	tcc	cgc	336
His	Tyr	Gly	Val	Val	Asp	Tyr	Leu	Ile	Lys	Pro	Phe	Gln	Ala	Ser	Arg	
			100					105					110			
ttt	gaa	gag	gcg	ctc	acc	ggc	tgg	cgg	caa	aag	aaa	atg	gcg	ctg	gaa	384
Phe	Glu	Glu	Ala	Leu	Thr	Gly	Trp	Arg	Gln	Lys	Lys	Met	Ala	Leu	Glu	
			115				120					125				
aaa	cat	cag	tat	tat	gac	cag	gcc	gag	ctt	gat	cag	cta	atc	cac	ggc	432
Lys	His	Gln	Tyr	Tyr	Asp	Gln	Ala	Glu	Leu	Asp	Gln	Leu	Ile	His	Gly	
			130			135					140					
agc	agc	tcc	aac	gaa	cag	gat	cct	cgt	cgc	ttg	cca	aaa	ggc	tta	acg	480
Ser	Ser	Ser	Asn	Glu	Gln	Asp	Pro	Arg	Arg	Leu	Pro	Lys	Gly	Leu	Thr	
					150					155					160	
ccg	cag	acg	tta	cgc	aca	ctg	tgc	cag	tgg	att	gac	gcg	cat	cag	gac	528
Pro	Gln	Thr	Leu	Arg	Thr	Leu	Cys	Gln	Trp	Ile	Asp	Ala	His	Gln	Asp	
				165				170						175		
tat	gaa	ttt	tca	acc	gac	gag	cta	gcc	aac	gag	gtt	aac	att	tcg	cgt	576
Tyr	Glu	Phe	Ser	Thr	Asp	Glu	Leu	Ala	Asn	Glu	Val	Asn	Ile	Ser	Arg	
			180					185					190			
gtt	tcc	tgc	cgt	aaa	tac	ctc	atc	tgg	ctg	gtc	aac	tgc	cac	atc	ttg	624
Val	Ser	Cys	Arg	Lys	Tyr	Leu	Ile	Trp	Leu	Val	Asn	Cys	His	Ile	Leu	
			195				200					205				
ttc	acc	agt	atc	cat	tat	ggc	gtc	acg	ggg	cgt	cca	gtt	tac	cgt	tac	672
Phe	Thr	Ser	Ile	His	Tyr	Gly	Val	Thr	Gly	Arg	Pro	Val	Tyr	Arg	Tyr	
			210			215					220					
cgt	att	cag	gca	gaa	cac	tac	tca	cta	ctg	aaa	caa	tat	tgc	caa	taa	720
Arg	Ile	Gln	Ala	Glu	His	Tyr	Ser	Leu	Leu	Lys	Gln	Tyr	Cys	Gln	*	
					230					235						

<210> 246

<211> 1632

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1632)

<400> 246

atg	aga	cat	tca	ttg	ccc	tac	cgc	atg	tta	cgc	aaa	cgt	ccg	atg	aaa	48
Met	Arg	His	Ser	Leu	Pro	Tyr	Arg	Met	Leu	Arg	Lys	Arg	Pro	Met	Lys	

1	5	10	15	
ttg agt acc aca gtg atc tta atg gtc agt gcg gta ctg ttc tcg gtg	96			
Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val				
20	25	30		
cta ttg gtg gtg cat ctg att tac ttc tcg caa atc agt gat atg acg	144			
Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr				
35	40	45		
cga gat ggg cta gcc aac aag gca ctg gca gtg gcg cgt acc ctc gcc	192			
Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala				
50	55	60		
gac tcg ccg gaa atc cgt cag ggc ttg cag aaa aaa ccg cag gag agt	240			
Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser				
65	70	75	80	
ggc atc cag gcc atc gcg gaa gcc gta cgc aaa cgc aac gat ctg ctg	288			
Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu				
85	90	95		
ttt att gtc gtt acc gat atg caa agt ctt cgc tac tcg cat cct gaa	336			
Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu				
100	105	110		
gcc cag cgt att ggt cag cca ttt aaa ggt gat gac atc ctt aaa gcg	384			
Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala				
115	120	125		
ctg aat ggc gaa gaa aat gtc gct atc aat cgc ggt ttt ctg gcg cag	432			
Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln				
130	135	140		
gct tta cgc gta ttt acc ccc atc tac gat gaa aat cat aaa caa att	480			
Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile				
145	150	155	160	
ggc gtg gtg gcg atc ggc ctt gag tta agc cgt gtg acc caa cag atc	528			
Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile				
165	170	175		
aat gac agt cgc tgg agc att atc tgg tcg gta tta ttt ggc atg ctg	576			
Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu				
180	185	190		
gtc gga ctg att ggc acc tgc att ctg gtt aag gta ctg aaa aaa atc	624			
Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile				
195	200	205		
ctt ttc ggc ctg gaa ccc tac gaa atc tcc acg ctg ttt gag caa cgc	672			
Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg				
210	215	220		
cag gcc atg ttg cag tct atc aaa gaa ggc gtc gtt gcc gtg gac gat	720			
Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp				
225	230	235	240	

cgc ggc gag gtc acg ctg atc aac gat gcc gca caa gaa ttg ctg aat	768
Arg Gly Glu Val Thr Leu Ile Asn Asp Ala Ala Gln Glu Leu Leu Asn	
245 250 255	
tac cgt aag tcg cag gac gat gag aaa ctg tcg acg cta agc cac tca	816
Tyr Arg Lys Ser Gln Asp Asp Glu Lys Leu Ser Thr Leu Ser His Ser	
260 265 270	
tgg tca cag gtg gta gat gtc tcg gaa gtg tta cgc gac ggt acc ccg	864
Trp Ser Gln Val Val Asp Val Ser Glu Val Leu Arg Asp Gly Thr Pro	
275 280 285	
cgc cgc gac gaa gag att acg att aaa gac cgg cta tta ctg atc aac	912
Arg Arg Asp Glu Glu Ile Thr Ile Lys Asp Arg Leu Leu Leu Ile Asn	
290 295 300	
acc gtt ccg gtg cgc agt aat ggc gtt atc atc ggt gcc att tca acc	960
Thr Val Pro Val Arg Ser Asn Gly Val Ile Ile Gly Ala Ile Ser Thr	
305 310 315 320	
ttc agg gac aaa act gaa gta cgt aaa ctg atg cag cga ctc gac ggt	1008
Phe Arg Asp Lys Thr Glu Val Arg Lys Leu Met Gln Arg Leu Asp Gly	
325 330 335	
ctg gtc aac tat gct gac gca ctt cgt gaa cga tcc cac gaa ttt atg	1056
Leu Val Asn Tyr Ala Asp Ala Leu Arg Glu Arg Ser His Glu Phe Met	
340 345 350	
aat aaa ttg cat gtg att ctc gga tta ttg cat ctg aag agt tat aag	1104
Asn Lys Leu His Val Ile Leu Gly Leu Leu His Leu Lys Ser Tyr Lys	
355 360 365	
cag ttg gaa gat tac att ctc aaa aca gcc aat aac tat cag gaa gag	1152
Gln Leu Glu Asp Tyr Ile Leu Lys Thr Ala Asn Asn Tyr Gln Glu Glu	
370 375 380	
att ggc tct ctg ctg ggt aag atc aaa tct ccg gtt atc gct ggt ttt	1200
Ile Gly Ser Leu Leu Gly Lys Ile Lys Ser Pro Val Ile Ala Gly Phe	
385 390 395 400	
tta atc agc aag att aac cgc gcg acc gat tta ggc cat acg ctg att	1248
Leu Ile Ser Lys Ile Asn Arg Ala Thr Asp Leu Gly His Thr Leu Ile	
405 410 415	
tta aac agt gaa agc cag ctg cca gac agc ggc agt gag gac cag gtc	1296
Leu Asn Ser Glu Ser Gln Leu Pro Asp Ser Gly Ser Glu Asp Gln Val	
420 425 430	
gcg acg ctg att acc acg ttg gga aat ctg ata gaa aac gcg ctg gag	1344
Ala Thr Leu Ile Thr Thr Leu Gly Asn Leu Ile Glu Asn Ala Leu Glu	
435 440 445	
gca tta ggg ccg gaa ccc gga ggc gaa att agc gta aca ttg cac tac	1392
Ala Leu Gly Pro Glu Pro Gly Gly Glu Ile Ser Val Thr Leu His Tyr	
450 455 460	

Arg	Glu	Lys	Met	Ile	Ala	Glu	Asn	Phe	Arg	Ser	Leu	Gly	Met	Ala	Leu		
			100				105						110				
gta	gaa	acc	ggc	atg	gca	tgg	ttc	tgg	ccc	gac	agt	cgc	gta	cgt	aaa	384	
Val	Glu	Thr	Gly	Met	Ala	Trp	Phe	Trp	Pro	Asp	Ser	Arg	Val	Arg	Lys		
			115				120						125				
tgg	ttt	gat	gtt	gaa	ggg	ttg	gat	aac	ctt	aaa	cgc	gca	caa	atg	caa	432	
Trp	Phe	Asp	Val	Glu	Gly	Leu	Asp	Asn	Leu	Lys	Arg	Ala	Gln	Met	Gln		
			130				135						140				
aat	cgc	ggc	gta	atg	gtt	gtc	ggc	gtc	cat	ttt	atg	tgc	ctg	gaa	ctg	480	
Asn	Arg	Gly	Val	Met	Val	Val	Gly	Val	His	Phe	Met	Ser	Leu	Glu	Leu		
145				150						155			160				
ggc	ggc	cgc	gtg	atg	gga	ctg	tgc	caa	cca	atg	atg	gct	acc	tat	cgt	528	
Gly	Gly	Arg	Val	Met	Gly	Leu	Cys	Gln	Pro	Met	Met	Ala	Thr	Tyr	Arg		
			165						170			175					
cca	cat	aat	aat	cag	ctg	atg	gaa	tgg	gtg	cag	acc	cgt	ggg	cgc	atg	576	
Pro	His	Asn	Asn	Gln	Leu	Met	Glu	Trp	Val	Gln	Thr	Arg	Gly	Arg	Met		
			180						185			190					
cgc	tct	aac	aaa	gcg	atg	atc	ggc	aga	aat	aat	ctg	cgc	ggc	att	gtc	624	
Arg	Ser	Asn	Lys	Ala	Met	Ile	Gly	Arg	Asn	Asn	Leu	Arg	Gly	Ile	Val		
			195						200			205					
ggt	gca	ctg	aag	aaa	ggt	gaa	gcg	gta	tgg	ttt	gct	ccc	gat	cag	gat	672	
Gly	Ala	Leu	Lys	Lys	Gly	Glu	Ala	Val	Trp	Phe	Ala	Pro	Asp	Gln	Asp		
			210			215						220					
tat	ggt	cgt	aaa	ggc	agc	tcc	ttc	gcg	ccg	ttc	ttt	gcg	gtg	gaa	aat	720	
Tyr	Gly	Arg	Lys	Gly	Ser	Ser	Phe	Ala	Pro	Phe	Phe	Ala	Val	Glu	Asn		
225				230						235			240				
gtc	gcc	aca	acc	aat	ggc	acc	tat	gtt	ctc	tcc	cgt	ctc	tct	ggc	gca	768	
Val	Ala	Thr	Thr	Asn	Gly	Thr	Tyr	Val	Leu	Ser	Arg	Leu	Ser	Gly	Ala		
			245						250			255					
gcc	atg	ttg	acc	gta	acg	atg	gta	aga	aaa	gcg	gat	tac	agc	gga	tat	816	
Ala	Met	Leu	Thr	Val	Thr	Met	Val	Arg	Lys	Ala	Asp	Tyr	Ser	Gly	Tyr		
			260						265			270					
cgt	ttg	ttc	atc	acc	cca	gag	atg	gaa	ggc	tac	ccg	aca	gat	gaa	aat	864	
Arg	Leu	Phe	Ile	Thr	Pro	Glu	Met	Glu	Gly	Tyr	Pro	Thr	Asp	Glu	Asn		
			275						280			285					
caa	gcc	gct	gcc	tat	atg	aac	aag	att	atc	gag	aaa	gag	atc	atg	cgc	912	
Gln	Ala	Ala	Ala	Tyr	Met	Asn	Lys	Ile	Ile	Glu	Lys	Glu	Ile	Met	Arg		
			290			295						300					
gca	ccg	gag	cag	tac	ctc	tgg	atc	cac	cgt	cgc	ttt	aaa	acg	cgc	ccg	960	
Ala	Pro	Glu	Gln	Tyr	Leu	Trp	Ile	His	Arg	Arg	Phe	Lys	Thr	Arg	Pro		
305				310						315			320				
gtg	gga	gaatcg	tcg	ttg	tac	att	taa									987	
Val	Gly	Glu	Ser	Ser	Leu	Tyr	Ile	*									

<210> 248
 <211> 264
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(264)

<400> 248
 ttg gct aat atc aaa tca gct aag aag cgc gcc att cag tct gaa aag 48
 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 gct cgt aag cac aac gca agc cgt cgc tct atg atg cgt act ttc atc 96
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 aag aaa gta tac gca gct atc gaa gct ggc gac aaa gct gct gca cag 144
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 aaa gca ttt aac gaa atg caa ccg atc gtg gac cgt cag gct gct aaa 192
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 ggt ctg atc cac aaa aac aaa gct gca cgt cat aag gct aac ctg act 240
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 gca cag atc aac aaa ctg gct taa 264
 Ala Gln Ile Asn Lys Leu Ala *
 85

<210> 249
 <211> 1293
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1293)

<400> 249
 atg cgc tat aat ggt tta aat aat atg ttt ttc cct ctt tgc ctg att 48
 Met Arg Tyr Asn Gly Leu Asn Asn Met Phe Phe Pro Leu Cys Leu Ile
 1 5 10 15
 aac gat aac cac tct gtc aca agt cca tca cat aca aag aaa aca aaa 96
 Asn Asp Asn His Ser Val Thr Ser Pro Ser His Thr Lys Lys Thr Lys
 20 25 30
 tca gat aat tac agc aaa cat cat aaa aac acg tta att gac aat aaa 144

Ser	Asp	Asn	Tyr	Ser	Lys	His	His	Lys	Asn	Thr	Leu	Ile	Asp	Asn	Lys		
35							40					45					
gcc	ctc	tct	ctt	ttc	aaa	atg	gat	gat	cat	gaa	aaa	gtg	ata	ggc	ttg	192	
Ala	Leu	Ser	Leu	Phe	Lys	Met	Asp	Asp	His	Glu	Lys	Val	Ile	Gly	Leu		
50						55				60							
att	cag	aaa	atg	aaa	aga	att	tat	gat	agt	tta	cca	tca	gga	aaa	atc	240	
Ile	Gln	Lys	Met	Lys	Arg	Ile	Tyr	Asp	Ser	Leu	Pro	Ser	Gly	Lys	Ile		
65					70				75						80		
acg	aaa	gaa	acg	gac	agg	aaa	ata	cat	aaa	tat	ttt	ata	gat	ata	gct	288	
Thr	Lys	Glu	Thr	Asp	Arg	Lys	Ile	His	Lys	Tyr	Phe	Ile	Asp	Ile	Ala		
				85				90						95			
tca	cat	gca	aat	aat	aaa	tgt	gac	gat	aga	att	acg	aga	aga	gtt	tac	336	
Ser	His	Ala	Asn	Asn	Lys	Cys	Asp	Asp	Arg	Ile	Thr	Arg	Arg	Val	Tyr		
			100				105				110						
ctt	aat	aaa	gat	aag	gaa	gtg	tca	att	aag	gtg	gta	tat	ttt	ata	aat	384	
Leu	Asn	Lys	Asp	Lys	Glu	Val	Ser	Ile	Lys	Val	Val	Tyr	Phe	Ile	Asn		
			115				120				125						
aat	gtc	acc	gtc	cat	aat	aat	act	atc	gaa	atc	cca	cag	aca	gta	aat	432	
Asn	Val	Thr	Val	His	Asn	Asn	Thr	Ile	Glu	Ile	Pro	Gln	Thr	Val	Asn		
130						135				140							
ggt	ggt	tac	gat	ttt	tca	cac	ctt	agc	ctg	aaa	ggt	atc	gtg	att	aaa	480	
Gly	Gly	Tyr	Asp	Phe	Ser	His	Leu	Ser	Leu	Lys	Gly	Ile	Val	Ile	Lys		
145					150				155						160		
gat	gaa	gat	tta	tcc	aat	tcg	aat	ttt	gca	ggt	tgc	aga	cta	caa	aac	528	
Asp	Glu	Asp	Leu	Ser	Asn	Ser	Asn	Phe	Ala	Gly	Cys	Arg	Leu	Gln	Asn		
			165				170				175						
gct	att	ttt	cag	gac	tgt	aat	atg	tat	aaa	acg	aat	ttt	aat	ttc	gcc	576	
Ala	Ile	Phe	Gln	Asp	Cys	Asn	Met	Tyr	Lys	Thr	Asn	Phe	Asn	Phe	Ala		
			180				185				190						
ata	atg	gaa	aaa	ata	ctt	ttt	gat	aat	tgt	att	ctc	gat	gac	tca	aat	624	
Ile	Met	Glu	Lys	Ile	Leu	Phe	Asp	Asn	Cys	Ile	Leu	Asp	Asp	Ser	Asn		
195						200				205							
ttc	gct	cag	ata	aaa	atg	act	gac	gga	act	cta	aat	tca	tgt	tcc	gct	672	
Phe	Ala	Gln	Ile	Lys	Met	Thr	Asp	Gly	Thr	Leu	Asn	Ser	Cys	Ser	Ala		
210						215				220							
atg	cat	gtt	caa	ttc	tac	aat	gca	aca	atg	aat	aga	gcc	aat	att	aaa	720	
Met	His	Val	Gln	Phe	Tyr	Asn	Ala	Thr	Met	Asn	Arg	Ala	Asn	Ile	Lys		
225					230				235						240		
aat	acc	ttc	ctt	gat	tat	tca	aat	ttt	tat	atg	gca	tac	atg	gct	gag	768	
Asn	Thr	Phe	Leu	Asp	Tyr	Ser	Asn	Phe	Tyr	Met	Ala	Tyr	Met	Ala	Glu		
			245				250				255						
gta	aat	ctt	tat	aaa	gta	ata	gcg	cca	tat	att	aat	tta	ttt	aga	gcc	816	
Val	Asn	Leu	Tyr	Lys													

260	265	270	
gac ctt agc ttc tct aaa ctt gat tta att aac ttt gaa cat gct gat	864		
Asp Leu Ser Phe Ser Lys Leu Asp Leu Ile Asn Phe Glu His Ala Asp			
275	280	285	
ctg tct cgt gtc aac ctg aat aaa gca acc ctc cag aat ata aac tta	912		
Leu Ser Arg Val Asn Leu Asn Lys Ala Thr Leu Gln Asn Ile Asn Leu			
290	295	300	
att gat agc aaa ctc ttt ttt acg cgg tta aca aat acg ttc ctc gaa	960		
Ile Asp Ser Lys Leu Phe Phe Thr Arg Leu Thr Asn Thr Phe Leu Glu			
305	310	315	320
atg gtt ata tgt acc gac tct aat atg gct aat gtt aat ttt aat aat	1008		
Met Val Ile Cys Thr Asp Ser Asn Met Ala Asn Val Asn Phe Asn Asn			
325	330	335	
gcc aat tta agc aat tgc cat ttc aac tgt tct gtt tta aca aaa gcc	1056		
Ala Asn Leu Ser Asn Cys His Phe Asn Cys Ser Val Leu Thr Lys Ala			
340	345	350	
tgg atg ttt aat atc cgt ctc tat cgt gtt aat ttc gat gag gct agc	1104		
Trp Met Phe Asn Ile Arg Leu Tyr Arg Val Asn Phe Asp Glu Ala Ser			
355	360	365	
gtc cag gga atg ggt att acc att ctc cgt ggt gag gaa aat atc tcc	1152		
Val Gln Gly Met Gly Ile Thr Ile Leu Arg Gly Glu Glu Asn Ile Ser			
370	375	380	
att aat agt gat atc ctg gta aca cta cag aaa ttc ttt gaa gaa gat	1200		
Ile Asn Ser Asp Ile Leu Val Thr Leu Gln Lys Phe Phe Glu Glu Asp			
385	390	395	400
tgt gcc act cat act ggc atg tca caa act gag gat aat ctt cat gca	1248		
Cys Ala Thr His Thr Gly Met Ser Gln Thr Glu Asp Asn Leu His Ala			
405	410	415	
gtc gct atg aag att act gca gat att atg caa gat gca gat tga	1293		
Val Ala Met Lys Ile Thr Ala Asp Ile Met Gln Asp Ala Asp *			
420	425	430	

<210> 250
 <211> 2652
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2652)

<400> 250

atg aac gaa caa tat tcc gca ttg cgt agt aat gtc agt atg ctc ggc	48
Met Asn Glu Gln Tyr Ser Ala Leu Arg Ser Asn Val Ser Met Leu Gly	
1	5
	10
	15

aaa gtg ctg gga gaa acc atc aag gat gcg ttg gga gaa cac att ctt	96
Lys Val Leu Gly Glu Thr Ile Lys Asp Ala Leu Gly Glu His Ile Leu	
20 25 30	
gaa cgc gta gaa act atc cgt aag ttg tcg aaa tct tca cgc gct ggc	144
Glu Arg Val Glu Thr Ile Arg Lys Leu Ser Lys Ser Ser Arg Ala Gly	
35 40 45	
aat gat gct aac cgc cag gag ttg ctc acc acc tta caa aat ttg tcg	192
Asn Asp Ala Asn Arg Gln Glu Leu Leu Thr Thr Leu Gln Asn Leu Ser	
50 55 60	
aac gac gag ctg ctg ccc gtt gcg cgt gcg ttt agt cag ttc ctg aac	240
Asn Asp Glu Leu Leu Pro Val Ala Arg Ala Phe Ser Gln Phe Leu Asn	
65 70 75 80	
ctg gcc aac acc gcc gag caa tac cac agc att tcg ccg aaa ggc gaa	288
Leu Ala Asn Thr Ala Glu Gln Tyr His Ser Ile Ser Pro Lys Gly Glu	
85 90 95	
gct gcc agc aac ccg gaa gtg atc gcc cgc acc ctg cgt aaa ctg aaa	336
Ala Ala Ser Asn Pro Glu Val Ile Ala Arg Thr Leu Arg Lys Leu Lys	
100 105 110	
aac cag ccg gaa ctg agc gaa gac acc atc aaa aaa gca gtg gaa tcg	384
Asn Gln Pro Glu Leu Ser Glu Asp Thr Ile Lys Lys Ala Val Glu Ser	
115 120 125	
ctg tcg ctg gaa ctg gtc ctc acg gct cac cca acc gaa att acc cgt	432
Leu Ser Leu Glu Leu Val Leu Thr Ala His Pro Thr Glu Ile Thr Arg	
130 135 140	
cgt aca ctg atc cac aaa atg gtg gaa gtg aac gcc tgt tta aaa cag	480
Arg Thr Leu Ile His Lys Met Val Glu Val Asn Ala Cys Leu Lys Gln	
145 150 155 160	
ctc gat aac aaa gat atc gct gac tac gaa cac aac cag ctg atg cgt	528
Leu Asp Asn Lys Asp Ile Ala Asp Tyr Glu His Asn Gln Leu Met Arg	
165 170 175	
cgc ctg cgc cag ttg atc gcc cag tca tgg cat acc gat gaa atc cgt	576
Arg Leu Arg Gln Leu Ile Ala Gln Ser Trp His Thr Asp Glu Ile Arg	
180 185 190	
aag ctg cgt cca agc ccg gta gat gaa gcc aaa tgg ggc ttt gcc gta	624
Lys Leu Arg Pro Ser Pro Val Asp Glu Ala Lys Trp Gly Phe Ala Val	
195 200 205	
gtg gaa aac agc ctg tgg caa ggc gta cca aat tac ctg cgc gaa ctg	672
Val Glu Asn Ser Leu Trp Gln Gly Val Pro Asn Tyr Leu Arg Glu Leu	
210 215 220	
aac gaa caa ctg gaa gag aac ctc ggc tac aaa ctg ccc gtc gaa ttt	720
Asn Glu Gln Leu Glu Glu Asn Leu Gly Tyr Lys Leu Pro Val Glu Phe	
225 230 235 240	

gtt ccg gtc cgt ttt act tcg tgg atg ggc ggc gac cgc gac ggc aac	768
Val Pro Val Arg Phe Thr Ser Trp Met Gly Gly Asp Arg Asp Gly Asn	
245 250 255	
ccg aac gtc act gcc gat atc acc cgc cac gtc ctg cta ctc agc cgc	816
Pro Asn Val Thr Ala Asp Ile Thr Arg His Val Leu Leu Leu Ser Arg	
260 265 270	
tgg aaa gcc acc gat ttg ttc ctg aaa gat att cag gtg ctg gtt tct	864
Trp Lys Ala Thr Asp Leu Phe Leu Lys Asp Ile Gln Val Leu Val Ser	
275 280 285	
gaa ctg tcg atg gtt gaa gcg acc cct gaa ctg ctg gcg ctg gtt ggc	912
Glu Leu Ser Met Val Glu Ala Thr Pro Glu Leu Leu Ala Leu Val Gly	
290 295 300	
gaa gaa ggt gcc gca gaa ccg tat cgc tat ctg atg aaa aac ctg cgt	960
Glu Glu Gly Ala Ala Glu Pro Tyr Arg Tyr Leu Met Lys Asn Leu Arg	
305 310 315 320	
tct cgc ctg atg gcg aca cag gca tgg ctg gaa gcg cgc ctg aaa ggc	1008
Ser Arg Leu Met Ala Thr Gln Ala Trp Leu Glu Ala Arg Leu Lys Gly	
325 330 335	
gaa gaa ctg cca aaa cca gaa ggc ctg ctg aca caa aac gaa gaa ctg	1056
Glu Glu Leu Pro Lys Pro Glu Gly Leu Leu Thr Gln Asn Glu Glu Leu	
340 345 350	
tgg gaa ccg ctc tac gct tgc tac cag tca ctt cag gcg tgt ggc atg	1104
Trp Glu Pro Leu Tyr Ala Cys Tyr Gln Ser Leu Gln Ala Cys Gly Met	
355 360 365	
ggg att atc gcc aac ggc gat ctg ctc gac acc ctg cgc cgc gtg aaa	1152
Gly Ile Ile Ala Asn Gly Asp Leu Leu Asp Thr Leu Arg Arg Val Lys	
370 375 380	
tgt ttc ggc gta ccg ctg gtc cgt att gat atc cgt cag gag agc acg	1200
Cys Phe Gly Val Pro Leu Val Arg Ile Asp Ile Arg Gln Glu Ser Thr	
385 390 395 400	
cgt cat acc gaa gcg ctg ggc gag ctg acc cgc tac ctc ggt atc ggc	1248
Arg His Thr Glu Ala Leu Gly Glu Leu Thr Arg Tyr Leu Gly Ile Gly	
405 410 415	
gac tac gaa agc tgg tca gag gcc gac aaa cag gcg ttc ctg atc cgc	1296
Asp Tyr Glu Ser Trp Ser Glu Ala Asp Lys Gln Ala Phe Leu Ile Arg	
420 425 430	
gaa ctg aac tcc aaa cgt ccg ctt ctg ccg cgc aac tgg caa cca agc	1344
Glu Leu Asn Ser Lys Arg Pro Leu Leu Pro Arg Asn Trp Gln Pro Ser	
435 440 445	
gcc gaa acg cgc gaa gtg ctc gat acc tgc cag gtg att gcc gaa gca	1392
Ala Glu Thr Arg Glu Val Leu Asp Thr Cys Gln Val Ile Ala Glu Ala	
450 455 460	
ccg caa ggc tcc att gcc gcc tac gtg atc tcg atg gcg aaa acg ccg	1440

Pro 465	Gln	Gly	Ser	Ile	Ala	Ala	Tyr	Val	Ile	Ser	Met	Ala	Lys	Thr	Pro 480	
					470						475					
tcc Ser	gac Asp	gta Val	ctg Leu	gct Ala	gtc Val	cac His	ctg Leu	ctg Leu	ctg Leu	aaa Lys	gaa Glu	gcg Ala	ggg Gly	atc Ile	ggg Gly	1488
					485						490					
ttt Phe	gcg Ala	atg Met	ccg Pro	gtt Val	gct Ala	ccg Pro	ctg Leu	ttt Phe	gaa Glu	acc Thr	ctc Leu	gat Asp	gat Asp	ctg Leu	aac Asn	1536
					500						505					
aac Asn	gcc Ala	aac Asn	gat Asp	gtc Val	atg Met	acc Thr	cag Gln	ctg Leu	ctc Leu	aat Asn	att Ile	gac Asp	tgg Trp	tat Tyr	cgt Arg	1584
					515						520					
ggc Gly	ctg Leu	att Ile	cag Gln	ggc Gly	aaa Lys	cag Gln	atg Met	gtg Val	atg Met	att Ile	ggc Gly	tat Tyr	tcc Ser	gac Asp	tca Ser	1632
					530						535					
gca Ala	aaa Lys	gat Asp	gcg Ala	gga Gly	gtg Val	atg Met	gca Ala	gct Ala	tcc Ser	tgg Trp	gcg Ala	caa Gln	tat Tyr	cag Gln	gca Ala	1680
					545						550					
cag Gln	gat Asp	gca Ala	tta Leu	atc Ile	aaa Lys	acc Thr	tgc Cys	gaa Glu	aaa Lys	gcg Ala	ggg Gly	att Ile	gag Glu	ctg Leu	acg Thr	1728
					565						570					
ttg Leu	ttc Phe	cac His	ggg Gly	cgc Arg	ggc Gly	ggg Gly	tcc Ser	att Ile	ggg Gly	cgc Arg	ggc Gly	ggc Gly	gca Ala	cct Pro	gct Ala	1776
					580						585					
cat His	gcg Ala	gcg Ala	ctg Leu	ctg Leu	tca Ser	caa Gln	ccg Pro	cca Pro	gga Gly	agc Ser	ctg Leu	aaa Lys	ggc Gly	ggc Gly	ctg Leu	1824
					595						600					
cgc Arg	gta Val	acc Thr	gaa Glu	cag Gln	ggc Gly	gag Glu	atg Met	atc Ile	cgc Arg	ttt Phe	aaa Lys	tat Tyr	ggg Gly	ctg Leu	cca Pro	1872
					610						615					
gaa Glu	atc Ile	acc Thr	gtc Val	agc Ser	agc Ser	ctg Leu	tgc Ser	ctt Leu	tat Tyr	acc Thr	ggg Gly	gcg Ala	att Ile	ctg Leu	gaa Glu	1920
					625						630					
gcc Ala	aac Asn	ctg Leu	ctg Leu	cca Pro	ccg Pro	ccg Pro	gag Glu	ccg Pro	aaa Lys	gag Glu	agc Ser	tgg Trp	cgt Arg	cgc Arg	att Ile	1968
					645						650					
atg Met	gat Asp	gaa Glu	ctg Leu	tca Ser	gtc Val	atc Ile	tcc Ser	tgc Cys	gat Asp	gtc Val	tac Tyr	cgc Arg	ggc Gly	tac Tyr	gta Val	2016
					660						665					
cgt Arg	gaa Glu	aac Asn	aaa Lys	gat Asp	ttt Phe	gtg Val	cct Pro	tac Tyr	ttc Phe	cgc Arg	tcc Ser	gct Ala	acg Thr	ccg Pro	gaa Glu	2064
					675						680					
caa Gln	gaa Glu	ctg Leu	ggc Gly	aaa Lys	ctg Leu	ccg Pro	ttg Leu	ggg Gly	tca Ser	cgt Arg	ccg Pro	gcg Ala	aaa Lys	cgt Arg	cgc Arg	2112

690	695	700	
cca acc ggc ggc gtc gag tca cta cgc gcc att ccg tgg atc ttc gcc			2160
Pro Thr Gly Gly Val Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala			
705	710	715	720
tgg acg caa aac cgt ctg atg ctc ccc gcc tgg ctg ggt gca ggt acg			2208
Trp Thr Gln Asn Arg Leu Met Leu Pro Ala Trp Leu Gly Ala Gly Thr			
	725	730	735
gcg ctg caa aaa gtg gtc gaa gac ggc aaa cag agc gag ctg gag gct			2256
Ala Leu Gln Lys Val Val Glu Asp Gly Lys Gln Ser Glu Leu Glu Ala			
	740	745	750
atg tgc cgc gat tgg cca ttc ttc tcg acg cgt ctc gcc atg ctg gag			2304
Met Cys Arg Asp Trp Pro Phe Phe Ser Thr Arg Leu Gly Met Leu Glu			
	755	760	765
atg gtc ttc gcc aaa gca gac ctg tgg ctg gcg gaa tac tat gac caa			2352
Met Val Phe Ala Lys Ala Asp Leu Trp Leu Ala Glu Tyr Tyr Asp Gln			
	770	775	780
cgc ctg gta gac aaa gca ctg tgg ccg tta ggt aaa gag tta cgc aac			2400
Arg Leu Val Asp Lys Ala Leu Trp Pro Leu Gly Lys Glu Leu Arg Asn			
	785	790	800
ctg caa gaa gaa gac atc aaa gtg gtg ctg gcg att gcc aac gat tcc			2448
Leu Gln Glu Glu Asp Ile Lys Val Val Leu Ala Ile Ala Asn Asp Ser			
	805	810	815
cat ctg atg gcc gat ctg ccg tgg att gca gag tct att cag cta cgg			2496
His Leu Met Ala Asp Leu Pro Trp Ile Ala Glu Ser Ile Gln Leu Arg			
	820	825	830
aat att tac acc gac ccg ctg aac gta ttg cag gcc gag ttg ctg cac			2544
Asn Ile Tyr Thr Asp Pro Leu Asn Val Leu Gln Ala Glu Leu Leu His			
	835	840	845
cgc tcc cgc cag gca gaa aaa gaa ggc cag gaa ccg gat cct cgc gtc			2592
Arg Ser Arg Gln Ala Glu Lys Glu Gly Gln Glu Pro Asp Pro Arg Val			
	850	855	860
gaa caa gcg tta atg gtc act att gcc ggg att gcg gca ggt atg cgt			2640
Glu Gln Ala Leu Met Val Thr Ile Ala Gly Ile Ala Ala Gly Met Arg			
	865	870	875
			880
aat acc ggc taa			2652
Asn Thr Gly *			

<210> 251
 <211> 1992
 <212> DNA
 <213> Escherichia coli
 <220>

<221> CDS

<222> (1)...(1992)

<400> 251

atg tcc tca cgt aaa gag ctt gcc aat gct att cgt gcg ctg agc atg	48
Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met	
1 5 10 15	
gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt	96
Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly	
20 25 30	
atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac	144
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn	
35 40 45	
ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac	192
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn	
50 55 60	
ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac	240
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr	
65 70 75 80	
gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa	288
Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys	
85 90 95	
act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc	336
Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr	
100 105 110	
acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att	384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile	
115 120 125	
gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att	432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile	
130 135 140	
gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa	480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu	
145 150 155 160	
ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt	528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly	
165 170 175	
aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac	576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His	
180 185 190	
gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac	624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr	
195 200 205	
ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc	672

435	440	445	
gcg ctg atg aaa cag cgt cag gtg atg gtt tac acc cac gac tcc atc Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile 450 455 460			1392
ggt ctg ggc gaa gac ggg ccg act cac cag ccg gtt gag cag gtc gct Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala 465 470 475 480			1440
tct ctg cgc gta acc ccg aac atg tct aca tgg cgt ccg tgt gac cag Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln 485 490 495			1488
gtt gaa tcc gcg gtc gcg tgg aaa tac ggt gtt gag cgt cag gac ggc Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly 500 505 510			1536
ccg acc gca ctg atc ctc tcc cgt cag aac ctg gcg cag cag gaa cga Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg 515 520 525			1584
act gaa gag caa ctg gca aac atc gcg cgc ggt ggt tat gtg ctg aaa Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys 530 535 540			1632
gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu 545 550 555 560			1680
gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val 565 570 575			1728
aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln 580 585 590			1776
gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg 595 600 605			1824
gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly 610 615 620			1872
ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro 625 630 635 640			1920
gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val 645 650 655			1968
gcg aaa gca aaa gaa ctg ctg taa Ala Lys Ala Lys Glu Leu Leu *			1992
660			

<210> 252
 <211> 459
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(459)

<400> 252
 atg ttc cgg gga gca acg tta gtc aat ctc gac agc aaa ggg cgc tta 48
 Met Phe Arg Gly Ala Thr Leu Val Asn Leu Asp Ser Lys Gly Arg Leu
 1 5 10 15
 tca gtg cct acc cgt tat cgg gaa cag ctg ctt gag aac gct gcc ggt 96
 Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly
 20 25 30
 caa atg gtt tgc acc att gac att tat cac ccg tgc ctg ctg ctt tac 144
 Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Leu Tyr
 35 40 45
 ccc ctg cct gaa tgg gaa att atc gag caa aaa tta tcg cgt ctg tcg 192
 Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser
 50 55 60
 agc atg aac ccg gtt gag cgc cgt gtg cag cgc cta ctg tta ggt cat 240
 Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His
 65 70 75 80
 gcc agc gaa tgt cag atg gat ggc gca ggt cga ttg tta atc gcg cca 288
 Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
 85 90 95
 gta ctg cgg caa cat gcc ggg ctg aca aaa gaa gtg atg ctg gtt gga 336
 Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
 100 105 110
 cag ttc aac aag ttt gag ctg tgg gat gaa aca acc tgg cat caa cag 384
 Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
 115 120 125
 gtc aag gaa gat atc gac gca gag cag ttg gct acc gga gac tta tcg 432
 Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
 130 135 140
 gag cga ctg cag gac ttg tct cta taa 459
 Glu Arg Leu Gln Asp Leu Ser Leu *
 145 150

<210> 253
 <211> 942
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(942)

<400> 253

atg atg gaa aac tat aaa cat act acg gtg ctg ctg gat gaa gcc gtt	48
Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val	
1 5 10 15	
aat ggc ctc aat atc cgt cct gat ggc atc tac att gat ggg act ttt	96
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe	
20 25 30	
ggt cgc ggt ggt cac tca cgt ctg atc ctc tcg cag ctt ggc gaa gag	144
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu	
35 40 45	
ggg cgt ttg ctg gcg atc gat cgc gac ccg cag gct atc gcc gtt gcg	192
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala	
50 55 60	
aag act att gat gat ccg cgc ttc tcc atc atc cac gga cct ttc tcc	240
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser	
65 70 75 80	
gcg ctg ggc gaa tac gtt gcc gag cgc gat ctt atc ggc aag atc gac	288
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp	
85 90 95	
ggc att ctc ctc gat ctt ggc gtc tct tca ccg caa ctt gat gat gct	336
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala	
100 105 110	
gaa cgt ggc ttt tcc ttt atg cgc gat ggt ccg ctg gac atg cgt atg	384
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met	
115 120 125	
gac cca acc cgt ggg cag tca gcc gct gaa tgg cta caa acc gca gaa	432
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu	
130 135 140	
gaa gcc gat atc gcc tgg gta ttg aaa acc tat ggt gaa gag cgt ttt	480
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe	
145 150 155 160	
gcc aaa cgc att gcc cgc gcc att gtc gag cgt aac cgc gaa cag ccg	528
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro	
165 170 175	
atg acc cgc acc aaa gaa ctg gcg gaa gtc gtg gct gct gca acg ccg	576
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro	
180 185 190	
gtg aaa gat aag ttt aaa cat ccc gcg acc cgt acc ttc cag gcg gtg	624
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val	
195 200 205	

cgc att tgg gta aac agt gaa ctg gag gag ata gag cag gcg cta aaa 672
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
210 215 220

agc tcg ctc aac gtg ctg gcc ccg ggt ggg cgg ctt tcg atc atc agc 720
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225 230 235 240

ttc cac tcg ctg gaa gac cgt att gtg aaa cgt ttt atg cgt gaa aac 768
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255

agc cgc ggt ccg caa gtt ccg gca ggg tta ccg atg act gaa gag cag 816
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
260 265 270

ctc aaa aaa ctg ggt ggc cgt cag ctg cga gca cta ggc aag tta atg 864
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285

ccg ggc gaa gaa gag gtg gct gag aac cct cgt gcc cgt agt tca gtt 912
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300

ctg cgt att gca gag agg acg aat gca tga 942
Leu Arg Ile Ala Glu Arg Thr Asn Ala *
305 310

<210> 254
<211> 366
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(366)

<400> 254
atg atc agc aga gtg aca gaa gct cta agc aaa gtt aaa gga tcg atg 48
Met Ile Ser Arg Val Thr Glu Ala Leu Ser Lys Val Lys Gly Ser Met
1 5 10 15

gga agc cac gag cgc cat gca ttg cct ggt gtt atc ggt gac gat ctt 96
Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
20 25 30

ttg cga ttt ggg aag ctg cca ctc tgc ctg ttc att tgc att att ttg 144
Leu Arg Phe Gly Lys Leu Pro Leu Cys Leu Phe Ile Cys Ile Ile Leu
35 40 45

acg gcg gtg act gtg gta acc acg gcg cac cat acc cgt tta ctg acc 192
Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr
50 55 60

gct cag cgc gaa caa ctg gtg ctg gag cga gat gct tta gac att gaa 240

Ala	Gln	Arg	Glu	Gln	Leu	Val	Leu	Glu	Arg	Asp	Ala	Leu	Asp	Ile	Glu	
65					70					75					80	
tgg	cgc	aac	ctg	atc	ctt	gaa	gag	aat	gcg	ctc	ggc	gac	cat	agc	cgg	288
Trp	Arg	Asn	Leu	Ile	Leu	Glu	Glu	Asn	Ala	Leu	Gly	Asp	His	Ser	Arg	
			85						90					95		
gtg	gaa	agg	atc	gcc	acg	gaa	aag	ctg	caa	atg	cag	cat	gtt	gat	ccg	336
Val	Glu	Arg	Ile	Ala	Thr	Glu	Lys	Leu	Gln	Met	Gln	His	Val	Asp	Pro	
			100					105					110			
tca	caa	gaa	aat	atc	gta	gtg	caa	aaa	taa							366
Ser	Gln	Glu	Asn	Ile	Val	Val	Gln	Lys	*							
		115					120									

<210> 255

<211> 1767

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1767)

<400> 255

atg	aaa	gca	gcg	gcg	aaa	acg	cag	aaa	cca	aaa	cgt	cag	gaa	gaa	cat	48
Met	Lys	Ala	Ala	Ala	Lys	Thr	Gln	Lys	Pro	Lys	Arg	Gln	Glu	Glu	His	
1				5					10					15		
gcc	aac	ttt	atc	agt	tgg	cgt	ttt	gcg	ttg	tta	tgc	ggc	tgt	att	ctc	96
Ala	Asn	Phe	Ile	Ser	Trp	Arg	Phe	Ala	Leu	Leu	Cys	Gly	Cys	Ile	Leu	
			20					25					30			
ctg	gcg	ctg	gct	ttt	ctg	ctc	gga	cgc	gta	gcg	tgg	tta	caa	gtt	atc	144
Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gly	Arg	Val	Ala	Trp	Leu	Gln	Val	Ile	
		35					40					45				
tcc	ccg	gat	atg	ctg	gtg	aaa	gag	ggc	gac	atg	cgt	tct	ctt	cgc	gtt	192
Ser	Pro	Asp	Met	Leu	Val	Lys	Glu	Gly	Asp	Met	Arg	Ser	Leu	Arg	Val	
	50					55				60						
cag	caa	gtt	tcc	acc	tcc	cgc	ggc	atg	att	act	gac	cgt	tct	ggt	cgc	240
Gln	Gln	Val	Ser	Thr	Ser	Arg	Gly	Met	Ile	Thr	Asp	Arg	Ser	Gly	Arg	
65					70					75				80		
ccg	tta	gcg	gtg	agc	gtg	ccg	gta	aaa	gcg	att	tgg	gct	gac	ccg	aaa	288
Pro	Leu	Ala	Val	Ser	Val	Pro	Val	Lys	Ala	Ile	Trp	Ala	Asp	Pro	Lys	
			85					90						95		
gaa	gtg	cat	gac	gct	ggc	ggt	atc	agc	gtc	ggt	gac	cgc	tgg	aag	gcg	336
Glu	Val	His	Asp	Ala	Gly	Gly	Ile	Ser	Val	Gly	Asp	Arg	Trp	Lys	Ala	
			100					105					110			
ctg	gct	aac	gcg	ctc	aat	att	ccg	ctg	gat	cag	ctt	tca	gcc	cgc	att	384
Leu	Ala	Asn	Ala	Leu	Asn	Ile	Pro	Leu	Asp	Gln	Leu	Ser	Ala	Arg	Ile	
		115					120					125				

aac gcc aac ccg aaa ggg cgc ttt att tat ctg gcg cgt cag gtg aac	432
Asn Ala Asn Pro Lys Gly Arg Phe Ile Tyr Leu Ala Arg Gln Val Asn	
130 135 140	
cct gac atg gcg gac tac atc aaa aaa ctg aaa ctg ccg ggg att cat	480
Pro Asp Met Ala Asp Tyr Ile Lys Lys Leu Lys Leu Pro Gly Ile His	
145 150 155 160	
ctg cgt gaa gag tct cgc cgt tac tat ccg tcc ggc gaa gtg act gct	528
Leu Arg Glu Glu Ser Arg Arg Tyr Tyr Pro Ser Gly Glu Val Thr Ala	
165 170 175	
cac ctc atc ggc ttt act aac gtc gat agt caa ggg att gag ggc gtt	576
His Leu Ile Gly Phe Thr Asn Val Asp Ser Gln Gly Ile Glu Gly Val	
180 185 190	
gag aag agt ttc gat aaa tgg ctt acc ggg cag ccg ggt gag cgc att	624
Glu Lys Ser Phe Asp Lys Trp Leu Thr Gly Gln Pro Gly Glu Arg Ile	
195 200 205	
gtg cgt aaa gac cgc tat ggt cgc gta att gaa gat att tct tct act	672
Val Arg Lys Asp Arg Tyr Gly Arg Val Ile Glu Asp Ile Ser Ser Thr	
210 215 220	
gac agc cag gca gcg cac aac ctg gcg ctg agt att gat gaa cgc ctg	720
Asp Ser Gln Ala Ala His Asn Leu Ala Leu Ser Ile Asp Glu Arg Leu	
225 230 235 240	
cag gcg ctg gtt tat cgc gaa ctg aac aac gcg gtg gcc ttt aac aag	768
Gln Ala Leu Val Tyr Arg Glu Leu Asn Asn Ala Val Ala Phe Asn Lys	
245 250 255	
gct gaa tct ggt agc gcc gtg ctg gtg gat gtc aac acc ggt gaa gtg	816
Ala Glu Ser Gly Ser Ala Val Leu Val Asp Val Asn Thr Gly Glu Val	
260 265 270	
ctg gcg atg gct aac agc ccg tca tac aac cct aac aat ctg agc ggc	864
Leu Ala Met Ala Asn Ser Pro Ser Tyr Asn Pro Asn Asn Leu Ser Gly	
275 280 285	
acg ccg aaa gag gcg atg cgt aac cgt acc atc acc gac gtg ttt gaa	912
Thr Pro Lys Glu Ala Met Arg Asn Arg Thr Ile Thr Asp Val Phe Glu	
290 295 300	
ccg ggc tca acg gtt aaa ccg atg gtg gta atg acc gcg ttg caa cgt	960
Pro Gly Ser Thr Val Lys Pro Met Val Val Met Thr Ala Leu Gln Arg	
305 310 315 320	
ggc gtg gtg cgg gaa aac tcg gta ctc aat acc att cct tat cga att	1008
Gly Val Val Arg Glu Asn Ser Val Leu Asn Thr Ile Pro Tyr Arg Ile	
325 330 335	
aac ggc cac gaa atc aaa gac gtg gca cgc tac agc gaa tta acc ctg	1056
Asn Gly His Glu Ile Lys Asp Val Ala Arg Tyr Ser Glu Leu Thr Leu	
340 345 350	

acc ggg gta tta cag aag tcg agt aac gtc ggt gtt tcc aag ctg gcg	1104
Thr Gly Val Leu Gln Lys Ser Ser Asn Val Gly Val Ser Lys Leu Ala	
355 360 365	
tta gcg atg ccg tcc tca gcg tta gta gat act tac tca cgt ttt gga	1152
Leu Ala Met Pro Ser Ser Ala Leu Val Asp Thr Tyr Ser Arg Phe Gly	
370 375 380	
ctg gga aaa gcg acc aat ttg ggg ttg gtc gga gaa cgc agt ggc tta	1200
Leu Gly Lys Ala Thr Asn Leu Gly Leu Val Gly Glu Arg Ser Gly Leu	
385 390 395 400	
tat cct caa aaa caa cgg tgg tct gac ata gag agg gcc acc ttc tct	1248
Tyr Pro Gln Lys Gln Arg Trp Ser Asp Ile Glu Arg Ala Thr Phe Ser	
405 410 415	
ttc ggc tac ggg cta atg gta aca cca tta cag tta gcg cga gtc tac	1296
Phe Gly Tyr Gly Leu Met Val Thr Pro Leu Gln Leu Ala Arg Val Tyr	
420 425 430	
gca act atc ggc agc tac ggc att tat cgc cca ctg tgc att acc aaa	1344
Ala Thr Ile Gly Ser Tyr Gly Ile Tyr Arg Pro Leu Ser Ile Thr Lys	
435 440 445	
gtt gac ccc ccg gtt ccc ggt gaa cgt gtc ttc ccg gaa tcc att gtc	1392
Val Asp Pro Pro Val Pro Gly Glu Arg Val Phe Pro Glu Ser Ile Val	
450 455 460	
cgc act gtg gtg cat atg atg gaa agc gtg gcg cta cca ggc ggc ggc	1440
Arg Thr Val Val His Met Met Glu Ser Val Ala Leu Pro Gly Gly Gly	
465 470 475 480	
ggc gtg aag gcg gcg att aaa ggc tat cgt atc gcc att aaa acc ggt	1488
Gly Val Lys Ala Ala Ile Lys Gly Tyr Arg Ile Ala Ile Lys Thr Gly	
485 490 495	
acc gcg aaa aag gtc ggg ccg gac ggt cgc tac atc aat aaa tat att	1536
Thr Ala Lys Lys Val Gly Pro Asp Gly Arg Tyr Ile Asn Lys Tyr Ile	
500 505 510	
gct tat acc gca ggc gtt gcg cct gcg agt cag ccg cgc ttc gcg ctg	1584
Ala Tyr Thr Ala Gly Val Ala Pro Ala Ser Gln Pro Arg Phe Ala Leu	
515 520 525	
gtt gtt gtt atc aac gat ccg cag gcg ggt aaa tac tac ggc ggc gcc	1632
Val Val Val Ile Asn Asp Pro Gln Ala Gly Lys Tyr Tyr Gly Gly Ala	
530 535 540	
gtt tcc gcg ccg gtc ttt ggt gcc atc atg ggc ggc gta ttg cgt acc	1680
Val Ser Ala Pro Val Phe Gly Ala Ile Met Gly Gly Val Leu Arg Thr	
545 550 555 560	
atg aac atc gag ccg gat gcg ctg aca acg ggc gat aaa aat gaa ttt	1728
Met Asn Ile Glu Pro Asp Ala Leu Thr Thr Gly Asp Lys Asn Glu Phe	
565 570 575	
gtg att aat caa ggc gag ggg aca ggt ggc aga tgc taa	1767

Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser *
 580 585

<210> 256
 <211> 1488
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1488)

<400> 256
 gtg gca gat cgt aat ttg cgc gac ctt ctt gct ccg tgg gtg cca gac 48
 Met Ala Asp Arg Asn Leu Arg Asp Leu Leu Ala Pro Trp Val Pro Asp
 1 5 10 15
 gca cct tcg cga gca ctg cga gag atg aca ctc gac agc cgt gtg gct 96
 Ala Pro Ser Arg Ala Leu Arg Glu Met Thr Leu Asp Ser Arg Val Ala
 20 25 30
 gcg gcg ggc gat ctc ttt gta gct gta gta ggt cat cag gcg gac ggg 144
 Ala Ala Gly Asp Leu Phe Val Ala Val Val Gly His Gln Ala Asp Gly
 35 40 45
 cgt cga tat atc ccg cag gcg ata gcg caa ggt gtg gct gcc att att 192
 Arg Arg Tyr Ile Pro Gln Ala Ile Ala Gln Gly Val Ala Ala Ile Ile
 50 55 60
 gca gag gcg aaa gat gag gcg acc gat ggt gaa atc cgt gaa atg cac 240
 Ala Glu Ala Lys Asp Glu Ala Thr Asp Gly Glu Ile Arg Glu Met His
 65 70 75 80
 ggc gta ccg gtc atc tat ctc agc cag ctc aac gag cgt tta tct gca 288
 Gly Val Pro Val Ile Tyr Leu Ser Gln Leu Asn Glu Arg Leu Ser Ala
 85 90 95
 ctg gcg ggc cgc ttt tac cat gaa ccc tct gac aat tta cgt ctc gtg 336
 Leu Ala Gly Arg Phe Tyr His Glu Pro Ser Asp Asn Leu Arg Leu Val
 100 105 110
 ggc gta acg ggc acc aac ggc aaa acc acg act acc cag ctg ttg gcg 384
 Gly Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr Gln Leu Leu Ala
 115 120 125
 cag tgg agc caa ctg ctt ggc gaa atc agc gcg gta atg ggc acc gtt 432
 Gln Trp Ser Gln Leu Leu Gly Glu Ile Ser Ala Val Met Gly Thr Val
 130 135 140
 ggt aac ggc ctg ctg ggg aaa gtg atc ccg aca gaa aat aca acc ggt 480
 Gly Asn Gly Leu Leu Gly Lys Val Ile Pro Thr Glu Asn Thr Thr Gly
 145 150 155 160
 tcg gca gtc gat gtt cag cat gag ctg gcg ggg ctg gtg gat cag ggc 528
 Ser Ala Val Asp Val Gln His Glu Leu Ala Gly Leu Val Asp Gln Gly
 165 170 175

gcg acg ttt tgc gca atg gaa gtt tcc tcc cac ggg ctg gta cag cac	576
Ala Thr Phe Cys Ala Met Glu Val Ser Ser His Gly Leu Val Gln His	
180 185 190	
cg t gtg gcg gca ttg aaa ttt gcg gcg tcc gtc ttt acc aac tta agc	624
Arg Val Ala Ala Leu Lys Phe Ala Ala Ser Val Phe Thr Asn Leu Ser	
195 200 205	
cg c gat cac ctt gat tat cat ggt gat atg gaa cac tac gaa gcc gcg	672
Arg Asp His Leu Asp Tyr His Gly Asp Met Glu His Tyr Glu Ala Ala	
210 215 220	
aaa tgg ctg ctt tat tct gag cat cat tgc ggt cag gcg att att aac	720
Lys Trp Leu Leu Tyr Ser Glu His His Cys Gly Gln Ala Ile Ile Asn	
225 230 235 240	
gcc gac gat gaa gtg ggc cgc cgc tgg ctg gca aaa ctg ccg gac gcg	768
Ala Asp Asp Glu Val Gly Arg Arg Trp Leu Ala Lys Leu Pro Asp Ala	
245 250 255	
gtt gcg gta tca atg gaa gat cat att aat ccg aac tgt cac gga cgc	816
Val Ala Val Ser Met Glu Asp His Ile Asn Pro Asn Cys His Gly Arg	
260 265 270	
tgg ttg aaa gcg acc gaa gtg aac tat cac gac agc ggt gcg acg att	864
Trp Leu Lys Ala Thr Glu Val Asn Tyr His Asp Ser Gly Ala Thr Ile	
275 280 285	
cg c ttt agc tca agt tgg ggc gat ggc gaa att gaa agc cat ctg atg	912
Arg Phe Ser Ser Ser Trp Gly Asp Gly Glu Ile Glu Ser His Leu Met	
290 295 300	
ggc gct ttt aac gtc agc aac ctg ctg ctc gcg ctg gcg aca ctg ttg	960
Gly Ala Phe Asn Val Ser Asn Leu Leu Leu Ala Leu Ala Thr Leu Leu	
305 310 315 320	
gca ctc ggc tat cca ctg gct gat ctg ctg aaa acc gcc gcg cgt ctg	1008
Ala Leu Gly Tyr Pro Leu Ala Asp Leu Leu Lys Thr Ala Ala Arg Leu	
325 330 335	
caa ccg gtt tgc gga cgt atg gaa gtg ttc act gcg cca ggc aaa ccg	1056
Gln Pro Val Cys Gly Arg Met Glu Val Phe Thr Ala Pro Gly Lys Pro	
340 345 350	
acg gtg gtg gtg gat tac gcg cat acg ccg gat gca ctg gaa aaa gcc	1104
Thr Val Val Val Asp Tyr Ala His Thr Pro Asp Ala Leu Glu Lys Ala	
355 360 365	
tta cag gcg gcg cgt ctg cac tgt gcg ggc aag ctg tgg tgt gtc ttt	1152
Leu Gln Ala Ala Arg Leu His Cys Ala Gly Lys Leu Trp Cys Val Phe	
370 375 380	
ggc tgt ggt ggc gat cgc gat aaa ggt aag cgt cca ctg atg ggc gca	1200
Gly Cys Gly Gly Asp Arg Asp Lys Gly Lys Arg Pro Leu Met Gly Ala	
385 390 395 400	

att gcc gaa gag ttt gct gac gtg gcg gtg gtg acg gac gat aac ccg 1248
 Ile Ala Glu Glu Phe Ala Asp Val Ala Val Val Thr Asp Asp Asn Pro
 405 410 415

cgt acc gaa gaa ccg cgt gcc atc atc aac gat att ctg gcg gga atg 1296
 Arg Thr Glu Glu Pro Arg Ala Ile Ile Asn Asp Ile Leu Ala Gly Met
 420 425 430

tta gat gcc gga cat gcc aaa gtg atg gaa ggc cgt gct gaa gcg gtg 1344
 Leu Asp Ala Gly His Ala Lys Val Met Glu Gly Arg Ala Glu Ala Val
 435 440 445

act tgc gcc gtt atg cag gct aaa gag aat gat gtg gta ctg gtc gcg 1392
 Thr Cys Ala Val Met Gln Ala Lys Glu Asn Asp Val Val Leu Val Ala
 450 455 460

ggc aaa ggc cat gaa gat tac cag att gtt ggc aat cag cgt ctg gac 1440
 Gly Lys Gly His Glu Asp Tyr Gln Ile Val Gly Asn Gln Arg Leu Asp
 465 470 475 480

tac tcc gat cgc gtc acg gtg gcg cgt ctg ctg ggg gtg att gca tga 1488
 Tyr Ser Asp Arg Val Thr Val Ala Arg Leu Leu Gly Val Ile Ala *
 485 490 495

<210> 257
 <211> 1359
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1359)

<400> 257

atg att agc gta acc ctt agc caa ctt acc gac att ctc aac ggt gaa 48
 Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1 5 10 15

ctg caa ggt gca gat atc acc ctt gat gct gta acc act gat acc cga 96
 Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
 20 25 30

aaa ctg acg ccg ggc tgc ctg ttt gtt gcc ctg aaa ggc gaa cgt ttt 144
 Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
 35 40 45

gat gcc cac gat ttt gcc gac cag gcg aaa gct ggc ggc gca ggc gca 192
 Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
 50 55 60

cta ctg gtt agc cgt ccg ctg gac atc gac ctg ccg cag tta atc gtc 240
 Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65 70 75 80

aag gat acg cgt ctg gcg ttt ggt gaa ctg gct gca tgg gtt cgc cag 288

Lys	Asp	Thr	Arg	Leu	Ala	Phe	Gly	Glu	Leu	Ala	Ala	Trp	Val	Arg	Gln		
				85					90						95		
caa	gtt	ccg	gcg	cgc	gtg	gtt	gct	ctg	acg	ggg	tcc	tcc	ggc	aaa	acc	336	
Gln	Val	Pro	Ala	Arg	Val	Val	Ala	Leu	Thr	Gly	Ser	Ser	Gly	Lys	Thr		
			100					105					110				
tcc	gtt	aaa	gag	atg	acg	gcg	gcg	att	tta	agc	cag	tgc	ggc	aac	acg	384	
Ser	Val	Lys	Glu	Met	Thr	Ala	Ala	Ile	Leu	Ser	Gln	Cys	Gly	Asn	Thr		
		115					120					125					
ctt	tat	acg	gca	ggc	aat	ctc	aac	aac	gac	atc	ggg	gta	ccg	atg	acg	432	
Leu	Tyr	Thr	Ala	Gly	Asn	Leu	Asn	Asn	Asp	Ile	Gly	Val	Pro	Met	Thr		
	130					135					140						
ctg	ttg	cgc	tta	acg	ccg	gaa	tac	gat	tac	gca	gtt	att	gaa	ctt	ggc	480	
Leu	Leu	Arg	Leu	Thr	Pro	Glu	Tyr	Asp	Tyr	Ala	Val	Ile	Glu	Leu	Gly		
	145				150					155					160		
gcg	aac	cat	cag	ggc	gaa	ata	gcc	tgg	act	gtg	agt	ctg	act	cgc	ccg	528	
Ala	Asn	His	Gln	Gly	Glu	Ile	Ala	Trp	Thr	Val	Ser	Leu	Thr	Arg	Pro		
			165						170					175			
gaa	gct	gcg	ctg	gtc	aac	aac	ctg	gca	gcg	gcg	cat	ctg	gaa	ggg	ttt	576	
Glu	Ala	Ala	Leu	Val	Asn	Asn	Leu	Ala	Ala	Ala	His	Leu	Glu	Gly	Phe		
			180					185					190				
ggc	tcg	ctt	gcg	ggg	gtc	gcg	aaa	gcg	aaa	ggg	gaa	atc	ttt	agc	ggc	624	
Gly	Ser	Leu	Ala	Gly	Val	Ala	Lys	Ala	Lys	Gly	Glu	Ile	Phe	Ser	Gly		
		195					200					205					
ctg	ccg	gaa	aac	ggg	atc	gcc	att	atg	aac	gcc	gac	aac	aac	gac	tgg	672	
Leu	Pro	Glu	Asn	Gly	Ile	Ala	Ile	Met	Asn	Ala	Asp	Asn	Asn	Asp	Trp		
	210					215					220						
ctg	aac	tgg	cag	agc	gta	att	ggc	tca	cgc	aaa	gtg	tgg	cgt	ttc	tca	720	
Leu	Asn	Trp	Gln	Ser	Val	Ile	Gly	Ser	Arg	Lys	Val	Trp	Arg	Phe	Ser		
	225				230				235						240		
ccc	aat	gcc	gcc	aac	agc	gat	ttc	acc	gcc	acc	aat	atc	cat	gtg	acc	768	
Pro	Asn	Ala	Ala	Asn	Ser	Asp	Phe	Thr	Ala	Thr	Asn	Ile	His	Val	Thr		
			245					250					255				
tcg	cac	ggg	acg	gaa	ttt	acc	cta	caa	acc	cca	acc	ggg	agc	gtc	gat	816	
Ser	His	Gly	Thr	Glu	Phe	Thr	Leu	Gln	Thr	Pro	Thr	Gly	Ser	Val	Asp		
			260					265					270				
gtt	ctg	ctg	ccg	ttg	ccg	ggg	cgt	cac	aat	att	gcg	aat	gcg	ctg	gca	864	
Val	Leu	Leu	Pro	Leu	Pro	Gly	Arg	His	Asn	Ile	Ala	Asn	Ala	Leu	Ala		
		275				280						285					
gcc	gct	gcg	ctc	tcc	atg	tcc	gtg	ggc	gca	acg	ctt	gat	gct	atc	aaa	912	
Ala	Ala	Ala	Leu	Ser	Met	Ser	Val	Gly	Ala	Thr	Leu	Asp	Ala	Ile	Lys		
	290					295					300						
gcg	ggg	ctg	gca	aat	ctg	aaa	gct	gtt	cca	ggc	cgt	ctg	ttc	ccc	atc	960	
Ala	Gly	Leu	Ala	Asn	Leu	Lys	Ala	Val	Pro	Gly	Arg	Leu	Phe	Pro	Ile		

305	310	315	320	
caa ctg gca gaa aac cag ttg ctg ctc gac gac tcc tac aac gcc aat				1008
Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn	325	330	335	
gtc ggt tca atg act gca gca gtc cag gta ctg gct gaa atg ccg ggc				1056
Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly	340	345	350	
tac cgc gtg ctg gtg gtg ggc gat atg gcg gaa ctg ggc gct gaa agc				1104
Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser	355	360	365	
gaa gcc tgc cat gta cag gtg ggc gag gcg gca aaa gct gct ggt att				1152
Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile	370	375	380	
gac cgc gtg tta agc gtg ggt aaa caa agc cat gct atc agc acc gcc				1200
Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala	385	390	400	
agc ggc gtt ggc gaa cat ttt gct gat aaa act gcg tta att acg cgt				1248
Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg	405	410	415	
ctt aaa tta ctg att gct gag caa cag gta att acg att tta gtt aag				1296
Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys	420	425	430	
ggt tca cgt agt gcc gcc atg gaa gag gta gta cgc gct tta cag gag				1344
Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu	435	440	445	
aat ggg aca tgt tag				1359
Asn Gly Thr Cys *	450			

<210> 258
 <211> 1083
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(1083)

<400> 258	
atg tta gtt tgg ctg gcc gaa cat ttg gtc aaa tat tat tcc ggc ttt	48
Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe	
1 5 10 15	
aac gtc ttt tcc tat ctg acg ttt cgc gcc atc gtc agc ctg ctg acc	96
Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr	
20 25 30	

gcg ctg ttc atc tca ttg tgg atg ggc ccg cgt atg att gct cat ttg	144
Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu	
35 40 45	
caa aaa ctt tcc ttt ggt cag gtg gtg cgt aac gac ggt cct gaa tca	192
Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser	
50 55 60	
cac ttc agc aag cgc ggt acg ccg acc atg ggc ggg att atg atc ctg	240
His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu	
65 70 75 80	
acg gcg att gtg atc tcc gta ctg ctg tgg gct tac ccg tcc aat ccg	288
Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro	
85 90 95	
tac gtc tgg tgc gtg ttg gtg gtg ctg gta ggt tac ggt gtt att ggc	336
Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly	
100 105 110	
ttt gtt gat gat tat cgc aaa gtg gtg cgt aaa gac acc aaa ggg ttg	384
Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu	
115 120 125	
atc gct cgt tgg aag tat ttc tgg atg tcg gtc att gcg ctg ggt gtc	432
Ile Ala Arg Trp Lys Tyr Phe Trp Met Ser Val Ile Ala Leu Gly Val	
130 135 140	
gcc ttc gcc ctg tac ctt gcc ggc aaa gac acg ccc gca acg cag ctg	480
Ala Phe Ala Leu Tyr Leu Ala Gly Lys Asp Thr Pro Ala Thr Gln Leu	
145 150 155 160	
gtg gtc cca ttc ttt aaa gat gtg atg ccg cag ctg ggg ctg ttc tac	528
Val Val Pro Phe Phe Lys Asp Val Met Pro Gln Leu Gly Leu Phe Tyr	
165 170 175	
att ctg ctg gct tac ttc gtc att gtg ggt act ggc aac gcg gta aac	576
Ile Leu Leu Ala Tyr Phe Val Ile Val Gly Thr Gly Asn Ala Val Asn	
180 185 190	
ctg acc gat ggt ctc gac ggc ctg gca att atg ccg acc gta ttt gtc	624
Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Phe Val	
195 200 205	
gcc ggt ggt ttt gcg ctg gtg gcg tgg gcg acc ggc aat atg aac ttt	672
Ala Gly Gly Phe Ala Leu Val Ala Trp Ala Thr Gly Asn Met Asn Phe	
210 215 220	
gcc agc tac ttg cat ata ccg tat ctg cga cac gcc ggg gaa ctg gtt	720
Ala Ser Tyr Leu His Ile Pro Tyr Leu Arg His Ala Gly Glu Leu Val	
225 230 235 240	
att gtc tgt acc gcg ata gtc ggg gca gga ctg ggc ttc ctg tgg ttt	768
Ile Val Cys Thr Ala Ile Val Gly Ala Gly Leu Gly Phe Leu Trp Phe	
245 250 255	
aac acc tat ccg gcg cag gtc ttt atg ggc gat gta ggt tcg ctg gcg	816

```

Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
    260                                265                                270

tta ggt ggt gcg tta ggc att atc gcc gta ctg cta cgt cag gaa ttc      864
Leu Gly Gly Ala Leu Gly Ile Ile Ala Val Leu Leu Arg Gln Glu Phe
    275                                280                                285

ctg ctg gtg att atg ggg ggc gtg ttc gtg gta gaa acg ctt tct gtc      912
Leu Leu Val Ile Met Gly Gly Val Phe Val Val Glu Thr Leu Ser Val
    290                                295                                300

atc ctg cag gtc ggc tcc ttt aaa ctg cgc gga caa cgt att ttc cgc      960
Ile Leu Gln Val Gly Ser Phe Lys Leu Arg Gly Gln Arg Ile Phe Arg
    305                                310                                315                                320

atg gca ccg att cat cac cac tat gaa ctg aaa ggc tgg ccg gaa ccg      1008
Met Ala Pro Ile His His His Tyr Glu Leu Lys Gly Trp Pro Glu Pro
    325                                330                                335

cgc gtc att gtg cgt ttc tgg att att tcg ctg atg ctg gtt ctg att      1056
Arg Val Ile Val Arg Phe Trp Ile Ile Ser Leu Met Leu Val Leu Ile
    340                                345                                350

ggt ctg gca acg ctg aag gta cgt taa                                  1083
Gly Leu Ala Thr Leu Lys Val Arg *
    355                                360

<210> 259
<211> 1317
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1317)

<400> 259
atg gct gat tat cag ggt aaa aat gtc gtc att atc ggc ctg ggc ctc      48
Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu
    1                                5                                10                                15

acc ggg ctt tcc tgc gtg gac ttt ttc ctc gct cgc ggt gtg acg ccg      96
Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro
    20                                25                                30

cgc gtt atg gat acg cgt atg aca ccg cct ggc ctg gat aaa tta ccc      144
Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
    35                                40                                45

gaa gcc gta gaa cgc cac acg ggc agt ctg aat gat gaa tgg ctg atg      192
Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
    50                                55                                60

gcg gca gat ctg att gtc gcc agt ccc ggt att gca ctg gcg cat cca      240
Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
    65                                70                                75                                80

```

tcc tta agc gct gcc gct gat gcc gga atc gaa atc gtt ggc gat atc	288
Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile	
85 90 95	
gag ctg ttc tgt cgc gaa gca caa gca ccg att gtg gcg att acc ggt	336
Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly	
100 105 110	
tct aac ggc aaa agc acg gtc acc acg cta gtg ggt gaa atg gcg aaa	384
Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys	
115 120 125	
gcg gcg ggg gtt aac gtt ggt gtg ggt ggc aat att ggc ctg cct gcg	432
Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala	
130 135 140	
ttg atg cta ctg gat gat gag tgt gaa ctg tac gtg ctg gaa ctg tcg	480
Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser	
145 150 155 160	
agc ttc cag ctg gaa acc acc tcc agc tta cag gcg gta gca gcg acc	528
Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr	
165 170 175	
att ctg aac gtg act gaa gat cat atg gat cgc tat ccg ttt ggt tta	576
Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu	
180 185 190	
caa cag tat cgt gca gca aaa ctg cgc att tac gaa aac gcg aaa gtt	624
Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val	
195 200 205	
tgc gtg gtt aat gct gat gat gcc tta aca atg ccg att cgc ggt gcg	672
Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala	
210 215 220	
gat gaa cgc tgc gtc agc ttt ggc gtc aac atg ggt gac tat cac ctg	720
Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu	
225 230 235 240	
aat cat cag cag ggc gaa acc tgg ctg cgg gtt aaa ggc gag aaa gtg	768
Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val	
245 250 255	
ctg aat gtg aaa gag atg aaa ctt tcc ggg cag cat aac tac acc aat	816
Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn	
260 265 270	
gcg ctg gcg gcg ctg gcg ctg gca gat gct gca ggg tta ccg cgt gcc	864
Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala	
275 280 285	
agc agc ctg aaa gcg tta acc aca ttc act ggt ctg ccg cat cgc ttt	912
Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe	
290 295 300	

```

gaa gtt gtg ctg gag cat aac ggc gta cgt tgg att aac gat tcg aaa 960
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys
305 310 315 320

gcg acc aac gtc ggc agt acg gaa gcg gcg ctg aat ggc ctg cac gta 1008
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val
325 330 335

gac ggc aca ctg cat ttg ttg ctg ggt ggc gat ggt aaa tcg gcg gac 1056
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp
340 345 350

ttt agc cca ctg gcg cgt tac ctg aat ggc gat aac gta cgt ctg tat 1104
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr
355 360 365

tgt ttc ggt cgt gac ggc gcg cag ctg gcg gcg cta cgc ccg gaa gtg 1152
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val
370 375 380

gca gaa caa acc gaa act atg gaa cag gcg atg cgc ttg ctg gct ccg 1200
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro
385 390 395 400

cgt gtt cag ccg ggc gat atg gtt ctg ctc tcc cca gcc tgt gcc agc 1248
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser
405 410 415

ctt gat cag ttc aag aac ttt gaa caa cga ggc aat gag ttt gcc cgt 1296
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg
420 425 430

ctg gcg aag gag tta ggt tga 1317
Leu Ala Lys Glu Leu Gly *
435

<210> 260
<211> 1245
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1245)

<400> 260
atg cgt tta tct ctc cct cgc ctg aaa atg ccg cgc ctg cca gga ttc 48
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe
1 5 10 15

agt atc ctg gtc tgg atc tcc acg gcg cta aag ggc tgg gtg atg ggc 96
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
20 25 30

tcg cgg gaa aaa gat acc gac agc ctg atc atg tac gat cgc acc tta 144
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu

```


35	40	45	
ctg tgg ctg acc ttc ggc ctc gcg gcg att ggc ttt atc atg gtg acc Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr 50 55 60			192
tcg gcg tca atg ccc ata ggg caa cgc tta acc aac gat ccg ttc ttc Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe 65 70 75 80			240
ttc gcg aag cgt gat ggt gtc tat ctg att ttg gcg ttt att ctg gcg Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala 85 90 95			288
atc att acg ctg cgt ctg ccg atg gag ttc tgg caa cgc tac agt gcc Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala 100 105 110			336
acg atg ctg ctc gga tct atc atc ctg ctg atg atc gtc ctg gta gtg Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val 115 120 125			384
ggc agc tcg gtt aaa ggg gca tcg cgt tgg atc gat ctc ggt ttg ctg Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu 130 135 140			432
cgt atc cag cct gcg gag ctg aca aaa ctg tcg ctg ttt tgc tat atc Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile 145 150 155 160			480
gcc aac tat ctg gtg cgt aaa ggc gac gaa gta cgt aat aac ctg cgc Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg 165 170 175			528
ggc ttc ctg aaa ccg atg ggc gtg att ctg gtg ttg gca gtg tta ctg Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu 180 185 190			576
ctg gca cag cca gac ctt ggt acg gtg gtg gtg ttg ttt gtg act acg Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr 195 200 205			624
ctg gcg atg ttg ttc ctg gcg gga gcg aaa ttg tgg cag ttc att gcc Leu Ala Met Leu Phe Leu Ala Gly Ala Lys Leu Trp Gln Phe Ile Ala 210 215 220			672
att atc ggt atg ggc att tca gcg gtt gtg ttg ctg ata ctc gcc gaa Ile Ile Gly Met Gly Ile Ser Ala Val Val Leu Leu Ile Leu Ala Glu 225 230 235 240			720
ccg tac cgt atc cgc cgt gtt acc gca ttc tgg aac ccg tgg gaa gat Pro Tyr Arg Ile Arg Arg Val Thr Ala Phe Trp Asn Pro Trp Glu Asp 245 250 255			768
ccc ttt ggc agc ggc tat cag tta acg caa tcg ctg atg gcg ttt ggt Pro Phe Gly Ser Gly Tyr Gln Leu Thr Gln Ser Leu Met Ala Phe Gly 260 265 270			816

```

cgc ggc gaa ctt tgg ggg caa ggt tta ggt aac tcg gta caa aaa ctg 864
Arg Gly Glu Leu Trp Gly Gln Gly Leu Gly Asn Ser Val Gln Lys Leu
      275                      280                      285

gag tat ctg ccg gaa gcg cac act gac ttt att ttc gcc att atc ggc 912
Glu Tyr Leu Pro Glu Ala His Thr Asp Phe Ile Phe Ala Ile Ile Gly
      290                      295                      300

gaa gaa ctg ggg tat gtc ggt gtg gtg ctg gca ctt tta atg gta ttc 960
Glu Glu Leu Gly Tyr Val Gly Val Val Leu Ala Leu Leu Met Val Phe
      305                      310                      315                      320

ttc gtc gct ttt cgc gcg atg tcg att ggc cgt aaa gca tta gaa att 1008
Phe Val Ala Phe Arg Ala Met Ser Ile Gly Arg Lys Ala Leu Glu Ile
      325                      330                      335

gac cac cgt ttt tcc ggt ttt ctc gcc tgt tct att ggc atc tgg ttt 1056
Asp His Arg Phe Ser Gly Phe Leu Ala Cys Ser Ile Gly Ile Trp Phe
      340                      345                      350

agc ttc cag gcg ctg gtt aac gta ggc gcg gcg gcg ggg atg tta ccg 1104
Ser Phe Gln Ala Leu Val Asn Val Gly Ala Ala Ala Gly Met Leu Pro
      355                      360                      365

acc aaa ggt ctg aca ttg ccg ctg atc agt tac ggt ggt tcg agc tta 1152
Thr Lys Gly Leu Thr Leu Pro Leu Ile Ser Tyr Gly Gly Ser Ser Leu
      370                      375                      380

ctg att atg tcg aca gcc atc atg atg ctg ttg cgt att gat tat gaa 1200
Leu Ile Met Ser Thr Ala Ile Met Met Leu Leu Arg Ile Asp Tyr Glu
      385                      390                      395                      400

acg cgt ctg gag aaa gcg cag gcg ttt gta cga ggt tca cga tga 1245
Thr Arg Leu Glu Lys Ala Gln Ala Phe Val Arg Gly Ser Arg *
      405                      410

```

<210> 261
 <211> 1068
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1068)

```

<400> 261
atg agt ggt caa gga aag cga tta atg gtg atg gca ggc gga acc ggt 48
Met Ser Gly Gln Gly Lys Arg Leu Met Val Met Ala Gly Gly Thr Gly
      1                      5                      10                      15

gga cat gta ttc ccg gga ctg gcg gtt gcg cac cat cta atg gct cag 96
Gly His Val Phe Pro Gly Leu Ala Val Ala His His Leu Met Ala Gln
      20                      25                      30

```

ggt tgg caa gtt cgc tgg ctg ggg act gcc gac cgt atg gaa gcg gac	144
Gly Trp Gln Val Arg Trp Leu Gly Thr Ala Asp Arg Met Glu Ala Asp	
35 40 45	
tta gtg cca aaa cat ggc atc gaa att gat ttc att cgt atc tct ggt	192
Leu Val Pro Lys His Gly Ile Glu Ile Asp Phe Ile Arg Ile Ser Gly	
50 55 60	
ctg cgt gga aaa ggt ata aaa gca ctg ata gct gcc ccg ctg cgt atc	240
Leu Arg Gly Lys Gly Ile Lys Ala Leu Ile Ala Ala Pro Leu Arg Ile	
65 70 75 80	
ttc aac gcc tgg cgt cag gcg cgg gcg att atg aaa gcg tac aaa cct	288
Phe Asn Ala Trp Arg Gln Ala Arg Ala Ile Met Lys Ala Tyr Lys Pro	
85 90 95	
gac gtg gtg ctc ggt atg gga ggc tac gtg tca ggt cca ggt ggt ctg	336
Asp Val Val Leu Gly Met Gly Gly Tyr Val Ser Gly Pro Gly Gly Leu	
100 105 110	
gcc gcg tgg tcg tta ggc att ccg gtt gta ctt cat gaa caa aac ggt	384
Ala Ala Trp Ser Leu Gly Ile Pro Val Val Leu His Glu Gln Asn Gly	
115 120 125	
att gcg ggc tta acc aat aaa tgg ctg gcg aag att gcc acc aaa gtg	432
Ile Ala Gly Leu Thr Asn Lys Trp Leu Ala Lys Ile Ala Thr Lys Val	
130 135 140	
atg cag gcg ttt cca ggt gct ttc cct aat gcg gaa gta gtg ggt aac	480
Met Gln Ala Phe Pro Gly Ala Phe Pro Asn Ala Glu Val Val Gly Asn	
145 150 155 160	
ccg gtg cgt acc gat gtg ttg gcg ctg ccg ttg ccg cag caa cgt ttg	528
Pro Val Arg Thr Asp Val Leu Ala Leu Pro Leu Pro Gln Gln Arg Leu	
165 170 175	
gct gga cgt gaa ggt ccg gtt cgt gtg ctg gta gtg ggt ggt tct cag	576
Ala Gly Arg Glu Gly Pro Val Arg Val Leu Val Val Gly Gly Ser Gln	
180 185 190	
ggc gca cgc att ctt aac cag aca atg ccg cag gtt gct gcg aaa ctg	624
Gly Ala Arg Ile Leu Asn Gln Thr Met Pro Gln Val Ala Ala Lys Leu	
195 200 205	
ggt gat tca gtc act atc tgg cat cag agc ggc aaa ggt tcg caa caa	672
Gly Asp Ser Val Thr Ile Trp His Gln Ser Gly Lys Gly Ser Gln Gln	
210 215 220	
tcc gtt gaa cag gcg tat gcc gaa gcg ggg caa ccg cag cat aaa gtg	720
Ser Val Glu Gln Ala Tyr Ala Glu Ala Gly Gln Pro Gln His Lys Val	
225 230 235 240	
acg gaa ttt att gat gat atg gcg gcg gcg tat gcg tgg gcg gat gtc	768
Thr Glu Phe Ile Asp Asp Met Ala Ala Ala Tyr Ala Trp Ala Asp Val	
245 250 255	
gtc gtt tgc cgc tcc ggt gcg tta acg gtg agt gaa atc gcc gcg gca	816

Val Val Cys Arg Ser Gly Ala Leu Thr Val Ser Glu Ile Ala Ala Ala	
260 265 270	
gga cta ccg gcg ttg ttt gtg ccg ttt caa cat aaa gac cgc cag caa	864
Gly Leu Pro Ala Leu Phe Val Pro Phe Gln His Lys Asp Arg Gln Gln	
275 280 285	
tac tgg aat gcg cta ccg ctg gaa aaa gcg ggc gca gcc aaa att atc	912
Tyr Trp Asn Ala Leu Pro Leu Glu Lys Ala Gly Ala Ala Lys Ile Ile	
290 295 300	
gag cag cca cag ctt agc gtg gat gct gtc gcc aac acc ctg gcc ggg	960
Glu Gln Pro Gln Leu Ser Val Asp Ala Val Ala Asn Thr Leu Ala Gly	
305 310 315 320	
tgg tcg cga gaa acc tta tta acc atg gca gaa cgc gcc cgc gct gca	1008
Trp Ser Arg Glu Thr Leu Leu Thr Met Ala Glu Arg Ala Arg Ala Ala	
325 330 335	
tcc att ccg gat gcc acc gag cga gtg gca aat gaa gtg agc cgg gtt	1056
Ser Ile Pro Asp Ala Thr Glu Arg Val Ala Asn Glu Val Ser Arg Val	
340 345 350	
gcc cgg gcg taa	1068
Ala Arg Ala *	
355	
<210> 262	
<211> 1476	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(1476)	
<400> 262	
atg aat aca caa caa ttg gca aaa ctg cgt tcc atc gtg ccc gaa atg	48
Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met	
1 5 10 15	
cgt cgc gtt cgg cac ata cat ttt gtc ggc att ggt ggt gcc ggt atg	96
Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met	
20 25 30	
ggc ggt att gcc gaa gtt ctg gcc aat gaa ggt tat cag atc agt ggt	144
Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly	
35 40 45	
tcc gat tta gcg cca aat ccg gtc acg cag cag tta atg aat ctg ggt	192
Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly	
50 55 60	
gcg acg att tat ttc aac cat cgc ccg gaa aac gta cgt gat gcc agc	240
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser	
65 70 75 80	

gtg	gtc	gtt	gtt	tcc	agc	gcg	att	tct	gcc	gat	aac	ccg	gaa	att	gtc	288
Val	Val	Val	Val	Ser	Ser	Ala	Ile	Ser	Ala	Asp	Asn	Pro	Glu	Ile	Val	
				85					90					95		
gcc	gct	cat	gaa	gcg	cgt	att	ccg	gtg	atc	cgt	cgt	gcc	gaa	atg	ctg	336
Ala	Ala	His	Glu	Ala	Arg	Ile	Pro	Val	Ile	Arg	Arg	Ala	Glu	Met	Leu	
			100					105					110			
gct	gag	tta	atg	cgt	ttt	cgt	cat	ggc	atc	gcc	att	gcc	gga	acg	cac	384
Ala	Glu	Leu	Met	Arg	Phe	Arg	His	Gly	Ile	Ala	Ile	Ala	Gly	Thr	His	
		115					120					125				
ggc	aaa	acg	aca	acc	acc	gcg	atg	gtt	tcc	agc	atc	tac	gca	gaa	gcg	432
Gly	Lys	Thr	Thr	Thr	Thr	Ala	Met	Val	Ser	Ser	Ile	Tyr	Ala	Glu	Ala	
	130						135				140					
ggg	ctc	gac	cca	acc	ttc	gtt	aac	ggc	ggg	ctg	gta	aaa	gcg	gcg	ggg	480
Gly	Leu	Asp	Pro	Thr	Phe	Val	Asn	Gly	Gly	Leu	Val	Lys	Ala	Ala	Gly	
145					150					155					160	
gtt	cat	gcg	cgt	ttg	ggg	cat	ggg	cgg	tac	ctg	att	gcc	gaa	gca	gat	528
Val	His	Ala	Arg	Leu	Gly	His	Gly	Arg	Tyr	Leu	Ile	Ala	Glu	Ala	Asp	
				165					170					175		
gag	agt	gat	gca	tcg	ttc	ctg	cat	ctg	caa	ccg	atg	gtg	gcg	att	gtc	576
Glu	Ser	Asp	Ala	Ser	Phe	Leu	His	Leu	Gln	Pro	Met	Val	Ala	Ile	Val	
			180					185					190			
acc	aat	atc	gaa	gcc	gac	cac	atg	gat	acc	tac	cag	ggc	gac	ttt	gag	624
Thr	Asn	Ile	Glu	Ala	Asp	His	Met	Asp	Thr	Tyr	Gln	Gly	Asp	Phe	Glu	
		195					200					205				
aat	tta	aaa	cag	act	ttt	att	aat	ttt	ctg	cac	aac	ctg	ccg	ttt	tac	672
Asn	Leu	Lys	Gln	Thr	Phe	Ile	Asn	Phe	Leu	His	Asn	Leu	Pro	Phe	Tyr	
	210					215					220					
ggg	cgt	gcg	gtg	atg	tgt	gtt	gat	gat	ccg	gtg	atc	cgc	gaa	ttg	tta	720
Gly	Arg	Ala	Val	Met	Cys	Val	Asp	Asp	Pro	Val	Ile	Arg	Glu	Leu	Leu	
225					230					235					240	
ccg	cga	gtg	ggg	cgt	cag	acc	acg	act	tac	ggc	ttc	agc	gaa	gat	gcc	768
Pro	Arg	Val	Gly	Arg	Gln	Thr	Thr	Thr	Tyr	Gly	Phe	Ser	Glu	Asp	Ala	
			245						250					255		
gac	gtg	cgt	gta	gaa	gat	tat	cag	cag	att	ggc	ccg	cag	ggg	cac	ttt	816
Asp	Val	Arg	Val	Glu	Asp	Tyr	Gln	Gln	Ile	Gly	Pro	Gln	Gly	His	Phe	
			260					265					270			
acg	ctg	ctg	cgc	cag	gac	aaa	gag	ccg	atg	cgc	gtc	acc	ctg	aat	gcg	864
Thr	Leu	Leu	Arg	Gln	Asp	Lys	Glu	Pro	Met	Arg	Val	Thr	Leu	Asn	Ala	
		275					280					285				
cca	ggg	cgt	cat	aac	gcg	ctg	aac	gcc	gca							

acg gaa gag ggc att gac gac gag gct att ttg cgg gcg ctt gaa agc 960
 Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser
 305 310 315 320

ttc cag ggg act ggt cgc cgt ttt gat ttc ctc ggt gaa ttc ccg ctg 1008
 Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu
 325 330 335

gag cca gtg aat ggt aaa agc ggt acg gca atg ctg gtc gat gac tac 1056
 Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr
 340 345 350

ggc cac cac ccg acg gaa gtg gac gcc acc att aaa gcg gcg cgc gca 1104
 Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala
 355 360 365

ggc tgg ccg gat aaa aac ctg gta atg ctg ttt cag ccg cac cgt ttt 1152
 Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe
 370 375 380

acc cgt acg cgc gac ctg tat gat gat ttc gcc aat gtg ctg acg cag 1200
 Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln
 385 390 395 400

gtt gat acc ctg ttg atg ctg gaa gtg tat ccg gct ggc gaa gcg cca 1248
 Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro
 405 410 415

att ccg gga gcg gac agc cgt tgc ctg tgt cgc aca att cgt gga cgt 1296
 Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg
 420 425 430

ggg aaa att gat ccc att ctg gtg ccg gat ccg gcg ccg gta gcc gag 1344
 Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu
 435 440 445

atg ctg gca ccg gta tta acc ggt aac gac ctg att ctc gtt cag ggg 1392
 Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly
 450 455 460

gct ggt aat att gga aaa att gcc cgt tct tta gct gaa atc aaa ctg 1440
 Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu
 465 470 475 480

aag ccg caa act ccg gag gaa gaa caa cat gac tga 1476
 Lys Pro Gln Thr Pro Glu Glu Glu Gln His Asp *
 485 490

<210> 263
 <211> 921
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(921)

<400> 263

atg act gat aaa atc gcg gtc ctg ttg ggt ggg acc tcc gct gag cgg	48
Met Thr Asp Lys Ile Ala Val Leu Leu Gly Gly Thr Ser Ala Glu Arg	
1 5 10 15	
gaa gtt tct ctg aat tct ggc gca gcg gtg tta gcc gga ctg cgt gaa	96
Glu Val Ser Leu Asn Ser Gly Ala Ala Val Leu Ala Gly Leu Arg Glu	
20 25 30	
ggc ggt att gac gcg tat cct gtc gac ccg aaa gaa gtc gac gtg acg	144
Gly Gly Ile Asp Ala Tyr Pro Val Asp Pro Lys Glu Val Asp Val Thr	
35 40 45	
caa ctg aag tcg atg ggc ttt cag aaa gtg ttt atc gcg cta cac ggt	192
Gln Leu Lys Ser Met Gly Phe Gln Lys Val Phe Ile Ala Leu His Gly	
50 55 60	
cgc ggc ggt gaa gat ggt acg ctg cag ggg atg ctc gag ctg atg ggc	240
Arg Gly Gly Glu Asp Gly Thr Leu Gln Gly Met Leu Glu Leu Met Gly	
65 70 75 80	
ttg cct tat acc gga agc gga gtg atg gca tct gcg ctt tca atg gat	288
Leu Pro Tyr Thr Gly Ser Gly Val Met Ala Ser Ala Leu Ser Met Asp	
85 90 95	
aaa cta cgc agc aaa ctt cta tgg caa ggt gcc ggt tta ccg gtc gcg	336
Lys Leu Arg Ser Lys Leu Leu Trp Gln Gly Ala Gly Leu Pro Val Ala	
100 105 110	
ccg tgg gta gcg tta acc cgc gca gag ttt gaa aaa ggc ctg agc gat	384
Pro Trp Val Ala Leu Thr Arg Ala Glu Phe Glu Lys Gly Leu Ser Asp	
115 120 125	
aag cag tta gca gaa att tct gct ctg ggt ttg ccg gtt atc gtt aag	432
Lys Gln Leu Ala Glu Ile Ser Ala Leu Gly Leu Pro Val Ile Val Lys	
130 135 140	
ccg agc cgc gaa ggt tcc agt gtg gga atg tca aaa gta gta gca gaa	480
Pro Ser Arg Glu Gly Ser Ser Val Gly Met Ser Lys Val Val Ala Glu	
145 150 155 160	
aat gct cta caa gat gca tta aga ttg gca ttt cag cac gat gaa gaa	528
Asn Ala Leu Gln Asp Ala Leu Arg Leu Ala Phe Gln His Asp Glu Glu	
165 170 175	
gta ttg att gaa aaa tgg cta agt ggg ccg gag ttc acg gtt gcg ata	576
Val Leu Ile Glu Lys Trp Leu Ser Gly Pro Glu Phe Thr Val Ala Ile	
180 185 190	
ctc ggt gaa gaa att tta ccg tca ata cgt att caa ccg tcc gga acc	624
Leu Gly Glu Glu Ile Leu Pro Ser Ile Arg Ile Gln Pro Ser Gly Thr	
195 200 205	
ttc tat gat tat gag gcg aag tat ctc tct gat gag aca cag tat ttc	672
Phe Tyr Asp Tyr Glu Ala Lys Tyr Leu Ser Asp Glu Thr Gln Tyr Phe	
210 215 220	

tgc ccc gca ggt ctg gaa gcg tca caa gag gcc aat ttg cag gca tta	720
Cys Pro Ala Gly Leu Glu Ala Ser Gln Glu Ala Asn Leu Gln Ala Leu	
225 230 235 240	
gtg ctg aaa gca tgg acg acg tta ggt tgc aaa gga tgg gga cgt att	768
Val Leu Lys Ala Trp Thr Thr Leu Gly Cys Lys Gly Trp Gly Arg Ile	
245 250 255	
gac gtt atg ctg gac agc gat gga cag ttt tat ctg ctg gaa gcc aat	816
Asp Val Met Leu Asp Ser Asp Gly Gln Phe Tyr Leu Leu Glu Ala Asn	
260 265 270	
acc tca ccg ggt atg acc agc cac agc ctg gtg ccg atg gcg gca cgt	864
Thr Ser Pro Gly Met Thr Ser His Ser Leu Val Pro Met Ala Ala Arg	
275 280 285	
cag gca ggt atg agc ttc tcg cag ttg gta gta cga att ctg gaa ctg	912
Gln Ala Gly Met Ser Phe Ser Gln Leu Val Val Arg Ile Leu Glu Leu	
290 295 300	
gcg,gac taa	921
Ala Asp *	
305	
<210> 264	
<211> 606	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(606)	
<400> 264	
atg gcg ctg cat gac gaa aac gtc gtc tgg cat agc cat ccg gtc act	48
Met Ala Leu His Asp Glu Asn Val Val Trp His Ser His Pro Val Thr	
1 5 10 15	
gtg caa caa cgc gag cta cac cac ggt cat cgt ggt gta gtg ctg tgg	96
Val Gln Gln Arg Glu Leu His His Gly His Arg Gly Val Val Leu Trp	
20 25 30	
ttt acc gcc ctc tcc ggg tcc ggt aaa tca acg gtc gcc ggg gcg ctg	144
Phe Thr Gly Leu Ser Gly Ser Gly Lys Ser Thr Val Ala Gly Ala Leu	
35 40 45	
gag gag gcg tta cat aaa ctc gcc gtc agt acg tat ctg ctg gat gcc	192
Glu Glu Ala Leu His Lys Leu Gly Val Ser Thr Tyr Leu Leu Asp Gly	
50 55 60	
gac aat gtt cgc cac gga tta tgc agc gat ctc ggt ttt agc gat gcc	240
Asp Asn Val Arg His Gly Leu Cys Ser Asp Leu Gly Phe Ser Asp Ala	
65 70 75 80	
gat cgt aaa gag aat atc cgt cgc gtc ggt gaa gtg gcg aat ttg atg	288


```

Asp Arg Lys Glu Asn Ile Arg Arg Val Gly Glu Val Ala Asn Leu Met
      85                                90                                95

gtt gaa gcc gga ctg gtg gtg ctg acc gca ttt atc tcg cca cac cgc 336
Val Glu Ala Gly Leu Val Val Leu Thr Ala Phe Ile Ser Pro His Arg
      100                                105                                110

gcc gaa cgc cag atg gtt cgc gaa cgc gta gga gaa ggg cgc ttt atc 384
Ala Glu Arg Gln Met Val Arg Glu Arg Val Gly Glu Gly Arg Phe Ile
      115                                120                                125

gaa gtg ttt gtc gat acg ccg ctg gcg att tgc gaa gcc cgc gat ccc 432
Glu Val Phe Val Asp Thr Pro Leu Ala Ile Cys Glu Ala Arg Asp Pro
      130                                135                                140

aaa ggc tta tat aag aaa gcg cgt gcc ggt gaa ctg cgc aac ttt acg 480
Lys Gly Leu Tyr Lys Lys Ala Arg Ala Gly Glu Leu Arg Asn Phe Thr
      145                                150                                155                                160

gga ata gat tcc gtt tac gaa gcg cct gaa tcg gca gaa att cat ctc 528
Gly Ile Asp Ser Val Tyr Glu Ala Pro Glu Ser Ala Glu Ile His Leu
      165                                170                                175

aat ggt gaa caa tta gta aca aat ttg gta cag caa tta tta gat ctg 576
Asn Gly Glu Gln Leu Val Thr Asn Leu Val Gln Gln Leu Leu Asp Leu
      180                                185                                190

ttg aga cag aac gat att atc aga tcc tga 606
Leu Arg Gln Asn Asp Ile Ile Arg Ser *
      195                                200

<210> 265
<211> 1428
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1428)

<400> 265
atg aac acc gca ctt gca caa caa atc gcc aat gaa ggc ggc gtc gaa 48
Met Asn Thr Ala Leu Ala Gln Gln Ile Ala Asn Glu Gly Gly Val Glu
      1                                5                                10                                15

gcc tgg atg att gcg caa caa cat aaa agc ctg ctg cgt ttt ctg acc 96
Ala Trp Met Ile Ala Gln Gln His Lys Ser Leu Leu Arg Phe Leu Thr
      20                                25                                30

tgt ggt agc gtc gat gac ggc aaa agt act ctg att ggt cgt ctg ctg 144
Cys Gly Ser Val Asp Asp Gly Lys Ser Thr Leu Ile Gly Arg Leu Leu
      35                                40                                45

cac gat acc cgc caa atc tac gaa gat cag ctc tca tcg ctg cat aac 192
His Asp Thr Arg Gln Ile Tyr Glu Asp Gln Leu Ser Ser Leu His Asn
      50                                55                                60

```

gac agt aag cgt cac ggc acc cag ggc gaa aag ctg gat ctg gct ctg	240
Asp Ser Lys Arg His Gly Thr Gln Gly Glu Lys Leu Asp Leu Ala Leu	
65 70 75 80	
ctg gtg gac ggc ctg caa gct gag cgc gaa cag ggc atc acc att gac	288
Leu Val Asp Gly Leu Gln Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp	
85 90 95	
gtg gcc tac cgc tat ttc tct acc gag aag cgt aaa ttt att atc gcc	336
Val Ala Tyr Arg Tyr Phe Ser Thr Glu Lys Arg Lys Phe Ile Ile Ala	
100 105 110	
gac acc cca ggg cac gag cag tac acc cgc aat atg gcg act ggc gca	384
Asp Thr Pro Gly His Glu Gln Tyr Thr Arg Asn Met Ala Thr Gly Ala	
115 120 125	
tcg aca tgt gaa ctg gcg atc tta ctg atc gat gcc cgt aaa ggc gtg	432
Ser Thr Cys Glu Leu Ala Ile Leu Leu Ile Asp Ala Arg Lys Gly Val	
130 135 140	
ctc gat caa acc cgt cgt cac agt ttt atc tcc aca ctg ttg ggg atc	480
Leu Asp Gln Thr Arg Arg His Ser Phe Ile Ser Thr Leu Leu Gly Ile	
145 150 155 160	
aaa cat ctg gtc gtg gcg atc aac aaa atg gat ctg gtg gat tac agt	528
Lys His Leu Val Val Ala Ile Asn Lys Met Asp Leu Val Asp Tyr Ser	
165 170 175	
gaa gag acg ttc acc cgt att cgt gaa gat tat ttg acc ttt gcc ggg	576
Glu Glu Thr Phe Thr Arg Ile Arg Glu Asp Tyr Leu Thr Phe Ala Gly	
180 185 190	
cag ctg ccg ggt aat ctg gat atc cgc ttt gtg ccg ctc tct gca ctg	624
Gln Leu Pro Gly Asn Leu Asp Ile Arg Phe Val Pro Leu Ser Ala Leu	
195 200 205	
gaa ggc gac aac gtg gca tcg caa agt gaa agt atg ccg tgg tac agc	672
Glu Gly Asp Asn Val Ala Ser Gln Ser Glu Ser Met Pro Trp Tyr Ser	
210 215 220	
ggg ccg aca ctg ctc gaa gtg ctg gaa acc gtg gag atc cag cga gtg	720
Gly Pro Thr Leu Leu Glu Val Leu Glu Thr Val Glu Ile Gln Arg Val	
225 230 235 240	
gtg gat gct cag cca atg cgc ttc ccg gtg cag tac gtt aat cgc ccg	768
Val Asp Ala Gln Pro Met Arg Phe Pro Val Gln Tyr Val Asn Arg Pro	
245 250 255	
aat ctc gat ttt cgt ggt tac gcc gga acg ctg gca tcc ggt cgc gtg	816
Asn Leu Asp Phe Arg Gly Tyr Ala Gly Thr Leu Ala Ser Gly Arg Val	
260 265 270	
gaa gtc ggg caa cgt gtc aaa gtg ctg ccc tct ggt gtg gaa tca aac	864
Glu Val Gly Gln Arg Val Lys Val Leu Pro Ser Gly Val Glu Ser Asn	
275 280 285	

gtc gcg cgg atc gtg act ttt gat ggt gat cgc gaa gaa gcc ttt gcc 912
Val Ala Arg Ile Val Thr Phe Asp Gly Asp Arg Glu Glu Ala Phe Ala
290 295 300

gga gaa gcg atc acc ctg gtg ctg acg gat gag atc gac atc agc cgt 960
Gly Glu Ala Ile Thr Leu Val Leu Thr Asp Glu Ile Asp Ile Ser Arg
305 310 315 320

ggc gat ctg ctg ctg gcg gca gac gaa gcg tta ccg gcg gtg cag agc 1008
Gly Asp Leu Leu Leu Ala Ala Asp Glu Ala Leu Pro Ala Val Gln Ser
325 330 335

gcg tcg gtg gat gtg gta tgg atg gcg gaa cag ccg ctt tct cca ggg 1056
Ala Ser Val Asp Val Val Trp Met Ala Glu Gln Pro Leu Ser Pro Gly
340 345 350

cag agt tac gac atc aaa att gcc ggt aag aag acg cgc gcg cgt gtt 1104
Gln Ser Tyr Asp Ile Lys Ile Ala Gly Lys Lys Thr Arg Ala Arg Val
355 360 365

gat ggc att cgc tat cag gtt gat att aat aac ctt acc cag cgt gaa 1152
Asp Gly Ile Arg Tyr Gln Val Asp Ile Asn Asn Leu Thr Gln Arg Glu
370 375 380

gtt gaa aac ctg cca ctg aat ggg atc ggc ctc gtg gat ctc act ttt 1200
Val Glu Asn Leu Pro Leu Asn Gly Ile Gly Leu Val Asp Leu Thr Phe
385 390 395 400

gac gag ccg ctg gtg tta gat cgt tat caa caa aat ccg gtg acg ggt 1248
Asp Glu Pro Leu Val Leu Asp Arg Tyr Gln Gln Asn Pro Val Thr Gly
405 410 415

ggg ctg att ttt atc gat cgc ctg agc aat gtg acc gtg ggt gcc ggt 1296
Gly Leu Ile Phe Ile Asp Arg Leu Ser Asn Val Thr Val Gly Ala Gly
420 425 430

atg gtg cac gag cca gtt agc cag gca act gct gcg cca tct gaa ttc 1344
Met Val His Glu Pro Val Ser Gln Ala Thr Ala Ala Pro Ser Glu Phe
435 440 445

agt gca ttc gaa ctg gaa ttg aat gct ctg gtt cgt cgc cac ttt ccg 1392
Ser Ala Phe Glu Leu Glu Leu Asn Ala Leu Val Arg Arg His Phe Pro
450 455 460

cac tgg ggc gcg cgc gat ttg ctg ggg gat aaa taa 1428
His Trp Gly Ala Arg Asp Leu Leu Gly Asp Lys *
465 470 475

<210> 266
<211> 384
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(384)

<400> 266

atg cgc cat cgt aag agt ggt cgt caa ctg aac cgc aac agc agc cat 48
Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
1 5 10 15

cgc cag gct atg ttc cgc aat atg gca ggt tca ctg gtt cgt cat gaa 96
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
20 25 30

atc atc aag acg act ctg cct aaa gcg aaa gag ctg cgc cgc gta gtt 144
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
35 40 45

gag ccg ctg att act ctt gcc aag act gat agc gtt gct aat cgt cgt 192
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
50 55 60

ctg gca ttc gcc cgt act cgt gat aac gag atc gtg gca aaa ctg ttt 240
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65 70 75 80

aac gaa ctg ggc ccg cgt ttc gcg agc cgt gcc ggt ggt tac act cgt 288
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
85 90 95

att ctg aag tgt ggc ttc cgt gca ggc gac aac gcg ccg atg gct tac 336
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
100 105 110

atc gag ctg gtt gat cgt tca gag aaa gca gaa gct gct gca gag taa 384
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu *
115 120 125

<210> 267

<211> 990

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(990)

<400> 267

atg cag ggt tct gtg aca gag ttt cta aaa ccg cgc ctg gtt gat atc 48
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
1 5 10 15

gag caa gtg agt tcg acg cac gcc aag gtg acc ctt gag cct tta gag 96
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
20 25 30

cgt ggc ttt ggc cat act ctg ggt aac gca ctg cgc cgt att ctg ctc 144
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu
35 40 45

tca tgc atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta	192
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val	
50 55 60	
cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa	240
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu	
65 70 75 80	
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat	288
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp	
85 90 95	
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca	336
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala	
100 105 110	
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac	384
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His	
115 120 125	
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc	432
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile	
130 135 140	
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat	480
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His	
145 150 155 160	
tgc gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc	528
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys	
165 170 175	
tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta	576
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val	
180 185 190	
gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac	624
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn	
195 200 205	
ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg	672
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu	
210 215 220	
gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct	720
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro	
225 230 235 240	
gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct	768
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro	
245 250 255	
gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca	816
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala	
260 265 270	

gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag 864
 Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu
 275 280 285

ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa 912
 Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys
 290 295 300

gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac 960
 Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn
 305 310 315 320

tgg cca ccg gca agc atc gct gac gag taa 990
 Trp Pro Pro Ala Ser Ile Ala Asp Glu *
 325

<210> 268

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(621)

<400> 268

atg gca aga tat ttg ggt cct aag ctc aag ctg agc cgt cgt gag ggc 48
 Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
 1 5 10 15

acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt 96
 Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
 20 25 30

aaa att gaa caa gct cct ggc cag cac ggt gcg cgt aaa ccg cgt ctg 144
 Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
 35 40 45

tct gac tat ggt gtg cag ttg cgt gaa aag caa aaa gtt cgc cgt atc 192
 Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
 50 55 60

tat ggt gtg ctg gag cgt cag ttc cgt aac tac tac aaa gaa gca gca 240
 Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala
 65 70 75 80

cgt ctg aaa ggc aac acc ggt gaa aac ctg ttg gct ctg ctg gaa ggt 288
 Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly
 85 90 95

cgt ctg gac aac gtt gta tac cgt atg ggc ttc ggt gcc act cgt gca 336
 Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala
 100 105 110

gaa gca cgt cag ctg gtt agc cat aaa gca att atg gta aac ggt cgt 384
 Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg

115	120	125	
gtt gtt aac atc gct tct tat cag gtt agt ccg aat gac gtt gta agc			432
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser			
130	135	140	
att cgt gag aaa gcg aag aag cag tct cgc gtg aaa gcc gct ctg gag			480
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu			
145	150	155	160
ctg gct gag cag cgt gaa aag cca acc tgg ctg gaa gtt gat gct ggc			528
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly			
165	170	175	
aag atg gaa ggt acg ttt aag cgt aag ccg gag cgt tct gat ctg tct			576
Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser			
180	185	190	
gcg gac att aac gaa cac ctg atc gtc gag ctt tac tcc aag taa			621
Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys *			
195	200	205	
<210> 269			
<211> 390			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(390)			
<400> 269			
atg gca aag gca cca att cgt gca cgt aaa cgt gta aga aaa caa gtc			48
Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val			
1	5	10	15
tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg			96
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val			
20	25	30	
act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt			144
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly			
35	40	45	
ggt tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag			192
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln			
50	55	60	
gtt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag			240
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys			
65	70	75	80
aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act			288
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr			
85	90	95	

att	cgt	gct	ctg	aac	gcc	gca	ggt	ttc	cgc	atc	act	aac	att	act	gat	336
Ile	Arg	Ala	Leu	Asn	Ala	Ala	Gly	Phe	Arg	Ile	Thr	Asn	Ile	Thr	Asp	
			100					105					110			

gtg	act	ccg	atc	cct	cat	aac	ggt	tgt	cgt	ccg	ccg	aaa	aaa	cgt	cgc	384
Val	Thr	Pro	Ile	Pro	His	Asn	Gly	Cys	Arg	Pro	Pro	Lys	Lys	Arg	Arg	
		115					120					125				

gta	taa															390
Val	*															

<210> 270
 <211> 357
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(357)

<400> 270																
gtg	gcc	cgt	ata	gca	ggc	att	aac	att	cct	gat	cat	aag	cat	gcc	gta	48
Met	Ala	Arg	Ile	Ala	Gly	Ile	Asn	Ile	Pro	Asp	His	Lys	His	Ala	Val	
	1			5					10					15		

atc	gca	tta	act	tcg	att	tat	ggc	gtc	ggc	aag	acc	cgt	tct	aaa	gcc	96
Ile	Ala	Leu	Thr	Ser	Ile	Tyr	Gly	Val	Gly	Lys	Thr	Arg	Ser	Lys	Ala	
			20					25					30			

atc	ctg	gct	gca	gcg	ggt	atc	gct	gaa	gat	gtt	aag	atc	agt	gag	ctg	144
Ile	Leu	Ala	Ala	Ala	Gly	Ile	Ala	Glu	Asp	Val	Lys	Ile	Ser	Glu	Leu	
		35				40						45				

tct	gaa	gga	caa	atc	gac	acg	ctg	cgt	gac	gaa	gtt	gcc	aaa	ttt	gtc	192
Ser	Glu	Gly	Gln	Ile	Asp	Thr	Leu	Arg	Asp	Glu	Val	Ala	Lys	Phe	Val	
	50				55					60						

gtt	gaa	ggt	gat	ctg	cgc	cgt	gaa	atc	agc	atg	agc	atc	aag	cgc	ctg	240
Val	Glu	Gly	Asp	Leu	Arg	Arg	Glu	Ile	Ser	Met	Ser	Ile	Lys	Arg	Leu	
	65			70					75					80		

atg	gat	ctt	ggt	tgc	tat	cgc	ggt	ttg	cgt	cat	cgt	cgt	ggt	ctc	ccg	288
Met	Asp	Leu	Gly	Cys	Tyr	Arg	Gly	Leu	Arg	His	Arg	Arg	Gly	Leu	Pro	
			85					90					95			

gtt	cgc	ggt	cag	cgt	acc	aag	acc	aac	gca	cgt	acc	cgt	aag	ggt	ccg	336
Val	Arg	Gly	Gln	Arg	Thr	Lys	Thr	Asn	Ala	Arg	Thr	Arg	Lys	Gly	Pro	
		100						105					110			

cgc	aaa	ccg	atc	aag	aaa	taa										357
Arg	Lys	Pro	Ile	Lys	Lys	*										
		115														

<210> 271
 <211> 1383
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1383)

<400> 271

atg acg caa tta acc atg aaa gac aaa att ggc tac ggg ctg gga gac	48
Met Thr Gln Leu Thr Met Lys Asp Lys Ile Gly Tyr Gly Leu Gly Asp	
1 5 10 15	
acc gcc tgc ggc ttc gtc tgg cag gcc acg atg ttc ctg ctg gcc tat	96
Thr Ala Cys Gly Phe Val Trp Gln Ala Thr Met Phe Leu Leu Ala Tyr	
20 25 30	
ttc tac acc gac gtc ttc ggc ctg tcg gcg ggg att atg ggc acg ctg	144
Phe Tyr Thr Asp Val Phe Gly Leu Ser Ala Gly Ile Met Gly Thr Leu	
35 40 45	
ttt ttg gtc tcc cgc gtg ctc gac gcc gtc acc gac ccg ctg atg ggg	192
Phe Leu Val Ser Arg Val Leu Asp Ala Val Thr Asp Pro Leu Met Gly	
50 55 60	
ctg ctg gta gac cgc acc cgc acg cgg cac ggc cag ttc cgc ccg ttc	240
Leu Leu Val Asp Arg Thr Arg Thr Arg His Gly Gln Phe Arg Pro Phe	
65 70 75 80	
ctg ctg tgg ggg gcc atc ccg ttc ggc atc gtc tgc gtg ctg acc ttc	288
Leu Leu Trp Gly Ala Ile Pro Phe Gly Ile Val Cys Val Leu Thr Phe	
85 90 95	
tac acg ccg gac ttc tcc gca cag gcc aag atc atc tac gcc tgc gtg	336
Tyr Thr Pro Asp Phe Ser Ala Gln Gly Lys Ile Ile Tyr Ala Cys Val	
100 105 110	
acc tac att ctc ctg acc ctg gtc tac acc ttc gtt aac gtg ccg tac	384
Thr Tyr Ile Leu Leu Thr Leu Val Tyr Thr Phe Val Asn Val Pro Tyr	
115 120 125	
tgc gcc atg ccg ggc gtc atc acc gcc gac ccg aaa gag cgt cac gcc	432
Cys Ala Met Pro Gly Val Ile Thr Ala Asp Pro Lys Glu Arg His Ala	
130 135 140	
ctg cag tcc tgg cgc ttc ttc ctg gcg gcg gcg ggc tcg ctc gct atc	480
Leu Gln Ser Trp Arg Phe Phe Leu Ala Ala Ala Gly Ser Leu Ala Ile	
145 150 155 160	
agc ggc atc gcg ctg ccg ctg gtg agc atc atc ggc aaa ggg gac gag	528
Ser Gly Ile Ala Leu Pro Leu Val Ser Ile Ile Gly Lys Gly Asp Glu	
165 170 175	
cag gtg ggc tac ttc ggc gcc atg tgc gtg ctg ggg ctg agc ggc gtg	576
Gln Val Gly Tyr Phe Gly Ala Met Cys Val Leu Gly Leu Ser Gly Val	
180 185 190	

gtg ctg ctc tac gtc tgc ttc ttc acg acc aaa gag cgc tac acc ttt	624
Val Leu Leu Tyr Val Cys Phe Phe Thr Thr Lys Glu Arg Tyr Thr Phe	
195 200 205	
gag gtg cag ccg ggc tgc tgc gtg gcg aaa gac ctt aag ctg ctg ctg	672
Glu Val Gln Pro Gly Ser Ser Val Ala Lys Asp Leu Lys Leu Leu Leu	
210 215 220	
ggc aac agc cag tgg cgc atc atg tgc gcg ttc aag atg atg gcg acc	720
Gly Asn Ser Gln Trp Arg Ile Met Cys Ala Phe Lys Met Met Ala Thr	
225 230 235 240	
tgc tcc aac gtg gtg cgc ggc ggg gcg acg ctc tac ttc gtg aaa tac	768
Cys Ser Asn Val Val Arg Gly Gly Ala Thr Leu Tyr Phe Val Lys Tyr	
245 250 255	
gtg atg gat cac ccg gag ttg gcg acc cag ttt tta ctt tac ggc agc	816
Val Met Asp His Pro Glu Leu Ala Thr Gln Phe Leu Leu Tyr Gly Ser	
260 265 270	
ctc gcc acc atg ttc ggc tgc ctt tgc tcc tca cgc ctg ctg ggc cgc	864
Leu Ala Thr Met Phe Gly Ser Leu Cys Ser Ser Arg Leu Leu Gly Arg	
275 280 285	
ttc gac cgc gtc acc gcc ttc aag tgg atc atc gtc gcc tac tgc ctg	912
Phe Asp Arg Val Thr Ala Phe Lys Trp Ile Ile Val Ala Tyr Ser Leu	
290 295 300	
atc agc ctg ctg att ttc gtc acc ccg gcg gag cac atc gcg ctc att	960
Ile Ser Leu Leu Ile Phe Val Thr Pro Ala Glu His Ile Ala Leu Ile	
305 310 315 320	
ttt gcc ctc aac atc ctg ttc ctg ttc gtc ttt aat acc acc acg ccg	1008
Phe Ala Leu Asn Ile Leu Phe Leu Phe Val Phe Asn Thr Thr Thr Pro	
325 330 335	
ctg cag tgg ctg atg gct tct gac gtg gtg gac tac gag gag agc cgc	1056
Leu Gln Trp Leu Met Ala Ser Asp Val Val Asp Tyr Glu Glu Ser Arg	
340 345 350	
agc ggt cgc cgc ctc gac ggg ctg gtg ttc tcc acc tac ctg ttc agc	1104
Ser Gly Arg Arg Leu Asp Gly Leu Val Phe Ser Thr Tyr Leu Phe Ser	
355 360 365	
ctg aag att ggc ctg gcg att ggc ggg gcg gtg gtg ggc tgg atc ctg	1152
Leu Lys Ile Gly Leu Ala Ile Gly Gly Ala Val Val Gly Trp Ile Leu	
370 375 380	
gcg tac gtc aac tat tcc gcc agc agc agc gtg cag ccg gtt gag gtg	1200
Ala Tyr Val Asn Tyr Ser Ala Ser Ser Ser Val Gln Pro Val Glu Val	
385 390 395 400	
ctc acc acc atc aaa att ctg ttc tgc gtg gtg ccg gtg gtg ctc tac	1248
Leu Thr Thr Ile Lys Ile Leu Phe Cys Val Val Pro Val Val Leu Tyr	
405 410 415	

gcg ggc atg ttc atc atg ctg tgc ctc tac aag ctc acc gat gcc cgc 1296
 Ala Gly Met Phe Ile Met Leu Ser Leu Tyr Lys Leu Thr Asp Ala Arg
 420 425 430

gtg gag gcc atc agc cgg cag ctg att aag cac cgc gcg gcg cag ggc 1344
 Val Glu Ala Ile Ser Arg Gln Leu Ile Lys His Arg Ala Ala Gln Gly
 435 440 445

gag gcc gtt ccc gac gcc gcg aca gcc gca tcc cat taa 1383
 Glu Ala Val Pro Asp Ala Ala Thr Ala Ala Ser His *
 450 455 460

<210> 272

<211> 1611

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1611)

<400> 272

atg gaa atc act aac ccg ata ctc acc ggc ttc aac ccg gac ccg tcc 48
 Met Glu Ile Thr Asn Pro Ile Leu Thr Gly Phe Asn Pro Asp Pro Ser
 1 5 10 15

ctg tgc cgc cag ggc gag gac tac tac atc gcc acc tcg acc ttc gag 96
 Leu Cys Arg Gln Gly Glu Asp Tyr Tyr Ile Ala Thr Ser Thr Phe Glu
 20 25 30

tgg ttc ccg ggc gtg cgc atc tac cac tcc cgt gac ctg aaa aac tgg 144
 Trp Phe Pro Gly Val Arg Ile Tyr His Ser Arg Asp Leu Lys Asn Trp
 35 40 45

tcg ctg gtc agc acc ccg ttg gac cgc gtg tcg atg ctg gac atg aag 192
 Ser Leu Val Ser Thr Pro Leu Asp Arg Val Ser Met Leu Asp Met Lys
 50 55 60

ggc aac ccg gac tcc ggc ggc atc tgg gcg ccg tgc ctg agc tac gcc 240
 Gly Asn Pro Asp Ser Gly Gly Ile Trp Ala Pro Cys Leu Ser Tyr Ala
 65 70 75 80

gac ggt aaa ttc tgg ctg ctc tac acc gac gtg aag att gtc gac tcg 288
 Asp Gly Lys Phe Trp Leu Leu Tyr Thr Asp Val Lys Ile Val Asp Ser
 85 90 95

ccg tgg aaa aac ggc cgc aac ttc ctc gtc acc gcg ccc tcc atc gag 336
 Pro Trp Lys Asn Gly Arg Asn Phe Leu Val Thr Ala Pro Ser Ile Glu
 100 105 110

ggg cca tgg agc gag cca atc ccg atg ggc aac ggc ggg ttt gac ccg 384
 Gly Pro Trp Ser Glu Pro Ile Pro Met Gly Asn Gly Gly Phe Asp Pro
 115 120 125

tcc ctg ttc cac gac gac gat ggc cgc aaa tac tat atc tac cgc ccg 432
 Ser Leu Phe His Asp Asp Asp Gly Arg Lys Tyr Tyr Ile Tyr Arg Pro


```

ggc aac gac tcg ctc aat tcg acc ttc acc caa tcg acc gtg gcg cgc 1152
Gly Asn Asp Ser Leu Asn Ser Thr Phe Thr Gln Ser Thr Val Ala Arg
370 375 380

cgc tgg cag cac ttc gcc ttc cgg gca gaa acg cgg atg gag ttc tcg 1200
Arg Trp Gln His Phe Ala Phe Arg Ala Glu Thr Arg Met Glu Phe Ser
385 390 395 400

ccg gtg cac ttc cag cag agc gcg ggg ctg acc tgc tac tac aac agc 1248
Pro Val His Phe Gln Gln Ser Ala Gly Leu Thr Cys Tyr Tyr Asn Ser
405 410 415

aaa aac tgg agc tac tgc ttt gtg gac tac gag gag gga cag ggt aga 1296
Lys Asn Trp Ser Tyr Cys Phe Val Asp Tyr Glu Glu Gly Gln Gly Arg
420 425 430

acc atc aaa gtt atc cag ctc gac cac aac gtg ccg tcg tgg ccg ctg 1344
Thr Ile Lys Val Ile Gln Leu Asp His Asn Val Pro Ser Trp Pro Leu
435 440 445

cac gag cag ccc att ccg gtg ccg gaa cat gcg gag agc gtc tgg ctg 1392
His Glu Gln Pro Ile Pro Val Pro Glu His Ala Glu Ser Val Trp Leu
450 455 460

cgg gtg gac gtg gat acg ctg gtc tac cgc tac agc tac tcg ttt gat 1440
Arg Val Asp Val Asp Thr Leu Val Tyr Arg Tyr Ser Tyr Ser Phe Asp
465 470 475 480

ggc gag acg tgg cac acc gtg ccg gtg acg tat gag gcg tgg aag ctg 1488
Gly Glu Thr Trp His Thr Val Pro Val Thr Tyr Glu Ala Trp Lys Leu
485 490 495

tcg gac gac tac atc ggc ggg cgc ggc ttc ttc acc ggc gcg ttt gtg 1536
Ser Asp Asp Tyr Ile Gly Gly Arg Gly Phe Phe Thr Gly Ala Phe Val
500 505 510

ggc ctg cac tgc gag gac atc agc ggc gac ggc tgc tac gcg gac ttc 1584
Gly Leu His Cys Glu Asp Ile Ser Gly Asp Gly Cys Tyr Ala Asp Phe
515 520 525

gac tac ttc acc tac gag ccg gtc taa 1611
Asp Tyr Phe Thr Tyr Glu Pro Val *
530 535

```

<210> 273
 <211> 978
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(978)

<400> 273
 ttg cat atg aaa aaa ata atc ttt gct ttt att ata tta ttt gtg ttt 48

Met	His	Met	Lys	Lys	Ile	Ile	Phe	Ala	Phe	Ile	Ile	Leu	Phe	Val	Phe		
1				5					10					15			
tta	ctc	cct	atg	att	att	ttt	tac	caa	ccc	tgg	gtc	aat	gca	tta	ccg	96	
Leu	Leu	Pro	Met	Ile	Ile	Phe	Tyr	Gln	Pro	Trp	Val	Asn	Ala	Leu	Pro		
			20					25					30				
tca	acg	ccc	cga	cac	gca	agt	cct	gag	caa	tta	gaa	aaa	aca	gtt	cgt	144	
Ser	Thr	Pro	Arg	His	Ala	Ser	Pro	Glu	Gln	Leu	Glu	Lys	Thr	Val	Arg		
		35					40					45					
tat	ctt	aca	caa	act	gtg	cat	cca	cgt	agt	gcc	gac	aat	att	gat	aat	192	
Tyr	Leu	Thr	Gln	Thr	Val	His	Pro	Arg	Ser	Ala	Asp	Asn	Ile	Asp	Asn		
	50					55					60						
ctg	aat	agg	tcc	gca	gaa	tat	ata	aaa	gag	gtc	ttt	gtc	agt	agc	ggc	240	
Leu	Asn	Arg	Ser	Ala	Glu	Tyr	Ile	Lys	Glu	Val	Phe	Val	Ser	Ser	Gly		
65					70					75					80		
gcc	aga	gtt	acc	tcg	cag	gac	gtc	ccc	att	acg	ggc	ggc	ccc	tac	aaa	288	
Ala	Arg	Val	Thr	Ser	Gln	Asp	Val	Pro	Ile	Thr	Gly	Gly	Pro	Tyr	Lys		
				85					90					95			
aac	att	gtt	gct	gat	tat	ggc	cct	gcc	gat	gga	ccg	ctg	att	att	att	336	
Asn	Ile	Val	Ala	Asp	Tyr	Gly	Pro	Ala	Asp	Gly	Pro	Leu	Ile	Ile	Ile		
			100					105					110				
ggc	gag	cat	tat	gac	tct	gcc	agc	agt	tat	gaa	aac	gat	caa	ttg	acc	384	
Gly	Ala	His	Tyr	Asp	Ser	Ala	Ser	Ser	Tyr	Glu	Asn	Asp	Gln	Leu	Thr		
		115				120						125					
tat	acg	ccg	ggc	gag	gat	gat	aac	gcc	agc	ggc	gtg	gca	gga	tta	ctc	432	
Tyr	Thr	Pro	Gly	Ala	Asp	Asp	Asn	Ala	Ser	Gly	Val	Ala	Gly	Leu	Leu		
	130					135					140						
gaa	ctg	gca	cgt	ttg	tta	cat	cag	caa	gta	ccg	aaa	aca	ggc	gtg	cag	480	
Glu	Leu	Ala	Arg	Leu	Leu	His	Gln	Gln	Val	Pro	Lys	Thr	Gly	Val	Gln		
145					150				155						160		
ctg	gtc	gcc	tat	gag	tcg	gaa	gaa	ccg	ccc	ttc	ttt	cgt	agc	gat	gaa	528	
Leu	Val	Ala	Tyr	Ala	Ser	Glu	Glu	Pro	Pro	Phe	Phe	Arg	Ser	Asp	Glu		
				165				170					175				
atg	ggg	agc	gag	gtg	cat	gca	gct	tcg	ctt	gag	cgt	cca	gtg	aaa	tta	576	
Met	Gly	Ser	Ala	Val	His	Ala	Ala	Ser	Leu	Glu	Arg	Pro	Val	Lys	Leu		
			180					185					190				
atg	ata	gca	ctg	gag	atg	att	ggc	tat	tac	gac	tct	gag	cct	gga	agc	624	
Met	Ile	Ala	Leu	Glu	Met	Ile	Gly	Tyr	Tyr	Asp	Ser	Ala	Pro	Gly	Ser		
	195					200						205					
cag	aat	tac	cct	tac	ccg	gca	atg	tcc	tgg	ctt	tat	ccc	gat	cgg	gga	672	
Gln	Asn	Tyr	Pro	Tyr	Pro	Ala	Met	Ser	Trp	Leu	Tyr	Pro	Asp	Arg	Gly		
	210					215					220						
gac	ttt	att	gcc	gtg	gtc	ggc	aga	ata	cag	gat	atc	aac	gcc	gtt	cgt	720	
Asp	Phe	Ile	Ala	Val	Val	Gly	Arg	Ile	Gln	Asp	Ile	Asn	Ala	Val	Arg		

225	230	235	240	
cag gta aaa gcg gca ttg ttg tca tct	cag gat tta tct gtt tat tct	768		
Gln Val Lys Ala Ala Leu Leu Ser Ser	Gln Asp Leu Ser Val Tyr Ser			
245	250	255		
atg aat acc cca ggg ttt att ccc ggt att gat ttc tct gac cac ctg	816			
Met Asn Thr Pro Gly Phe Ile Pro Gly Ile Asp Phe Ser Asp His Leu				
260	265	270		
aat tat tgg caa cac gat att ccc gcc ata atg att act gac acc gct	864			
Asn Tyr Trp Gln His Asp Ile Pro Ala Ile Met Ile Thr Asp Thr Ala				
275	280	285		
ttt tat cgt aat aaa caa tac cac ttg ccc ggt gat acc gca gac aga	912			
Phe Tyr Arg Asn Lys Gln Tyr His Leu Pro Gly Asp Thr Ala Asp Arg				
290	295	300		
ttg aat tat cag aaa atg gct cag gta gtg gat ggt gtt ata act ttg	960			
Leu Asn Tyr Gln Lys Met Ala Gln Val Val Asp Gly Val Ile Thr Leu				
305	310	315	320	
tta tac aac agt aaa taa	978			
Leu Tyr Asn Ser Lys *				
325				
<210> 274				
<211> 963				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(963)				
<400> 274				
gtg atg atc aaa acg cgt ttt tct cgc tgg cta acg ttt ttt acg ttc	48			
Met Met Ile Lys Thr Arg Phe Ser Arg Trp Leu Thr Phe Phe Thr Phe				
1	5	10	15	
gcc gct gcc gtg gcg ctg gcg cta ccg gca aaa gcc aac acc tgg ccg	96			
Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro				
20	25	30		
ctg ccg cca gcg ggc agt cgt ctg gtt ggc gaa aac aaa ttt cat gtg	144			
Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val				
35	40	45		
gtg gaa aat gac ggt ggt tct ctg gaa gcc atc gcc aaa aaa tac aac	192			
Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn				
50	55	60		
gtc ggc ttt ctc gct ctg tta cag gct aac ccc ggc gtt gat cct tac	240			
Val Gly Phe Leu Ala Leu Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr				
65	70	75	80	

gta ccg cgc gcg ggc agc gtg tta acg atc ccg ttg caa acc cta ctt	288
Val Pro Arg Ala Gly Ser Val Leu Thr Ile Pro Leu Gln Thr Leu Leu	
85 90 95	
cca gat gcg ccg cgc gaa ggc att gtg atc aac att gcg gag ctg cgt	336
Pro Asp Ala Pro Arg Glu Gly Ile Val Ile Asn Ile Ala Glu Leu Arg	
100 105 110	
ctc tat tac tac ccg ccg ggt aaa aat tcg gta acc gtg tat cca ata	384
Leu Tyr Tyr Tyr Pro Pro Gly Lys Asn Ser Val Thr Val Tyr Pro Ile	
115 120 125	
ggt att ggt cag tta ggt ggt gac acg ctg aca ccg aca atg gtg acc	432
Gly Ile Gly Gln Leu Gly Gly Asp Thr Leu Thr Pro Thr Met Val Thr	
130 135 140	
acc gtt tca gac aaa cgt gca aac cca acc tgg acg cca acg gca aac	480
Thr Val Ser Asp Lys Arg Ala Asn Pro Thr Trp Thr Pro Thr Ala Asn	
145 150 155 160	
atc cgc gcc cgt tat aaa gca cag gga att gag ttg cct gcg gta gtg	528
Ile Arg Ala Arg Tyr Lys Ala Gln Gly Ile Glu Leu Pro Ala Val Val	
165 170 175	
ccg gct gga ctg gat aac cca atg ggc cat cat gcg att cgt ctg gcg	576
Pro Ala Gly Leu Asp Asn Pro Met Gly His His Ala Ile Arg Leu Ala	
180 185 190	
gcc tat ggc ggc gtt tat ttg ctt cat ggt acg aac gcc gat ttc ggc	624
Ala Tyr Gly Gly Val Tyr Leu Leu His Gly Thr Asn Ala Asp Phe Gly	
195 200 205	
att ggc atg cgg gta agt tct ggc tgt att cgt ctg cgg gat gac gat	672
Ile Gly Met Arg Val Ser Ser Gly Cys Ile Arg Leu Arg Asp Asp Asp	
210 215 220	
atc aaa aca ctc ttt agc cag gtc acc cca ggc acc aaa gtg aat atc	720
Ile Lys Thr Leu Phe Ser Gln Val Thr Pro Gly Thr Lys Val Asn Ile	
225 230 235 240	
atc aac act ccg ata aaa gtc tct gcc gaa cca aac ggt gcg cgt ctg	768
Ile Asn Thr Pro Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu	
245 250 255	
gtt gaa gta cat cag ccg ctg tca gag aag att gat gac gat ccg cag	816
Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Asp Pro Gln	
260 265 270	
ctg ctg cca att acg ctg aat agc gca atg caa tca ttt aaa gat gca	864
Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala	
275 280 285	
gca caa act gac gct gaa gtg atg caa cat gtg atg gat gtc cgt tcc	912
Ala Gln Thr Asp Ala Glu Val Met Gln His Val Met Asp Val Arg Ser	
290 295 300	
ggg atg ccg gtg gat gtc cgc cgt cat caa gtg agc cca caa acg ctg	960

gtt aat acc gca ctt atc cgc ctg atc tat cca caa cgt ttt ctg ggt	528
Val Asn Thr Ala Leu Ile Arg Leu Ile Tyr Pro Gln Arg Phe Leu Gly	
165 170 175	
aga ggg atg ggc ata aac tcg ttt att gtt gcc gtc tct tct gct gcc	576
Arg Gly Met Gly Ile Asn Ser Phe Ile Val Ala Val Ser Ser Ala Ala	
180 185 190	
ggg ccg aca att gct gca gca atc ctc tcc atc gca tcc tgg aaa tgg	624
Gly Pro Thr Ile Ala Ala Ala Ile Leu Ser Ile Ala Ser Trp Lys Trp	
195 200 205	
tta ttt tta atc aac gta ccg tta ggt att atc gcc ctg ctt ctg gcg	672
Leu Phe Leu Ile Asn Val Pro Leu Gly Ile Ile Ala Leu Leu Leu Ala	
210 215 220	
atg cgt ttt ctg cca ccc aat ggt tct cgc gcc agt aaa ccc cgt ttc	720
Met Arg Phe Leu Pro Pro Asn Gly Ser Arg Ala Ser Lys Pro Arg Phe	
225 230 235 240	
gac ctg ccc agc gcc gtg atg aac gcg tta acc ttc ggc ctg ctt atc	768
Asp Leu Pro Ser Ala Val Met Asn Ala Leu Thr Phe Gly Leu Leu Ile	
245 250 255	
act gcg ttg agt ggt ttc gct cag ggg caa tcg ctg acg tta att gct	816
Thr Ala Leu Ser Gly Phe Ala Gln Gly Gln Ser Leu Thr Leu Ile Ala	
260 265 270	
gcg gaa ctg gtg gta atg gtt gtt gtt ggt att ttc ttt att cgc cgc	864
Ala Glu Leu Val Val Met Val Val Val Gly Ile Phe Phe Ile Arg Arg	
275 280 285	
cag ctt tct ctt ccc gta ccg ctg cta ccg gtg gat tta ctg cgt atc	912
Gln Leu Ser Leu Pro Val Pro Leu Leu Pro Val Asp Leu Leu Arg Ile	
290 295 300	
ccg ctg ttt tca ctt tct att tgc aca tct gtt tgc tct ttc tgc gca	960
Pro Leu Phe Ser Leu Ser Ile Cys Thr Ser Val Cys Ser Phe Cys Ala	
305 310 315 320	
caa atg ctg gca atg gtt tcc ctg ccc ttt tac ctg caa acc gtg ctc	1008
Gln Met Leu Ala Met Val Ser Leu Pro Phe Tyr Leu Gln Thr Val Leu	
325 330 335	
ggg cgt agt gaa gtc gaa aca ggt tta ctt ctg aca ccg tgg ccg tta	1056
Gly Arg Ser Glu Val Glu Thr Gly Leu Leu Leu Thr Pro Trp Pro Leu	
340 345 350	
gca acg atg gtg atg gct ccg ctg gca ggc tat ttg att gaa cgc gta	1104
Ala Thr Met Val Met Ala Pro Leu Ala Gly Tyr Leu Ile Glu Arg Val	
355 360 365	
cat gca gga ttg ctg ggg gct tta ggg ttg ttc atc atg gct gcg ggg	1152
His Ala Gly Leu Leu Gly Ala Leu Gly Leu Phe Ile Met Ala Ala Gly	
370 375 380	

```

ctt ttt tcc ctg gtt ctg ctg ccc gcg tca cct gcg gat atc aat att 1200
Leu Phe Ser Leu Val Leu Leu Pro Ala Ser Pro Ala Asp Ile Asn Ile
385                390                395                400

atc tgg ccg atg atc tta tgt ggt gct gga ttt ggc tta ttc cag tca 1248
Ile Trp Pro Met Ile Leu Cys Gly Ala Gly Phe Gly Leu Phe Gln Ser
                405                410                415

ccc aat aac cac acc att att acc tcc gcg cct cgc gaa cgt agc ggt 1296
Pro Asn Asn His Thr Ile Ile Thr Ser Ala Pro Arg Glu Arg Ser Gly
                420                425                430

gga gcc agt ggc atg tta gga acg gct cgt cta ctg ggt cag agt agc 1344
Gly Ala Ser Gly Met Leu Gly Thr Ala Arg Leu Leu Gly Gln Ser Ser
                435                440                445

ggc gcg gcg ctg gtg gcg ctg atg cta aat cag ttt gga gat aat ggt 1392
Gly Ala Ala Leu Val Ala Leu Met Leu Asn Gln Phe Gly Asp Asn Gly
                450                455                460

aca cac gtc tcg ctg atg gct gcg gct att ctg gca gtg att gct gcc 1440
Thr His Val Ser Leu Met Ala Ala Ala Ile Leu Ala Val Ile Ala Ala
465                470                475                480

tgt gtc agt ggt tta cgt atc act cag cca cga tcc agg gca taa 1485
Cys Val Ser Gly Leu Arg Ile Thr Gln Pro Arg Ser Arg Ala *
                485                490

<210> 276
<211> 1434
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1434)

<400> 276
atg aaa gta acg ctg cca gag ttt gaa cgt gca gga gtg atg gtg gtt 48
Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
1                5                10                15

ggt gat gtg atg ctg gat cgt tac tgg tac ggc ccc acc agt cgt atc 96
Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
                20                25                30

tcg ccg gaa gcg ccg gtg ccc gtg gtt aaa gtg aat acc atc gaa gaa 144
Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
35                40                45

cgt ccg ggc ggc gcg gct aac gtg gcg atg aat atc gct tct ctc ggt 192
Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
50                55                60

gct aat gca cgc ctg gtc ggg ttg acg ggc att gac gat gca gcg cgc 240

```

Ala 65	Asn	Ala	Arg	Leu	Val 70	Gly	Leu	Thr	Gly	Ile 75	Asp	Asp	Ala	Ala	Arg 80	
gcg Ala	ctg Leu	agt Ser	aaa Lys	tct Ser 85	ctg Leu	gcc Ala	gac Asp	gtc Val	aac Asn 90	gtc Val	aaa Lys	tgc Cys	gac Asp	ttc Phe 95	gtt Val	288
tct Ser	gta Val	ccg Pro	acg Thr 100	cat His	ccg Pro	acc Thr	att Ile	acc Thr 105	aaa Lys	tta Leu	cgg Arg	gta Val	ctt Leu 110	tcc Ser	cgc Arg	336
aac Asn	caa Gln 115	cag Gln	ctg Leu	atc Ile	cgt Arg	ctg Leu 120	gat Asp	ttt Phe	gaa Glu	gaa Glu	ggc Gly 125	ttc Phe	gaa Glu	ggc Gly	ggt Val	384
gat Asp 130	ccg Pro	cag Gln	ccg Pro	ctg Leu	cac His	gag Glu 135	cgg Arg	att Ile	aat Asn	cag Gln	gcg Ala 140	ctg Leu	agt Ser	tcg Ser	att Ile	432
ggc Gly 145	gcg Ala	ctg Leu	gtg Val	ctt Leu	tct Ser 150	gac Asp	tac Tyr	gcc Ala	aaa Lys	ggc Gly 155	gcg Ala	ctg Leu	gca Ala	agc Ser	gta Val 160	480
cag Gln	cag Gln	atg Met	atc Ile	caa Gln 165	ctg Leu	gcg Ala	cgt Arg	aaa Lys	gcg Ala 170	ggc Gly	ggt Val	ccg Pro	gtg Val	ctg Leu 175	att Ile	528
gat Asp	cca Pro	aaa Lys 180	ggc Gly	acc Thr	gat Asp	ttt Phe	gag Glu	cgc Arg	tac Tyr	cgc Arg	ggc Gly	gct Ala	acg Thr 190	ctg Leu	tta Leu	576
acg Thr	ccg Pro	aat Asn 195	ctc Leu	tcg Ser	gaa Glu	ttt Phe 200	gaa Glu	gct Ala	gtt Val	gtc Val	ggc Gly 205	aaa Lys	tgt Cys	aag Lys	acc Thr	624
gaa Glu 210	gaa Glu	gag Glu	att Ile	gtt Val	gag Glu	cgc Arg 215	ggc Gly	atg Met	aaa Lys	ctg Leu	att Ile 220	gcc Ala	gat Asp	tac Tyr	gaa Glu	672
ctc Leu 225	tcg Ser	gct Ala	ctg Leu	tta Leu	gtg Val 230	acc Thr	cgt Arg	tcc Ser	gaa Glu	cag Gln 235	ggc Gly	atg Met	tcg Ser	ctg Leu 240	ctg Leu	720
caa Gln	ccg Pro	ggc Gly	aaa Lys 245	gcg Ala	ccg Pro	ctg Leu	cat His	atg Met	cca Pro 250	acc Thr	caa Gln	gcg Ala	cag Gln	gaa Glu 255	gtg Val	768
tat Tyr	gac Asp	gtt Val	acc Thr 260	ggc Gly	gag Ala	ggc Gly	gac Asp	acg Thr 265	gtg Val	att Ile	ggc Gly	gtc Val	ctg Leu 270	gag Ala	gca Ala	816
acg Thr	ctg Leu	gca Ala 275	gag Ala	ggc Gly	aat Asn	tcg Ser	ctg Leu 280	gaa Glu	gaa Glu	gcc Ala	tgc Cys 285	ttc Phe	ttt Phe	gcc Ala	aat Asn	864
gag Ala	gag Ala	gct Ala	ggc Gly	gtg Val	gtg Val	gtc Val	ggc Gly	aaa Lys	ctg Leu	gga Gly	acc Thr	tcc Ser	acg Thr	gtt Val	tcg Ser	912

290	295	300	
ccg atc gag ctg gaa aat gct gta cgt gga cgt gca gat aca ggc ttt			960
Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe			
305	310	315	320
ggc gtg atg acc gaa gag gaa ctg aag ctg gcc gta gcg gca gcg cgt			1008
Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Arg			
	325	330	335
aaa cgt ggt gaa aaa gtg gtg atg acc aac ggt gtc ttt gac atc ctg			1056
Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu			
	340	345	350
cac gcc ggg cac gtc tct tat ctg gca aat gcc cgc aag ctg ggt gac			1104
His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp			
	355	360	365
cgc ttg att gtt gcc gtc aac agc gat gcc tcc acc aaa cgg ctg aaa			1152
Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys			
	370	375	380
ggg gat tcc cgc ccg gta aac cca ctc gaa cag cgt atg att gtg ctg			1200
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu			
	385	390	400
ggc gca ctg gaa gcg gtc gac tgg gta gtg tcg ttt gaa gag gac acg			1248
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr			
	405	410	415
ccg cag cgc ttg atc gcc ggg atc ttg cca gat ctg ctg gtg aaa ggc			1296
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly			
	420	425	430
ggc gac tat aaa cca gaa gag att gcc ggg agt aaa gaa gtc tgg gcc			1344
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala			
	435	440	445
aac ggt ggc gaa gtg ttg gtg ctc aac ttt gaa gac ggt tgc tcg acg			1392
Asn Gly Glu Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr			
	450	455	460
acc aac atc atc aag aag atc caa cag gat aaa aaa ggc taa			1434
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly *			
	465	470	475

<210> 277
 <211> 2841
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2841)

```

<400> 277
atg aag ccg ctc tct tca ccg tta cag cag tac tgg cag acc gtt gtt 48
Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
 1          5          10          15

gag cgg ctg cca gag cct tta gcc gag gaa tca ctt agc gca cag gcg 96
Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
      20          25          30

aag tca gta ctt act ttt agt gat ttt gtg cag gac agc gtg att gcg 144
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
      35          40          45

cat cca gag tgg ctg acg gaa ctg gaa agc caa ccg ccg cag gcc gac 192
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
      50          55          60

gaa tgg cag cat tac gcg gca tgg ttg cag gag gcg ctc tgt aat gtg 240
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
      65          70          75          80

agt gac gaa gcc ggg tta atg cgc gag ctg cgg cta ttc cgg cgg cgc 288
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
      85          90          95

att atg gtg cgc atc gcc tgg gcg caa acg ctg gca ctg gtt act gaa 336
Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
      100          105          110

gag agc ata ttg cag cag ctc agc tat ctg gcg gag acg ctg att gtt 384
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
      115          120          125

gcg gcg cgt gac tgg ctg tat gac gcc tgc tgc cgc gag tgg gga acg 432
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
      130          135          140

ccg tgc aat gcg cag ggc gaa gcg caa ccg ctg ctg att tta ggc atg 480
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
      145          150          155          160

ggt aag ctg ggc ggt ggg gag ctg aat ttc tcc tct gat atc gat ctg 528
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
      165          170          175

att ttt gcc tgg ccg gaa cat ggt tgt acg cag ggt gga cgc cgg gaa 576
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
      180          185          190

ctg gat aac gcg cag ttt ttt acc cgc atg ggg cag cgg ctg att aaa 624
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
      195          200          205

gtg ctg gat caa cca acg cag gat ggc ttc gtc tat cgc gtg gat atg 672
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
      210          215          220

```

cg	g	ctg	cg	t	g	g	a	a	g	g	cg	ctg	gtg	ctg	a	g	t	g	c	720
Arg	Leu	Arg	Pro	Phe	Gly	Glu	Ser	Gly	Pro	Leu	Val	Leu	Ser	Phe	Ala					
225					230					235					240					
gc	g	ttg	g	a	g	a	t	t	a	c	a	g	a	g	c	a	g	g	g	768
Ala	Leu	Glu	Asp	Tyr	Tyr	Gln	Glu	Gln	Gly	Arg	Asp	Trp	Glu	Arg	Tyr					
				245					250						255					
gc	a	t	g	t	c	a	a	g	c	g	a	t	t	a	g	g	c	t	c	816
Ala	Met	Val	Lys	Ala	Arg	Ile	Met	Gly	Asp	Ser	Glu	Gly	Val	Tyr	Ala					
			260					265						270						
a	a	c	g	a	g	t	t	c	g	a	t	c	t	a	c	a	t	c	a	864
Asn	Glu	Leu	Arg	Ala	Met	Leu	Arg	Pro	Phe	Val	Phe	Arg	Arg	Tyr	Ile					
			275					280						285						
g	a	t	t	c	a	g	t	t	c	a	a	a	a	a	a	a	a	a	a	912
Asp	Phe	Ser	Val	Ile	Gln	Ser	Leu	Arg	Asn	Met	Lys	Gly	Met	Ile	Ala					
			290					295						300						
c	g	t	a	a	c	a	c	t	a	a	c	a	a	a	a	a	a	a	a	960
Arg	Glu	Val	Arg	Arg	Arg	Gly	Leu	Thr	Asp	Asn	Ile	Lys	Leu	Gly	Ala					
			305			310								315					320	
g	g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1008
Gly	Gly	Ile	Arg	Glu	Ile	Glu	Phe	Ile	Val	Gln	Val	Phe	Gln	Leu	Ile					
				325					330					335						
c	g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1056
Arg	Gly	Gly	Arg	Glu	Pro	Ser	Leu	Gln	Ser	Arg	Ser	Leu	Leu	Pro	Thr					
			340					345						350						
c	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1104
Leu	Ser	Ala	Ile	Ala	Glu	Leu	His	Leu	Leu	Ser	Glu	Asn	Asp	Ala	Glu					
			355					360						365						
c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1152
Gln	Leu	Arg	Val	Ala	Tyr	Leu	Phe	Leu	Arg	Arg	Leu	Glu	Asn	Leu	Leu					
			370					375						380						
c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1200
Gln	Ser	Ile	Asn	Asp	Glu	Gln	Thr	Gln	Thr	Leu	Pro	Ser	Asp	Glu	Leu					
			385			390				395					400					
a	a	t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1248
Asn	Arg	Ala	Arg	Leu	Ala	Trp	Ala	Met	Asp	Phe	Ala	Asp	Trp	Pro	Gln					
				405					410						415					
c	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1296
Leu	Thr	Gly	Ala	Leu	Thr	Ala	His	Met	Thr	Asn	Val	Arg	Arg	Val	Phe					
			420					425						430						
a	a	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1344
Asn	Glu	Leu	Ile	Gly	Asp	Asp	Glu	Ser	Glu	Thr	Gln	Glu	Glu	Ser	Leu					
			435					440						445						
t	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	1392

Ser	Glu	Gln	Trp	Arg	Glu	Leu	Trp	Gln	Asp	Ala	Leu	Gln	Glu	Asp	Asp	
450						455					460					
act	acg	cca	gtg	ctg	gcg	cat	ctt	agc	gag	gat	gat	cgc	aaa	cag	gtg	1440
Thr	Thr	Pro	Val	Leu	Ala	His	Leu	Ser	Glu	Asp	Asp	Arg	Lys	Gln	Val	
465					470					475					480	
cta	acg	ctg	att	gcc	gat	ttc	cgc	aaa	gag	ctg	gat	aag	cgc	acc	atc	1488
Leu	Thr	Leu	Ile	Ala	Asp	Phe	Arg	Lys	Glu	Leu	Asp	Lys	Arg	Thr	Ile	
				485					490					495		
ggg	ccg	cga	gga	cgt	cag	gtg	ctc	gac	cat	ctg	atg	ccg	cat	ctg	cta	1536
Gly	Pro	Arg	Gly	Arg	Gln	Val	Leu	Asp	His	Leu	Met	Pro	His	Leu	Leu	
			500					505					510			
agt	gat	gtc	tgt	gcg	cgt	gaa	gac	gct	gcc	gtt	acg	ctg	tcg	cgc	att	1584
Ser	Asp	Val	Cys	Ala	Arg	Glu	Asp	Ala	Ala	Val	Thr	Leu	Ser	Arg	Ile	
		515					520					525				
acc	gcc	ttg	ctg	gtg	ggg	att	gtt	acc	cgc	acc	acc	tat	tta	gaa	ttg	1632
Thr	Ala	Leu	Leu	Val	Gly	Ile	Val	Thr	Arg	Thr	Thr	Tyr	Leu	Glu	Leu	
	530					535					540					
ctc	agt	gaa	ttc	ccc	gcg	gcg	ctt	aaa	cat	ttg	att	tct	ctg	tgt	gcc	1680
Leu	Ser	Glu	Phe	Pro	Ala	Ala	Leu	Lys	His	Leu	Ile	Ser	Leu	Cys	Ala	
545					550					555					560	
gcg	tcg	ccg	atg	att	gcc	agc	cag	ctg	gcg	cgt	tat	cca	tta	ttg	ctg	1728
Ala	Ser	Pro	Met	Ile	Ala	Ser	Gln	Leu	Ala	Arg	Tyr	Pro	Leu	Leu	Leu	
				565					570					575		
gat	gaa	ttg	ctc	gat	cca	aac	acc	ctt	tac	cag	ccg	acg	gcg	acc	gat	1776
Asp	Glu	Leu	Leu	Asp	Pro	Asn	Thr	Leu	Tyr	Gln	Pro	Thr	Ala	Thr	Asp	
			580					585					590			
gcc	tac	cgc	gat	gag	ttg	cgc	cag	tat	ttg	ctg	cgc	gtg	ccg	gaa	gat	1824
Ala	Tyr	Arg	Asp	Glu	Leu	Arg	Gln	Tyr	Leu	Leu	Arg	Val	Pro	Glu	Asp	
		595					600					605				
gac	gaa	gag	caa	cag	ctt	gag	gcg	ctg	cgt	cag	ttc	aaa	cag	gcg	cag	1872
Asp	Glu	Glu	Gln	Gln	Leu	Glu	Ala	Leu	Arg	Gln	Phe	Lys	Gln	Ala	Gln	
	610					615					620					
ctg	tta	cgc	atc	gcc	gca	gcg	gat	atc	gcc	ggc	acg	cta	ccg	gtg	atg	1920
Leu	Leu	Arg	Ile	Ala	Ala	Ala	Asp	Ile	Ala	Gly	Thr	Leu	Pro	Val	Met	
625					630					635					640	
aaa	gtg	agc	gat	cac	tta	acc	tgg	ctg	gcg	gaa	gcc	atg	ata	gat	gcc	1968
Lys	Val	Ser	Asp	His	Leu	Thr	Trp	Leu	Ala	Glu	Ala	Met	Ile	Asp	Ala	
				645					650					655		
gtc	gtt	cag	cag	gcg	tgg	gtt	caa	atg	gtt	gcc	cgc	tac	ggc	aag	ccg	2016
Val	Val	Gln	Gln													

675	680	685	
ggc aag ctg ggc ggc tgg gag tta ggc tac agt tcc gat ctt gac ctt Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu 690 695 700			2112
atc ttc ctc cat gat tgc cca atg gat gcg atg act gac ggt gag cgg Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg 705 710 715 720			2160
gaa atc gac ggg cgg cag ttt tat ctg cgt ctg gcg caa cgc att atg Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met 725 730 735			2208
cat ctg ttc agt acg cgt acc tct tcc ggc att ttg tat gaa gtg gat His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp 740 745 750			2256
gct cga ctg cgt ccg tcc ggg gcg gcg gga atg ctg gtg aca tcc gca Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala 755 760 765			2304
gaa gca ttt gcc gat tat cag aaa aac gag gcc tgg acg tgg gaa cat Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His 770 775 780			2352
cag gcg ctg gtg cgt gcg cgt gta gtg tac ggc gat ccg cag ctc acc Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr 785 790 795 800			2400
gcg cac ttt gac gca gtg cgt cgc gag att atg acg ctg ccg cgt gaa Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu 805 810 815			2448
ggt aaa act ctg caa acg gaa gtg cgg gaa atg cgc gag aaa atg cgc Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg 820 825 830			2496
gct cat ctc ggc aat aaa cat cgc gat cgc ttt gat atc aaa gct gat Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp 835 840 845			2544
gaa ggg gga att acc gat atc gaa ttt att acc caa tat ctg gtg ttg Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu 850 855 860			2592
cgc tac gct cat gaa aaa ccg aag tta acg cgc tgg tca gac aac gtg Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg Trp Ser Asp Asn Val 865 870 875 880			2640
cgt att ctg gaa cta ctg gcg caa aac gac att atg gaa gag cag gaa Arg Ile Leu Glu Leu Leu Ala Gln Asn Asp Ile Met Glu Glu Gln Glu 885 890 895			2688
gcg atg gcg ctg acc cgt gct tac act acg ctt cgc gat gaa ctt cat Ala Met Ala Leu Thr Arg Ala Tyr Thr Thr Leu Arg Asp Glu Leu His 900 905 910			2736

cat	ctg	gca	tta	cag	gaa	ttg	ccg	ggc	cat	gtg	tcg	gag	gat	tgc	ttc	2784
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe	
	915						920					925				

acc	gca	gag	cgt	gaa	ctg	gtg	cgg	gca	agc	tgg	cag	aag	tgg	ctg	gtg	2832
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val	
	930					935					940					

gaa	gaa	tga														2841
Glu	Glu	*														
945																

<210> 278
 <211> 1302
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1302)

<400>	278																
atg	gct	cag	gaa	atc	gaa	tta	aag	ttt	att	gtt	aat	cac	agt	gcc	gtt	48	
Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val		
1				5					10					15			

gag	gcg	ttg	cgt	gac	cat	ctc	aat	acg	ctg	ggc	ggc	gag	cac	cat	gac	96	
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp		
			20					25					30				

ccc	gtg	cag	ttg	ctg	aat	att	tac	tac	gaa	acg	ccg	gat	aac	tgg	ctg	144	
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu		
		35					40					45					

cgt	ggg	cac	gat	atg	ggc	tta	cgt	att	cgt	ggc	gaa	aac	ggg	cgc	tat	192	
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr		
	50					55					60						

gag	atg	acc	atg	aaa	gtt	gca	gga	aga	gtg	aca	ggc	ggc	tta	cat	cag	240	
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln		
	65				70					75					80		

cgc	ccg	gaa	tat	aac	gtg	gcg	ttg	agc	gaa	ccg	acg	ctc	gac	ctg	gcg	288	
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala		
				85					90					95			

cag	tta	ccg	acg	gaa	gtc	tgg	ccg	aac	ggc	gaa	ttg	ccc	gcc	gat	ctc	336	
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu		
		100						105					110				

gcc	tcc	cgc	gtg	cag	ccg	ctg	ttc	agc	acc	gat	ttt	tat	cgc	gaa	aaa	384	
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys		
		115					120					125					

tgg	ctg	gtg	gcg	gtc	gat	ggg	agc	caa	att	gaa	atc	gcc	ctc	gac	cag	432	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln		
130						135					140						
ggg	gaa	gtg	aaa	gcg	ggt	gaa	ttt	gct	gaa	cct	atc	tgt	gag	ctg	gaa	480	
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu		
145					150					155					160		
ctg	gaa	ctg	ctt	agc	ggc	gac	acg	cgc	gcg	gtg	ctg	aaa	ctg	gcg	aac	528	
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn		
				165					170						175		
caa	ctg	gta	tcg	caa	acc	gga	tta	cgc	cag	ggc	agc	ctg	agc	aaa	gcg	576	
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala		
			180					185						190			
gcg	cgt	ggc	tat	cat	ctg	gcg	cag	ggc	aat	ccg	gcg	cgt	gaa	atc	aaa	624	
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys		
		195					200					205					
ccg	acc	acc	att	ttg	cat	gtt	gcg	gca	aaa	gcc	gat	gtg	gaa	cag	ggg	672	
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly		
		210				215					220						
ctg	gaa	gcg	gcg	ctc	gag	ctg	gcg	tta	gcg	caa	tgg	cag	tat	cat	gaa	720	
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu		
225					230					235					240		
gaa	ctg	tgg	gta	cgc	ggc	aac	gat	gcg	gcg	aaa	gaa	cag	gtg	ctg	gca	768	
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala		
			245						250						255		
gcc	att	agc	ctg	gtc	cgt	cat	acg	ctg	atg	ctg	ttc	ggc	ggc	att	gtg	816	
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val		
		260						265					270				
ccg	cgt	aaa	gcg	agc	act	cac	tta	cgt	gat	ctg	ctg	act	caa	tgc	gag	864	
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu		
		275					280					285					
gcg	acc	att	gct	tct	gcg	gtg	tct	gcc	gtg	acg	gcg	gtc	tac	tct	acc	912	
Ala	Thr	Ile	Ala	Ser	Ala	Val	Ser	Ala	Val	Thr	Ala	Val	Tyr	Ser	Thr		
	290					295					300						
gaa	acg	gca	atg	gcg	aag	ctg	gcg	ttg	acc	gaa	tgg	ttg	gta	agc	aaa	960	
Glu	Thr	Ala	Met	Ala	Lys	Leu	Ala	Leu	Thr	Glu	Trp	Leu	Val	Ser	Lys		
305					310					315					320		
gca	tgg	cag	cca	ttt	tta	gat	gcc	aaa	gcg	cag	ggc	aaa	atc	agc	gac	1008	
Ala	Trp	Gln	Pro	Phe	Leu	Asp	Ala	Lys	Ala	Gln	Gly	Lys	Ile	Ser	Asp		
			325						330						335		
tcc	ttc	aaa	cgc	ttt	gcc	gat	atc	cat	ctt	tcc	cgc	cat	gcc	gct	gaa	1056	
Ser	Phe	Lys	Arg	Phe	Ala	Asp	Ile	His	Leu	Ser	Arg	His	Ala	Ala	Glu		
		340						345					350				
ctg	aaa	agc	gtt	ttc	tgc	cag	ccg	tta	ggc	gat	cgc	tac	cgt	gac	cag	1104	
Leu	Lys	Ser	Val	Phe	Cys	Gln	Pro	Leu	Gly	Asp	Arg	Tyr	Arg	Asp	Gln		

355	360	365	
ttg cca cgc ctg acg cgt gat att gac tca ata ctg ttg ctg gcg ggt	1152		
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly			
370 375 380			
tac tat gat cct gtc gtc gcg caa gcc tgg ctg gag aac tgg cag ggg	1200		
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly			
385 390 395 400			
ctg cat cac gct att gcg acc ggg caa cgc atc gaa att gaa cat ttc	1248		
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe			
405 410 415			
cgt aat gag gca aac aat cag gaa ccg ttc tgg ttg cac agc gga aaa	1296		
Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys			
420 425 430			
cgt taa	1302		
Arg *			
<210> 279			
<211> 624			
<212> DNA			
<213> Escherichia coli			
<220>			
<221> CDS			
<222> (1)...(624)			
<400> 279			
gtg ctc aac aaa ctc tcc tta ctg ctg aaa gac gca ggt att tcg ctt	48		
Met Leu Asn Lys Leu Ser Leu Leu Leu Lys Asp Ala Gly Ile Ser Leu			
1 5 10 15			
acc gat cac cag aaa aac cag ctt att gcc tac gtg aat atg ctg cat	96		
Thr Asp His Gln Lys Asn Gln Leu Ile Ala Tyr Val Asn Met Leu His			
20 25 30			
aaa tgg aac aaa gcg tac aac ctg act tcg gtc cgc gat cct aat gag	144		
Lys Trp Asn Lys Ala Tyr Asn Leu Thr Ser Val Arg Asp Pro Asn Glu			
35 40 45			
atg ctg gta cgc cat att ctc gat agc att gtg gtg gca ccg tat ctg	192		
Met Leu Val Arg His Ile Leu Asp Ser Ile Val Val Ala Pro Tyr Leu			
50 55 60			
caa ggt gaa cgg ttt atc gat gtc ggc acc gga cca gga ctg cca ggc	240		
Gln Gly Glu Arg Phe Ile Asp Val Gly Thr Gly Pro Gly Leu Pro Gly			
65 70 75 80			
att cca ctc tct atc gtg cgt cct gaa gcc cat ttc act ctg ttg gat	288		
Ile Pro Leu Ser Ile Val Arg Pro Glu Ala His Phe Thr Leu Leu Asp			
85 90 95			

```

agc ctt ggt aaa cgc gtg cgt ttc ctt cgt cag gtg caa cat gag ctt 336
Ser Leu Gly Lys Arg Val Arg Phe Leu Arg Gln Val Gln His Glu Leu
      100                      105                      110

aaa ctg gag aat att gaa cca gta cag agc agg gta gaa gag ttt cct 384
Lys Leu Glu Asn Ile Glu Pro Val Gln Ser Arg Val Glu Glu Phe Pro
      115                      120                      125

tca gag ccg cca ttt gat ggc gta att agc cgc gct ttt gcc tct ctg 432
Ser Glu Pro Pro Phe Asp Gly Val Ile Ser Arg Ala Phe Ala Ser Leu
      130                      135                      140

aac gat atg gtg agc tgg tgc cac cat ctt cct ggt gag caa ggc cgt 480
Asn Asp Met Val Ser Trp Cys His His Leu Pro Gly Glu Gln Gly Arg
      145                      150                      155                      160

ttc tac gcg ctg aaa ggg caa atg ccg gaa gat gaa atc gct ttg ttg 528
Phe Tyr Ala Leu Lys Gly Gln Met Pro Glu Asp Glu Ile Ala Leu Leu
      165                      170                      175

ccc gaa gaa tat cag gtc gaa tca gtg gtt aaa ctt cag gtt cca gcc 576
Pro Glu Glu Tyr Gln Val Glu Ser Val Val Lys Leu Gln Val Pro Ala
      180                      185                      190

ctg gat ggc gaa cgt cat ctg gtg gtg att aaa gca aat aaa att taa 624
Leu Asp Gly Glu Arg His Leu Val Val Ile Lys Ala Asn Lys Ile *
      195                      200                      205

<210> 280
<211> 1890
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1890)

<400> 280
atg ttt tat ccg gat cct ttt gac gtc atc atc att ggc ggg ggt cat 48
Met Phe Tyr Pro Asp Pro Phe Asp Val Ile Ile Ile Gly Gly Gly His
      1           5           10           15

gca ggc acc gag gcc gcg atg gcc gcg gcg cgt atg ggt caa cag act 96
Ala Gly Thr Glu Ala Ala Met Ala Ala Ala Arg Met Gly Gln Gln Thr
      20           25           30

ctg ctt ttg aca cac aat atc gac act ctg ggg cag atg agc tgc aac 144
Leu Leu Leu Thr His Asn Ile Asp Thr Leu Gly Gln Met Ser Cys Asn
      35           40           45

ccg gcg atc ggc ggt att ggg aag gga cat ctg gta aaa gaa gtg gat 192
Pro Ala Ile Gly Gly Ile Gly Lys Gly His Leu Val Lys Glu Val Asp
      50           55           60

gca ctc ggc ggt ctg atg gcg aaa gcg atc gat cag gcg ggt atc cag 240

```


338

```

ttt gcc cct gcg ttg aca gac gaa cag gcg gcg gaa cag gtt gag att 1632
Phe Ala Pro Ala Leu Thr Asp Glu Gln Ala Ala Glu Gln Val Glu Ile
    530                535                540

cag gtt aaa tac gaa ggt tat atc gcg cgc cag caa gat gag atc gaa 1680
Gln Val Lys Tyr Glu Gly Tyr Ile Ala Arg Gln Gln Asp Glu Ile Glu
545                550                555                560

aag cag ctg cgt aac gag aac acc ctg cta ccc gcg aca ctg gat tac 1728
Lys Gln Leu Arg Asn Glu Asn Thr Leu Leu Pro Ala Thr Leu Asp Tyr
    565                570                575

cgc cag gta tcc ggt ctt tct aac gaa gtg atc gcc aaa ctt aac gat 1776
Arg Gln Val Ser Gly Leu Ser Asn Glu Val Ile Ala Lys Leu Asn Asp
    580                585                590

cac aaa cca gcc tct atc ggc caa gct tcg cgt att tct ggc gtc acg 1824
His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr
    595                600                605

cct gcg gcc atc tcc att ctg ctg gtg tgg ctg aaa aaa cag ggt atg 1872
Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met
    610                615                620

ctg cgt cgt agc gca taa
Leu Arg Arg Ser Ala *
625

<210> 281
<211> 444
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(444)

<400> 281
atg gca gat atc act ctt atc agc ggc agc acc ctc ggc ggt gcc gaa 48
Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu
    1                5                10                15

tat gta gca gaa cac ctg gct gaa aag ctg gaa gag gcg ggt ttt acc 96
Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr
    20                25                30

acc gaa acg ctg cac ggt ccg ctg tta gaa gat tta cct gcc tca ggg 144
Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly
    35                40                45

atc tgg ctg gtt atc agc tcc acc cac ggt gcc gga gat att ccg gac 192
Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp
    50                55                60

aac ctt tct cct ttc tat gaa gca ttg cag gaa cag aag ccc gat ctt 240

```



```

Asn Leu Ser Pro Phe Tyr Glu Ala Leu Gln Glu Gln Lys Pro Asp Leu
 65              70              75              80

tct gca gtc cgc ttt ggc gca atc ggt att ggc agt cgt gaa tat gac   288
Ser Ala Val Arg Phe Gly Ala Ile Gly Ile Gly Ser Arg Glu Tyr Asp
      85              90              95

acc ttt tgt ggg gct atc gat aaa ctc gag gca gaa ctc aaa aat tcc   336
Thr Phe Cys Gly Ala Ile Asp Lys Leu Glu Ala Glu Leu Lys Asn Ser
      100             105             110

ggg gca aaa cag aca ggc gaa aca ctg aag atc aac att ctt gat cac   384
Gly Ala Lys Gln Thr Gly Glu Thr Leu Lys Ile Asn Ile Leu Asp His
      115             120             125

gac att ccg gaa gat ccg gca gaa gaa tgg ctg gga tgc tgg gtt aat   432
Asp Ile Pro Glu Asp Pro Ala Glu Glu Trp Leu Gly Ser Trp Val Asn
      130             135             140

tta ctc aaa taa
Leu Leu Lys *
145

<210> 282
<211> 456
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(456)

<400> 282
gtg ggt cag cga aac gtt tgc ctg atg gag aaa aaa atg aaa aaa ggc   48
Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
  1              5              10              15

acc gtt ctt aat tct gat att tca tgc gtg atc tcc cgt ctg gga cat   96
Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
      20              25              30

acc gat acg ctg gtg gtg tgt gat gct ggt tta ccc atc ccc aaa agt   144
Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser
      35              40              45

aca acg cgt atc gat atg gca tta acc cag ggt gta cct tct ttt atg   192
Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
      50              55              60

cag gtg ctg ggc gtc gtc aca aat gaa atg cag gtc gag gcg gcc att   240
Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
      65              70              75              80

atc gcg gaa gag atc aaa cac cat aat ccg caa ctc cac gaa acg ttg   288
Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
      85              90              95

```

```

ctc act cac ctt gag cag ctg caa aaa cac cag gga aat acc att gaa 336
Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
      100                      105                      110

att cgt tac acc acg cat gaa caa ttc aaa caa caa acc gca gaa agt 384
Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser
      115                      120                      125

cag gcg gta att cgc agc gga gaa tgt tct ccg tat gcg aat atc att 432
Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile
      130                      135                      140

ctc tgt gct ggc gtg acg ttc tga 456
Leu Cys Ala Gly Val Thr Phe *
      145                      150

<210> 283
<211> 1506
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1506)

<400> 283
atg gaa gca tta ctt cag ctt aaa ggc atc gat aaa gcc ttc ccg ggc 48
Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly
      1                      5                      10                      15

gta aaa gcc ctc tcg ggc gca gcg tta aat gtc tat ccg ggc cgc gtg 96
Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val
      20                      25                      30

atg gcg ctg gtg ggc gaa aac ggc gcg ggt aaa tcc acc atg atg aaa 144
Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys
      35                      40                      45

gtg ctt act ggc atc tat act cgc gat gcc ggt acg ctt tta tgg ctg 192
Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu
      50                      55                      60

ggg aaa gaa acg aca ttt acc ggg cca aaa tct tcc cag gaa gcc ggg 240
Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly
      65                      70                      75                      80

att ggg att atc cat cag gaa ctg aac ctg atc ccg cag ttg acc att 288
Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile
      85                      90                      95

gcc gaa aac att ttc ctc ggt cgt gag ttt gtt aat cgc ttt ggc aaa 336
Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys
      100                      105                      110

att gac tgg aaa acc atg tat gcc gaa gcg gat aaa ttg ctg gct aaa 384

```

Ile Asp Trp Lys Thr Met Tyr Ala Glu Ala Asp Lys Leu Leu Ala Lys	
115	120
125	
ctt aac ctg cgc ttt aaa agc gac aag ctg gtg ggc gat ctt tcc atc	432
Leu Asn Leu Arg Phe Lys Ser Asp Lys Leu Val Gly Asp Leu Ser Ile	
130	135
140	
ggt gac cag caa atg gtt gaa atc gcc aaa gtg ctg agc ttt gag tcg	480
Gly Asp Gln Gln Met Val Glu Ile Ala Lys Val Leu Ser Phe Glu Ser	
145	150
155	160
aaa gtc atc att atg gat gaa ccg acc gat gcg ctg acc gat acc gaa	528
Lys Val Ile Ile Met Asp Glu Pro Thr Asp Ala Leu Thr Asp Thr Glu	
165	170
175	
acc gaa tcc ctg ttc cgc gtc atc cgc gag ctg aaa tcg caa ggc cgc	576
Thr Glu Ser Leu Phe Arg Val Ile Arg Glu Leu Lys Ser Gln Gly Arg	
180	185
190	
ggt att gtc tat atc tcc cac cgc atg aaa gaa atc ttc gag att tgc	624
Gly Ile Val Tyr Ile Ser His Arg Met Lys Glu Ile Phe Glu Ile Cys	
195	200
205	
gat gac gtt acc gtt ttt cgt gat ggg caa ttt att gct gag cgc gaa	672
Asp Asp Val Thr Val Phe Arg Asp Gly Gln Phe Ile Ala Glu Arg Glu	
210	215
220	
gtg gca tca ctg acc gaa gat tcg ctg att gag atg atg gtg ggt cgc	720
Val Ala Ser Leu Thr Glu Asp Ser Leu Ile Glu Met Met Val Gly Arg	
225	230
235	240
aag ctg gaa gat caa tat ccg cac ctg gac aaa gcg ccg gga gat atc	768
Lys Leu Glu Asp Gln Tyr Pro His Leu Asp Lys Ala Pro Gly Asp Ile	
245	250
255	
cgc ctg aaa gtc gat aat ctc tgc gga cct ggc gtt aac gat gtc tct	816
Arg Leu Lys Val Asp Asn Leu Cys Gly Pro Gly Val Asn Asp Val Ser	
260	265
270	
ttt act tta cgc aaa ggc gaa att ctt ggc gtc tct ggt ttg atg ggc	864
Phe Thr Leu Arg Lys Gly Glu Ile Leu Gly Val Ser Gly Leu Met Gly	
275	280
285	
gca ggt cgt acc gaa ctg atg aaa gtg ctc tac ggc gca cta ccg cgc	912
Ala Gly Arg Thr Glu Leu Met Lys Val Leu Tyr Gly Ala Leu Pro Arg	
290	295
300	
acc agc ggt tac gtc acc ctg gat ggg cat gaa gtc gtt acc cgt tca	960
Thr Ser Gly Tyr Val Thr Leu Asp Gly His Glu Val Val Thr Arg Ser	
305	310
315	320
ccg cag gat ggc ctg gca aac ggc att gtg tat atc tcc gaa gac cgt	1008
Pro Gln Asp Gly Leu Ala Asn Gly Ile Val Tyr Ile Ser Glu Asp Arg	
325	330
335	
aaa cgt gac ggt tta gtg ttg ggc atg tca gta aaa gag aac atg tcg	1056
Lys Arg Asp Gly Leu Val Leu Gly Met Ser Val Lys Glu Asn Met Ser	

340	345	350	
ctg aca gcg ctg cgc tac ttc agc cgc gct ggc ggc agt ttg aag cat			1104
Leu Thr Ala Leu Arg Tyr Phe Ser Arg Ala Gly Gly Ser Leu Lys His			
355	360	365	
gcc gat gaa cag cag gct gtg agt gat ttc att cgt ctg ttt aat gtg			1152
Ala Asp Glu Gln Gln Ala Val Ser Asp Phe Ile Arg Leu Phe Asn Val			
370	375	380	
aaa act ccg tcg atg gaa cag gca att ggt ctg ctt tcc ggt ggc aat			1200
Lys Thr Pro Ser Met Glu Gln Ala Ile Gly Leu Leu Ser Gly Gly Asn			
385	390	395	400
cag caa aaa gtg gcg att gcc cgc ggt ctg atg aca cgc ccc aaa gtg			1248
Gln Gln Lys Val Ala Ile Ala Arg Gly Leu Met Thr Arg Pro Lys Val			
405	410	415	
ttg atc ctt gat gaa cct acc cgt ggc gta gat gtc ggc gcg aaa aaa			1296
Leu Ile Leu Asp Glu Pro Thr Arg Gly Val Asp Val Gly Ala Lys Lys			
420	425	430	
gag atc tat caa ctg att aac cag ttc aaa gcc gat ggc ttg agc atc			1344
Glu Ile Tyr Gln Leu Ile Asn Gln Phe Lys Ala Asp Gly Leu Ser Ile			
435	440	445	
att ctg gtg tca tcg gag atg cca gaa gta tta ggc atg agc gat cgc			1392
Ile Leu Val Ser Ser Glu Met Pro Glu Val Leu Gly Met Ser Asp Arg			
450	455	460	
atc atc gtc atg cat gaa ggg cat ctc agc ggg gaa ttt act cgt gag			1440
Ile Ile Val Met His Glu Gly His Leu Ser Gly Glu Phe Thr Arg Glu			
465	470	475	480
cag gcc acc cag gaa gtg tta atg gct gcc gct gtg ggc aag ctt aat			1488
Gln Ala Thr Gln Glu Val Leu Met Ala Ala Ala Val Gly Lys Leu Asn			
485	490	495	
cgc gtg aat cag gag taa			1506
Arg Val Asn Gln Glu *			
500			

<210> 284

<211> 966

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(966)

<400> 284

atg aca acc cag act gtc tct ggt cgc cgt tat ttc acg aaa gcg tgg	48
Met Thr Thr Gln Thr Val Ser Gly Arg Arg Tyr Phe Thr Lys Ala Trp	
1	5
	10
	15

ctg atg gag cag aaa tcg ctt atc gct ctg ctg gtg ctg atc gcg att	96
Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile	
20 25 30	
gtc tcg acg tta agc ccg aac ttt ttc acc atc aat aac tta ttc aat	144
Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn	
35 40 45	
att ctc cag caa acc tca gtg aac gcc att atg gcg gtc ggg atg acg	192
Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr	
50 55 60	
ctg gtg atc ctg acg tcg ggc atc gac tta tcg gta ggt tct ctg ttg	240
Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu	
65 70 75 80	
gcg ctg acc ggc gca gtt gct gca tct atc gtc ggc att gaa gtc aat	288
Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn	
85 90 95	
gcg ctg gtg gct gtc gct gct gct ctc gcg tta ggt gcc gca att ggt	336
Ala Leu Val Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly	
100 105 110	
gcg gta acc ggg gtg att gta gcg aaa ggt cgc gtc cag gcg ttt atc	384
Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile	
115 120 125	
gct acg ctg gtt atg atg ctt tta ctg cgc ggc gtg acc atg gtt tat	432
Ala Thr Leu Val Met Met Leu Leu Leu Arg Gly Val Thr Met Val Tyr	
130 135 140	
acc aac ggt agc cca gtg aat acc ggc ttt act gag aac gcc gat ctg	480
Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu	
145 150 155 160	
ttt ggc tgg ttt ggt att ggt cgt ccg ctg ggc gta ccg acg cca gtc	528
Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val	
165 170 175	
tgg atc atg ggg att gtc ttc ctc gcg gcc tgg tac atg ctg cat cac	576
Trp Ile Met Gly Ile Val Phe Leu Ala Ala Trp Tyr Met Leu His His	
180 185 190	
acg cgt ctg ggg cgt tac atc tac gcg ctg ggc ggc aac gaa gcg gca	624
Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala	
195 200 205	
acg cgt ctt tct ggt atc aac gtc aat aaa atc aaa atc atc gtc tat	672
Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr	
210 215 220	
tct ctt tgt ggt ctg ctg gca tcg ctg gcc ggg atc att gaa gtg gcg	720
Ser Leu Cys Gly Leu Leu Ala Ser Leu Ala Gly Ile Ile Glu Val Ala	
225 230 235 240	
cgt ctc tcc tcc gca caa ccc acg gcg ggg act ggc tat gag ctg gat	768

ggt aat gct gtg aag atg gct aac cag gcg aac atc ccg gtt atc act 336
 Gly Asn Ala Val Lys Met Ala Asn Gln Ala Asn Ile Pro Val Ile Thr
 100 105 110

ctt gac cgc cag gca acg aaa ggt gaa gtg gtg agc cac att gct tct 384
 Leu Asp Arg Gln Ala Thr Lys Gly Glu Val Val Ser His Ile Ala Ser
 115 120 125

gat aac gta ctg ggc ggc aaa atc gct ggt gat tac atc gcg aag aaa 432
 Asp Asn Val Leu Gly Gly Lys Ile Ala Gly Asp Tyr Ile Ala Lys Lys
 130 135 140

gcg ggt gaa ggt gcc aaa gtt atc gag ctg caa ggc att gct ggt aca 480
 Ala Gly Glu Gly Ala Lys Val Ile Glu Leu Gln Gly Ile Ala Gly Thr
 145 150 155 160

tcc gca gcc cgt gaa cgt ggc gaa ggc ttc cag cag gcc gtt gct gct 528
 Ser Ala Ala Arg Glu Arg Gly Glu Gly Phe Gln Gln Ala Val Ala Ala
 165 170 175

cac aag ttt aat gtt ctt gcc agc cag cca gca gat ttt gat cgc att 576
 His Lys Phe Asn Val Leu Ala Ser Gln Pro Ala Asp Phe Asp Arg Ile
 180 185 190

aaa ggt ttg aac gta atg cag aac ctg ttg acc gct cat ccg gat gtt 624
 Lys Gly Leu Asn Val Met Gln Asn Leu Leu Thr Ala His Pro Asp Val
 195 200 205

cag gct gta ttc gcg cag aat gat gaa atg gcg ctg ggc gcg ctg cgc 672
 Gln Ala Val Phe Ala Gln Asn Asp Glu Met Ala Leu Gly Ala Leu Arg
 210 215 220

gca ctg caa act gcc ggt aaa tcg gat gtg atg gtc gtc gga ttt gac 720
 Ala Leu Gln Thr Ala Gly Lys Ser Asp Val Met Val Val Gly Phe Asp
 225 230 235 240

ggt aca ccg gat ggc gaa aaa gcg gtg aat gat ggc aaa cta gca gcg 768
 Gly Thr Pro Asp Gly Glu Lys Ala Val Asn Asp Gly Lys Leu Ala Ala
 245 250 255

act atc gct cag cta ccc gat cag att ggc gcg aaa ggc gtc gaa acc 816
 Thr Ile Ala Gln Leu Pro Asp Gln Ile Gly Ala Lys Gly Val Glu Thr
 260 265 270

gca gat aaa gtg ctg aaa ggc gag aaa gtt cag gct aag tat ccg gtt 864
 Ala Asp Lys Val Leu Lys Gly Glu Lys Val Gln Ala Lys Tyr Pro Val
 275 280 285

gat ctg aaa ctg gtt gtt aag cag tag 891
 Asp Leu Lys Leu Val Val Lys Gln *
 290 295

<210> 286
 <211> 930
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(930)

<400> 286

atg	caa	aac	gca	ggc	agc	ctc	gtt	gtt	ctt	ggc	agc	att	aat	gct	gac	48
Met	Gln	Asn	Ala	Gly	Ser	Leu	Val	Val	Leu	Gly	Ser	Ile	Asn	Ala	Asp	
1			5						10					15		
cac	att	ctt	aat	ctt	caa	tct	ttt	cct	act	cca	ggc	gaa	acc	gta	acc	96
His	Ile	Leu	Asn	Leu	Gln	Ser	Phe	Pro	Thr	Pro	Gly	Glu	Thr	Val	Thr	
			20					25					30			
ggt	aac	cac	tat	cag	gtt	gca	ttt	ggc	ggc	aaa	ggc	gcg	aat	cag	gct	144
Gly	Asn	His	Tyr	Gln	Val	Ala	Phe	Gly	Gly	Lys	Gly	Ala	Asn	Gln	Ala	
		35					40					45				
gtg	gct	gct	ggg	cgt	agc	ggc	gcg	aat	atc	gcg	ttt	att	gcc	tgt	acg	192
Val	Ala	Ala	Gly	Arg	Ser	Gly	Ala	Asn	Ile	Ala	Phe	Ile	Ala	Cys	Thr	
		50				55					60					
ggt	gat	gac	agc	att	ggt	gag	agc	gtt	cgc	cag	cag	ctc	gcc	act	gat	240
Gly	Asp	Asp	Ser	Ile	Gly	Glu	Ser	Val	Arg	Gln	Gln	Leu	Ala	Thr	Asp	
	65				70				75					80		
aac	att	gat	att	act	ccg	gtc	agc	gtg	atc	aaa	ggc	gaa	tca	aca	ggt	288
Asn	Ile	Asp	Ile	Thr	Pro	Val	Ser	Val	Ile	Lys	Gly	Glu	Ser	Thr	Gly	
				85					90					95		
gtg	gcg	ctg	att	ttt	gtt	aat	ggc	gaa	ggt	gag	aat	gtc	atc	ggt	att	336
Val	Ala	Leu	Ile	Phe	Val	Asn	Gly	Glu	Gly	Glu	Asn	Val	Ile	Gly	Ile	
			100					105					110			
cat	gcc	ggc	gct	aat	gct	gcc	ctt	tcc	ccg	gcg	ctg	gtg	gaa	gcg	caa	384
His	Ala	Gly	Ala	Asn	Ala	Ala	Leu	Ser	Pro	Ala	Leu	Val	Glu	Ala	Gln	
		115					120					125				
cgt	gag	cgt	att	gcc	aac	gcg	tca	gca	tta	tta	atg	cag	ctg	gaa	tca	432
Arg	Glu	Arg	Ile	Ala	Asn	Ala	Ser	Ala	Leu	Leu	Met	Gln	Leu	Glu	Ser	
	130					135					140					
cca	ctc	gaa	agt	gtg	atg	gca	gcg	gcg	aaa	atc	gcc	cat	caa	aat	aag	480
Pro	Leu	Glu	Ser	Val	Met	Ala	Ala	Ala	Lys	Ile	Ala	His	Gln	Asn	Lys	
	145				150				155						160	
act	atc	gtt	gcg	ctt	aac	ccg	gct	ccg	gct	cgc	gaa	ctt	cct	gac	gaa	528
Thr	Ile	Val	Ala	Leu	Asn	Pro	Ala	Pro	Ala	Arg	Glu	Leu	Pro	Asp	Glu	
				165				170						175		
ctg	ctg	gcg	ctg	gtg	gac	att	att	acg	cca	aac	gaa	acg	gaa	gca	gaa	576
Leu	Leu	Ala	Leu	Val	Asp	Ile	Ile	Thr	Pro	Asn	Glu	Thr	Glu	Ala	Glu	
			180					185					190			
aag	ctc	acc	ggt	att	cgt	gtt	gaa	aat	gat	gaa	gat	gca	gcg	aag	gcg	624
Lys	Leu	Thr	Gly	Ile	Arg	Val	Glu	Asn	Asp	Glu	Asp	Ala	Ala	Lys	Ala	

195	200	205	
gcg cag gta ctg cat gaa aaa ggt atc cgt act gta ctg att act tta			672
Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu			
210	215	220	
gga agt cgt ggt gta tgg gct agc gtg aat ggt gaa ggt cag cgc gtt			720
Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val			
225	230	235	240
cct gga ttc cgg gtg cag gct gtc gat acc att gct gcc gga gat acc			768
Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr			
245	250	255	
ttt aac ggt gcg tta atc acg gca ttg ctg gaa gaa aaa cca ttg cca			816
Phe Asn Gly Ala Leu Ile Thr Ala Leu Leu Glu Glu Lys Pro Leu Pro			
260	265	270	
gag gcg att cgt ttt gcc cat gct gcc gct gcg att gcc gta aca cgt			864
Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ala Ile Ala Val Thr Arg			
275	280	285	
aaa ggc gca caa cct tcc gta ccg tgg cgt gaa gag atc gac gca ttt			912
Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe			
290	295	300	
tta gac agg cag agg tga			930
Leu Asp Arg Gln Arg *			
305			
<210> 287			
<211> 38			
<212> PRT			
<213> Escherichia coli			
<400> 287			
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile			
1 5 10 15			
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys			
20 25 30			
His Lys Gln Arg Gln Gly			
35			
<210> 288			
<211> 443			
<212> PRT			
<213> Escherichia coli			
<400> 288			
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu			
1 5 10 15			
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val			
20 25 30			
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val			
35 40 45			

Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
 50 55 60
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65 70 75 80
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
 85 90 95
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
 100 105 110
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
 115 120 125
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
 130 135 140
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
 145 150 155 160
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
 165 170 175
 Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
 225 230 235 240
 Gln Arg Arg Ile Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
 245 250 255
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
 260 265 270
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
 275 280 285
 Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
 290 295 300
 Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
 305 310 315 320
 Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
 325 330 335
 Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
 340 345 350
 Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
 355 360 365
 Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
 370 375 380
 Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
 385 390 395 400
 Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
 405 410 415
 Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
 420 425 430
 Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
 435 440

<210> 289

<211> 144

<212> PRT

<213> Escherichia coli

<400> 289

Met	Arg	Leu	Asn	Thr	Leu	Ser	Pro	Ala	Glu	Gly	Ser	Lys	Lys	Ala	Gly
1				5					10					15	
Lys	Arg	Leu	Gly	Arg	Gly	Ile	Gly	Ser	Gly	Leu	Gly	Lys	Thr	Gly	Gly
		20					25						30		
Arg	Gly	His	Lys	Gly	Gln	Lys	Ser	Arg	Ser	Gly	Gly	Gly	Val	Arg	Arg
		35				40						45			
Gly	Phe	Glu	Gly	Gly	Gln	Met	Pro	Leu	Tyr	Arg	Arg	Leu	Pro	Lys	Phe
	50					55				60					
Gly	Phe	Thr	Ser	Arg	Lys	Ala	Ala	Ile	Thr	Ala	Glu	Ile	Arg	Leu	Ser
65					70					75					80
Asp	Leu	Ala	Lys	Val	Glu	Gly	Gly	Val	Val	Asp	Leu	Asn	Thr	Leu	Lys
			85					90						95	
Ala	Ala	Asn	Ile	Ile	Gly	Ile	Gln	Ile	Glu	Phe	Ala	Lys	Val	Ile	Leu
		100					105						110		
Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr
	115					120						125			
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu
	130					135						140			

<210> 290

<211> 59

<212> PRT

<213> Escherichia coli

<400> 290

Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg
1				5					10					15	
Leu	Pro	Lys	His	Lys	Ala	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Arg	Arg	Ile
		20					25						30		
Gly	His	Thr	Val	Glu	Arg	Glu	Asp	Thr	Pro	Ala	Ile	Arg	Gly	Met	Ile
		35				40						45			
Asn	Ala	Val	Ser	Phe	Met	Val	Lys	Val	Glu	Glu					
	50					55									

<210> 291

<211> 167

<212> PRT

<213> Escherichia coli

<400> 291

Met	Ala	His	Ile	Glu	Lys	Gln	Ala	Gly	Glu	Leu	Gln	Glu	Lys	Leu	Ile
1			5					10						15	
Ala	Val	Asn	Arg	Val	Ser	Lys	Thr	Val	Lys	Gly	Gly	Arg	Ile	Phe	Ser
		20					25						30		
Phe	Thr	Ala	Leu	Thr	Val	Val	Gly	Asp	Gly	Asn	Gly	Arg	Val	Gly	Phe
		35				40						45			
Gly	Tyr	Gly	Lys	Ala	Arg	Glu	Val	Pro	Ala	Ala	Ile	Gln	Lys	Ala	Met
	50					55					60				
Glu	Lys	Ala	Arg	Arg	Asn	Met	Ile	Asn	Val	Ala	Leu	Asn	Asn	Gly	Thr
65					70					75					80
Leu	Gln	His	Pro	Val	Lys	Gly	Val	His	Thr	Gly	Ser	Arg	Val	Phe	Met
			85					90						95	
Gln	Pro	Ala	Ser	Glu	Gly	Thr	Gly	Ile	Ile	Ala	Gly	Gly	Ala	Met	Arg
		100					105						110		

Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160
 Val Glu Glu Ile Leu Gly Lys
 165

<210> 292
 <211> 117
 <212> PRT
 <213> Escherichia coli

<400> 292
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
 35 40 45
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50 55 60
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
 65 70 75 80
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
 85 90 95
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
 100 105 110
 Ala Gly Leu Gln Phe
 115

<210> 293
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 293
 Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
 1 5 10 15
 Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
 20 25 30
 Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
 35 40 45
 Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
 50 55 60
 Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
 65 70 75 80
 Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
 85 90 95
 Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
 100 105 110
 Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
 115 120 125
 Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val

130		135		140											
Ala	Ala	Asp	Leu	Arg	Ala	Tyr	Arg	Arg	Pro	Glu	Pro	Tyr	Lys	Gly	Lys
145		150		155						160					
Gly	Val	Arg	Tyr	Ala	Asp	Glu	Val	Val	Arg	Thr	Lys	Glu	Ala	Lys	Lys
		165							170					175	
Lys															

<210> 294
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 294
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1 5 10 15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
20 25 30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
35 40 45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
50 55 60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65 70 75 80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
85 90 95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
100 105 110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
115 120 125
Val Ala
130

<210> 295
 <211> 101
 <212> PRT
 <213> Escherichia coli

<400> 295
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1 5 10 15
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
20 25 30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
35 40 45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
50 55 60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65 70 75 80
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
85 90 95
Lys Lys Ala Ser Trp
100

<210> 296
 <211> 179
 <212> PRT
 <213> Escherichia coli

<400> 296

Met	Ala	Lys	Leu	His	Asp	Tyr	Tyr	Lys	Asp	Glu	Val	Val	Lys	Lys	Leu
1				5					10					15	
Met	Thr	Glu	Phe	Asn	Tyr	Asn	Ser	Val	Met	Gln	Val	Pro	Arg	Val	Glu
			20					25					30		
Lys	Ile	Thr	Leu	Asn	Met	Gly	Val	Gly	Glu	Ala	Ile	Ala	Asp	Lys	Lys
		35					40					45			
Leu	Leu	Asp	Asn	Ala	Ala	Ala	Asp	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Lys
	50					55					60				
Pro	Leu	Ile	Thr	Lys	Ala	Arg	Lys	Ser	Val	Ala	Gly	Phe	Lys	Ile	Arg
65					70					75					80
Gln	Gly	Tyr	Pro	Ile	Gly	Cys	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met
				85					90					95	
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg
			100					105					110		
Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr
		115					120					125			
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp
	130					135					140				
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala
145					150					155					160
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro
				165					170					175	
Phe	Arg	Lys													

<210> 297
 <211> 104
 <212> PRT
 <213> Escherichia coli

<400> 297

Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly
1				5					10					15	
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly
		20						25					30		
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro
		35					40					45			
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala
	50					55					60				
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala
65					70				75						80
Asp	Arg	Val	Gly	Phe	Arg	Phe	Glu	Asp	Gly	Lys	Lys	Val	Arg	Phe	Phe
				85					90					95	
Lys	Ser	Asn	Ser	Glu	Thr	Ile	Lys								
			100												

<210> 298
 <211> 123
 <212> PRT

<213> Escherichia coli

<400> 298

Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
1 5 10 15
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
20 25 30
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
35 40 45
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
50 55 60
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65 70 75 80
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
85 90 95
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
100 105 110
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
115 120

<210> 299

<211> 485

<212> PRT

<213> Escherichia coli

<400> 299

Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg
1 5 10 15
Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe
20 25 30
Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile
35 40 45
Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile
50 55 60
Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val
65 70 75 80
Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn
85 90 95
Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn
100 105 110
Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser
115 120 125
Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser
130 135 140
Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr
145 150 155 160
Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met
165 170 175
Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly
180 185 190
Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly
195 200 205
Val Gly Leu Leu Val Leu Ile Val Val Ile Gly Phe Asn Cys Cys Arg
210 215 220
Ser Pro Leu Leu Arg Met Gly Gly Ile Ala Ile Gly Leu Cys Val Gly
225 230 235 240

130	135	140
His Pro Gln Ser Val Asp	Ala Leu Phe Glu Ala	Ala Ser His Ile Asn
145	150	155
Met Arg Met Ile Ala Gly	Lys Val Met Met Asp	Arg Asn Ala Pro Asp
165	170	175
Tyr Leu Leu Asp Thr Ala	Glu Ser Ser Tyr His	Gln Ser Lys Glu Leu
180	185	190
Ile Glu Arg Trp His Lys	Asn Gly Arg Leu Leu	Tyr Ala Ile Thr Pro
195	200	205
Arg Phe Ala Pro Thr Ser	Ser Pro Glu Gln Met	Ala Met Ala Gln Arg
210	215	220
Leu Lys Glu Glu Tyr Pro	Asp Thr Trp Val His	Thr His Leu Cys Glu
225	230	235
Asn Lys Asp Glu Ile Ala	Trp Val Lys Ser Leu	Tyr Pro Asp His Asp
245	250	255
Gly Tyr Leu Asp Val Tyr	His Gln Tyr Gly Leu	Thr Gly Lys Asn Cys
260	265	270
Val Phe Ala His Cys Val	His Leu Glu Glu Lys	Glu Trp Asp Arg Leu
275	280	285
Ser Glu Thr Lys Ser Ser	Ile Ala Phe Cys Pro	Thr Ser Asn Leu Tyr
290	295	300
Leu Gly Ser Gly Leu Phe	Asn Leu Lys Lys Ala	Trp Gln Lys Lys Val
305	310	315
Lys Val Gly Met Gly Thr	Asp Ile Gly Ala Gly	Thr Thr Phe Asn Met
325	330	335
Leu Gln Thr Leu Asn Glu	Ala Tyr Lys Val Leu	Gln Leu Gln Gly Tyr
340	345	350
Arg Leu Ser Ala Tyr Glu	Ala Phe Tyr Leu Ala	Thr Leu Gly Gly Ala
355	360	365
Lys Ser Leu Gly Leu Asp	Asp Leu Ile Gly Asn	Phe Leu Pro Gly Lys
370	375	380
Glu Ala Asp Phe Val Val	Met Glu Pro Thr Ala	Thr Pro Leu Gln Gln
385	390	395
Leu Arg Tyr Asp Asn Ser	Val Ser Leu Val Asp	Lys Leu Phe Val Met
405	410	415
Met Thr Leu Gly Asp Asp	Arg Ser Ile Tyr Arg	Thr Tyr Val Asp Gly
420	425	430
Arg Leu Val Tyr Glu Arg	Asn	
435		

<210> 301
 <211> 189
 <212> PRT
 <213> Escherichia coli

<400> 301
 Met Ser Gly Asp Ile Leu Gln Thr Pro Asp Ala Pro Lys Pro Gln Gly
 1 5 10 15
 Ala Leu Asp Asn Tyr Phe Lys Ile Thr Ala Arg Gly Ser Thr Val Arg
 20 25 30
 Gln Glu Val Leu Ala Gly Leu Thr Thr Phe Leu Ala Met Val Tyr Ser
 35 40 45
 Val Ile Val Val Pro Gly Met Leu Gly Lys Ala Gly Phe Pro Pro Ala
 50 55 60
 Ala Val Phe Val Ala Thr Cys Leu Val Ala Gly Phe Gly Ser Leu Leu
 65 70 75 80

Met Gly Leu Trp Ala Asn Leu Pro Met Ala Ile Gly Cys Ala Ile Ser
85 90 95
Leu Thr Ala Phe Thr Ala Phe Ser Leu Val Leu Gly Gln Gln Ile Ser
100 105 110
Val Pro Val Ala Leu Gly Ala Val Phe Leu Met Gly Val Ile Phe Thr
115 120 125
Ala Ile Ser Val Thr Gly Val Arg Thr Trp Ile Leu Arg Asn Leu Pro
130 135 140
Met Gly Ile Ala His Gly Thr Gly Ile Gly Ile Gly Leu Phe Leu Leu
145 150 155 160
Leu Ile Ala Ala Asn Gly Val Gly Met Val Ile Lys Asn Pro Ile Glu
165 170 175
Gly Leu Gln Trp Arg Ser Val Arg Leu Pro Pro Ser Arg
180 185

<210> 302

<211> 276

<212> PRT

<213> Escherichia coli

<400> 302

Met Ala Leu Gly Ala Phe Thr Ser Phe Pro Val Met Met Ser Leu Leu
1 5 10 15
Gly Leu Ala Val Ile Phe Gly Leu Glu Lys Cys Arg Val Pro Gly Gly
20 25 30
Ile Leu Leu Val Ile Ile Ala Ile Ser Ile Ile Gly Leu Ile Phe Asp
35 40 45
Pro Ala Val Lys Tyr His Gly Leu Val Ala Met Pro Ser Leu Thr Gly
50 55 60
Glu Asp Gly Lys Ser Leu Ile Phe Ser Leu Asp Ile Met Gly Ala Leu
65 70 75 80
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val
85 90 95
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu
100 105 110
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser
115 120 125
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala
130 135 140
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr
145 150 155 160
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe
165 170 175
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala
180 185 190
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp
195 200 205
Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe
210 215 220
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val
225 230 235 240
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn
245 250 255
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly
260 265 270
Gly Trp Ala Ile

<210> 303

<211> 466

<212> PRT

<213> Escherichia coli

<400> 303

```

Met Asn Ser Glu Gly Gly Lys Pro Gly Asn Val Leu Thr Val Asn Gly
 1          5          10          15
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly
          20          25          30
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln
          35          40          45
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln
          50          55          60
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly
65          70          75          80
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr
          85          90          95
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr
          100          105          110
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn
          115          120          125
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu
          130          135          140
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Asn Ser Leu Phe Ser
145          150          155          160
His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu
          165          170          175
His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly
          180          185          190
His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn
          195          200          205
Arg Tyr Val Leu Gln Leu Gly Gly Asp Leu Ala Gln Trp Ser Ser Asn
          210          215          220
Ala Gln Asp Arg Trp His Leu Gly Val Met Ala Gly Tyr Ala Asn Gln
225          230          235          240
His Ser Asn Thr Gln Ser Asn Arg Val Gly Tyr Lys Ser Asp Gly Arg
          245          250          255
Ile Ser Gly Tyr Ser Ala Gly Leu Tyr Ala Thr Trp Tyr Gln Asn Asp
          260          265          270
Ala Asn Lys Thr Gly Ala Tyr Val Asp Ser Trp Ala Leu Tyr Asn Trp
          275          280          285
Phe Asp Asn Ser Val Ser Ser Asp Asn Arg Ser Ala Asp Asp Tyr Asp
          290          295          300
Ser Arg Gly Val Thr Ala Ser Val Glu Gly Gly Tyr Thr Phe Glu Ala
305          310          315          320
Gly Thr Phe Ser Gly Ser Glu Gly Thr Leu Asn Thr Trp Tyr Val Gln
          325          330          335
Pro Gln Ala Gln Ile Thr Trp Met Gly Val Lys Asp Ser Asp His Thr
          340          345          350
Arg Lys Asp Gly Thr Arg Ile Glu Thr Glu Gly Asp Gly Asn Val Gln
          355          360          365
Thr Arg Leu Gly Val Lys Thr Tyr Leu Asn Ser His His Gln Arg Asp
          370          375          380

```

Asp Gly Lys Gln Arg Glu Phe Gln Pro Tyr Ile Glu Ala Asn Trp Ile
 385 390 395 400
 Asn Asn Ser Lys Val Tyr Ala Val Lys Met Asn Gly Gln Thr Val Gly
 405 410 415
 Arg Glu Gly Ala Arg Asn Leu Gly Glu Val Arg Thr Gly Val Glu Ala
 420 425 430
 Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
 435 440 445
 Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
 450 455 460
 Ser Trp
 465

<210> 304
 <211> 1325
 <212> PRT
 <213> Escherichia coli

<400> 304
 Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
 1 5 10 15
 Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
 20 25 30
 Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
 35 40 45
 Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
 50 55 60
 Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
 65 70 75 80
 Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
 85 90 95
 Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly
 100 105 110
 Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp
 115 120 125
 Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln
 130 135 140
 Ser Gly Thr Gly Thr Leu Asn Ile Lys Gln Lys Gly His Val Asp Gly
 145 150 155 160
 Gly Tyr Leu Arg Leu Gly Ser Ser Thr Gly Gly Val Gly Thr Val Asn
 165 170 175
 Val Glu Gly Glu Asp Ser Val Leu Thr Thr Glu Leu Phe Glu Ile Gly
 180 185 190
 Ser Tyr Gly Thr Gly Ser Leu Asn Ile Thr Asp Lys Gly Tyr Val Thr
 195 200 205
 Ser Ser Ile Val Ala Ile Leu Gly Tyr Gln Ala Gly Ser Asn Gly Gln
 210 215 220
 Val Val Val Glu Lys Gly Gly Glu Trp Leu Ile Lys Asn Asn Asp Ser
 225 230 235 240
 Ser Ile Glu Phe Gln Ile Gly Asn Gln Gly Thr Gly Glu Ala Thr Ile
 245 250 255
 Arg Glu Gly Gly Leu Val Thr Ala Glu Asn Thr Ile Ile Gly Gly Asn
 260 265 270
 Ala Thr Gly Ile Gly Thr Leu Asn Val Gln Asp Gln Asp Ser Val Ile
 275 280 285
 Thr Val Arg Arg Leu Tyr Asn Gly Tyr Phe Gly Asn Gly Thr Val Asn

	290					295					300				
Ile 305	Ser	Asn	Asn	Gly	Leu 310	Ile	Asn	Asn	Lys	Glu 315	Tyr	Ser	Leu	Val	Gly 320
Val	Gln	Asp	Gly	Ser 325	His	Gly	Val	Val	Asn 330	Val	Thr	Asp	Lys	Gly	His 335
Trp	Asn	Phe	Leu 340	Gly	Thr	Gly	Glu	Ala 345	Phe	Arg	Tyr	Ile	Tyr	Ile	Gly 350
Asp	Ala	Gly 355	Asp	Gly	Glu	Leu	Asn 360	Val	Ser	Ser	Glu	Gly 365	Lys	Val	Asp
Ser	Gly 370	Ile	Ile	Thr	Ala	Gly 375	Met	Lys	Glu	Thr	Gly 380	Thr	Gly	Asn	Ile
Thr 385	Val	Lys	Asp	Lys	Asn 390	Ser	Val	Ile	Thr	Asn 395	Leu	Gly	Thr	Asn	Leu 400
Gly	Tyr	Asp	Gly 405	His	Gly	Glu	Met	Asn 410	Ile	Ser	Asn	Gln	Gly	Leu	Val 415
Val	Ser	Asn 420	Gly	Ser	Ser	Leu	Gly 425	Tyr	Gly	Glu	Thr	Gly 430	Val	Gly	Gly
Asn	Val	Ser 435	Ile	Thr	Thr	Gly 440	Gly	Met	Trp	Glu	Val	Asn 445	Lys	Asn	Val
Tyr	Thr 450	Thr	Ile	Gly	Val	Ala 455	Gly	Val	Gly	Asn 460	Leu	Asn	Ile	Ser	Asp
Gly 465	Gly	Lys	Phe	Val	Ser 470	Gln	Asn	Ile	Thr	Phe 475	Leu	Gly	Asp	Lys	Ala 480
Ser	Gly	Ile	Gly 485	Thr	Leu	Asn	Leu	Met 490	Asp	Ala	Thr	Ser	Ser	Phe	Asp 495
Thr	Val	Gly 500	Ile	Asn	Val	Gly	Asn 505	Phe	Gly	Ser	Gly	Ile	Val	Asn	Val
Ser	Asn 515	Gly	Ala	Thr	Leu	Asn 520	Ser	Thr	Gly	Tyr	Gly	Phe 525	Ile	Gly	Gly
Asn 530	Ala	Ser	Gly	Lys	Gly 535	Ile	Val	Asn	Ile	Ser	Thr 540	Asp	Ser	Leu	Trp
Asn 545	Leu	Lys	Thr	Ser 550	Ser	Thr	Asn	Ala	Gln	Leu 555	Leu	Gln	Val	Gly	Val 560
Leu	Gly	Thr	Gly 565	Glu	Leu	Asn	Ile	Thr 570	Thr	Gly	Gly	Ile	Val	Lys	Ala 575
Arg	Asp	Thr 580	Gln	Ile	Ala	Leu	Asn 585	Asp	Lys	Ser	Lys	Gly	Asp	Val	Arg
Val	Asp 595	Gly	Gln	Asn	Ser	Leu 600	Leu	Glu	Thr	Phe 605	Asn	Met	Tyr	Val	Gly
Thr	Ser 610	Gly	Thr	Gly 615	Thr	Leu	Thr	Leu	Thr	Asn 620	Asn	Gly	Thr	Leu	Asn
Val 625	Glu	Gly	Gly	Glu 630	Val	Tyr	Leu	Gly	Val	Phe 635	Glu	Pro	Ala	Val	Gly 640
Thr	Leu	Asn	Ile 645	Gly	Ala	Ala	His	Gly 650	Glu	Ala	Ala	Ala	Asp	Ala	Gly 655
Phe	Ile	Thr 660	Asn	Ala	Thr	Lys	Val 665	Glu	Phe	Gly	Leu	Gly	Glu	Gly	Val
Phe	Val 675	Phe	Asn	His	Thr	Asn 680	Asn	Ser	Asp	Ala	Gly	Tyr	Gln	Val	Asp
Met	Leu 690	Ile	Thr	Gly 695	Asp	Asp	Lys	Asp	Gly	Lys	Val	Ile	His	Asp	Ala
Gly 705	His	Thr	Val	Phe 710	Asn	Ala	Gly	Asn	Thr	Tyr 715	Ser	Gly	Lys	Thr	Leu 720
Val	Asn	Asp	Gly 725	Leu	Leu	Thr	Ile	Ala 730	Ser	His	Thr	Ala	Asp	Gly	Val 735
Thr	Gly	Met 740	Gly	Ser 745	Ser	Glu	Val	Thr 745	Ile	Ala	Asn	Pro	Gly	Thr	Leu

Asp	Ile	Leu	Ala	Ser	Thr	Asn	Ser	Ala	Gly	Asp	Tyr	Thr	Leu	Thr	Asn
		755					760					765			
Ala	Leu	Lys	Gly	Asp	Gly	Leu	Met	Arg	Val	Gln	Leu	Ser	Ser	Ser	Asp
		770					775					780			
Lys	Met	Phe	Gly	Phe	Thr	His	Ala	Thr	Gly	Thr	Glu	Phe	Ala	Gly	Val
785					790					795					800
Ala	Gln	Leu	Lys	Asp	Ser	Thr	Phe	Thr	Leu	Glu	Arg	Asp	Asn	Thr	Ala
				805						810					815
Ala	Leu	Thr	His	Ala	Met	Leu	Gln	Ser	Asp	Ser	Glu	Asn	Thr	Thr	Ser
			820					825					830		
Val	Lys	Val	Gly	Glu	Gln	Ser	Ile	Gly	Gly	Leu	Ala	Met	Asn	Gly	Gly
		835					840					845			
Thr	Ile	Ile	Phe	Asp	Thr	Asp	Ile	Pro	Ala	Ala	Thr	Leu	Ala	Glu	Gly
		850				855					860				
Tyr	Ile	Ser	Val	Asp	Thr	Leu	Val	Val	Gly	Ala	Gly	Asp	Tyr	Thr	Trp
865					870					875					880
Lys	Gly	Arg	Asn	Tyr	Gln	Val	Asn	Gly	Thr	Gly	Asp	Val	Leu	Ile	Asp
				885						890					895
Val	Pro	Lys	Pro	Trp	Asn	Asp	Pro	Met	Ala	Asn	Asn	Pro	Leu	Thr	Thr
			900					905					910		
Leu	Asn	Leu	Leu	Glu	His	Asp	Asp	Ser	His	Val	Gly	Val	Gln	Leu	Val
		915					920					925			
Lys	Ala	Gln	Thr	Val	Ile	Gly	Ser	Gly	Gly	Ser	Leu	Thr	Leu	Arg	Asp
		930				935					940				
Leu	Gln	Gly	Asp	Glu	Val	Glu	Ala	Asp	Lys	Thr	Leu	His	Ile	Ala	Gln
945					950					955					960
Asn	Gly	Thr	Val	Val	Ala	Glu	Gly	Asp	Tyr	Gly	Phe	Arg	Leu	Thr	Thr
				965					970					975	
Ala	Pro	Gly	Asn	Gly	Leu	Tyr	Val	Asn	Tyr	Gly	Leu	Lys	Ala	Leu	Asn
			980					985					990		
Ile	His	Gly	Gly	Gln	Lys	Leu	Thr	Leu	Ala	Glu	His	Gly	Gly	Ala	Tyr
		995					1000					1005			
Gly	Ala	Thr	Ala	Asp	Met	Ser	Ala	Lys	Ile	Gly	Gly	Glu	Gly	Asp	Leu
		1010				1015					1020				
Ala	Ile	Asn	Thr	Val	Arg	Gln	Val	Ser	Leu	Ser	Asn	Gly	Gln	Asn	Asp
1025					1030					1035					1040
Tyr	Gln	Gly	Ala	Thr	Tyr	Val	Gln	Met	Gly	Thr	Leu	Arg	Thr	Asp	Ala
				1045					1050					1055	
Asp	Gly	Ala	Leu	Gly	Asn	Thr	Arg	Glu	Leu	Asn	Ile	Ser	Asn	Ala	Ala
			1060					1065					1070		
Ile	Val	Asp	Leu	Asn	Gly	Ser	Thr	Gln	Thr	Val	Glu	Thr	Phe	Thr	Gly
		1075					1080					1085			
Gln	Met	Gly	Ser	Thr	Val	Leu	Phe	Lys	Glu	Gly	Ala	Leu	Thr	Val	Asn
		1090				1095					11				

<210> 306
 <211> 274
 <212> PRT
 <213> Escherichia coli

<400> 306
 Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
 1 5 10 15
 Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
 20 25 30
 His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
 35 40 45
 Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
 50 55 60
 Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
 65 70 75 80
 Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
 85 90 95
 Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
 100 105 110
 Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
 115 120 125
 His His Asp His Glu His His His Asp His Gly His His His His His
 130 135 140
 Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
 145 150 155 160
 Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
 165 170 175
 Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
 180 185 190
 Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
 195 200 205
 Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
 210 215 220
 Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
 225 230 235 240
 Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
 245 250 255
 Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
 260 265 270
 Met Arg

<210> 307
 <211> 172
 <212> PRT
 <213> Escherichia coli

<400> 307
 Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys

50		55		60											
Asn	Lys	Met	Leu	Leu	Gly	Ala	Leu	Leu	Leu	Val	Thr	Ser	Ala	Ala	Trp
65					70					75					80
Ala	Ala	Pro	Ala	Thr	Ala	Gly	Ser	Thr	Asn	Thr	Ser	Gly	Ile	Ser	Lys
			85						90					95	
Tyr	Glu	Leu	Ser	Phe	Ile	Ala	Asp	Phe	Lys	His	Phe	Lys	Pro	Gly	
		100					105					110			
Asp	Thr	Val	Pro	Glu	Met	Tyr	Arg	Thr	Asp	Glu	Tyr	Asn	Ile	Lys	Gln
		115					120					125			
Trp	Gln	Leu	Arg	Asn	Leu	Pro	Ala	Pro	Asp	Ala	Gly	Thr	His	Trp	Thr
	130					135					140				
Tyr	Met	Gly	Gly	Ala	Tyr	Val	Leu	Ile	Ser	Asp	Thr	Asp	Gly	Lys	Ile
145					150					155					160
Ile	Lys	Ala	Tyr	Asp	Gly	Glu	Ile	Phe	Tyr	His	Arg				
			165						170						

<210> 308
 <211> 344
 <212> PRT
 <213> Escherichia coli

<400> 308

Met	Glu	Ile	Arg	Ile	Met	Leu	Phe	Ile	Leu	Met	Met	Met	Val	Met	Pro
1				5					10					15	
Val	Ser	Tyr	Ala	Ala	Cys	Tyr	Ser	Glu	Leu	Ser	Val	Gln	His	Asn	Leu
			20					25					30		
Val	Val	Gln	Gly	Asp	Phe	Ala	Leu	Thr	Gln	Thr	Gln	Met	Ala	Thr	Tyr
		35					40					45			
Glu	His	Asn	Phe	Asn	Asp	Ser	Ser	Cys	Val	Ser	Thr	Asn	Thr	Ile	Thr
	50					55					60				
Pro	Met	Ser	Pro	Ser	Asp	Ile	Ile	Val	Gly	Leu	Tyr	Asn	Asp	Thr	Ile
65					70				75						80
Lys	Leu	Asn	Leu	His	Phe	Glu	Trp	Thr	Asn	Lys	Asn	Asn	Ile	Thr	Leu
			85						90				95		
Ser	Asn	Asn	Gln	Thr	Ser	Phe	Thr	Ser	Gly	Tyr	Ser	Val	Thr	Val	Thr
			100					105					110		
Pro	Ala	Ala	Ser	Asn	Ala	Lys	Val	Asn	Val	Ser	Ala	Gly	Gly	Gly	Gly
	115					120						125			
Ser	Val	Met	Ile	Asn	Gly	Val	Ala	Thr	Leu	Ser	Ser	Ala	Ser	Ser	Ser
	130					135					140				
Thr	Arg	Gly	Ser	Ala	Ala	Val	Gln	Phe	Leu	Leu	Cys	Leu	Leu	Gly	Gly
145					150					155					160
Lys	Ser	Trp	Asp	Ala	Cys	Val	Asn	Ser	Tyr	Arg	Asn	Ala	Leu	Ala	Gln
			165						170					175	
Asn	Ala	Gly	Val	Tyr	Ser	Phe	Asn	Leu	Thr	Leu	Ser	Tyr	Asn	Pro	Ile
		180						185					190		
Thr	Thr	Thr	Cys	Lys	Pro	Asp	Asp	Leu	Leu	Ile	Thr	Leu	Asp	Ser	Ile
	195					200						205			
Pro	Val	Ser	Gln	Leu	Pro	Ala	Thr	Gly	Asn	Lys	Ala	Thr	Ile	Asn	Ser
	210					215					220				
Lys	Gln	Gly	Asp	Ile	Ile	Leu	Arg	Cys	Lys	Asn	Leu	Leu	Gly	Gln	Gln
225					230				235						240
Asn	Gln	Thr	Ser	Arg	Lys	Met	Gln	Val	Tyr	Leu	Ser	Ser	Ser	Asp	Leu
			245						250					255	
Leu	Thr	Asn	Ser	Asn	Thr	Ile	Leu	Lys	Gly	Ala	Glu	Asp	Asn	Gly	Val
		260						265						270	

[illegible]

<400> 309															
Met 1	Leu	Arg	Met	Thr 5	Pro	Leu	Ala	Ser	Ala 10	Ile	Val	Ala	Leu	Leu 15	Leu
Gly	Ile	Glu	Ala 20	Tyr	Ala	Ala	Glu	Glu 25	Thr	Phe	Asp	Thr	His 30	Phe	Met
Ile	Gly	Gly 35	Met	Lys	Asp	Gln	Gln 40	Val	Ala	Asn	Ile	Arg 45	Leu	Asp	Asp
Asn	Gln 50	Pro	Leu	Pro	Gly	Gln 55	Tyr	Asp	Ile	Asp	Ile 60	Tyr	Val	Asn	Lys
Gln 65	Trp	Arg	Gly	Lys 70	Tyr	Glu	Ile	Ile	Val	Lys 75	Asp	Asn	Pro	Gln	Glu 80
Thr	Cys	Leu	Ser	Arg 85	Glu	Val	Ile	Lys 90	Arg	Leu	Gly	Ile	Asn 95	Ser	Asp
Asn	Phe	Ala	Ser 100	Gly	Lys	Gln	Cys	Leu 105	Thr	Phe	Glu	Gln	Leu 110	Val	Gln
Gly	Gly 115	Ser	Tyr	Thr	Trp	Asp	Ile 120	Gly	Val	Phe	Arg	Leu 125	Asp	Phe	Ser
Val	Pro 130	Gln	Ala	Trp	Val	Glu 135	Leu	Glu	Ser	Gly 140	Tyr	Val	Pro	Pro	
Glu 145	Asn	Trp	Glu	Arg 150	Gly	Ile	Asn	Ala	Phe	Tyr 155	Thr	Ser	Tyr	Tyr	Leu 160
Ser	Gln	Tyr	Tyr	Ser 165	Asp	Tyr	Lys	Ala	Ser 170	Gly	Asn	Asn	Lys	Ser	Thr
Tyr	Val	Arg	Phe 180	Asn	Ser	Gly	Leu	Asn 185	Leu	Leu	Gly	Trp	Gln 190	Leu	His
Ser	Asp	Ala 195	Ser	Phe	Ser	Lys	Thr 200	Asn	Asn	Asn	Pro	Gly 205	Val	Trp	Lys
Ser	Asn 210	Thr	Leu	Tyr	Leu	Glu 215	Arg	Gly	Phe	Ala	Gln 220	Leu	Leu	Gly	Thr
Leu 225	Arg	Val	Gly	Asp 230	Met	Tyr	Thr	Ser	Ser	Asp 235	Ile	Phe	Asp	Ser	Val 240
Arg	Phe	Arg	Gly 245	Val	Arg	Leu	Phe	Arg	Asp 250	Met	Gln	Met	Leu	Pro	Asn
Ser	Lys	Gln 260	Asn	Phe	Thr	Pro	Arg	Val 265	Gln	Gly	Ile	Ala	Gln 270	Ser	Asn
Ala	Leu 275	Val	Thr	Ile	Glu	Gln	Asn 280	Gly	Phe	Val	Val	Tyr 285	Gln	Lys	Glu
Val	Pro 290	Pro	Gly	Pro	Phe	Ala 295	Ile	Thr	Asp	Leu	Gln	Leu	Ala	Gly	Gly
Gly	Ala	Asp	Leu	Asp	Val	Ser	Val	Lys	Glu	Ala	Asp	Gly	Ser	Val	Thr

305					310					315					320
Thr	Tyr	Leu	Val	Pro	Tyr	Ala	Ala	Val	Pro	Asn	Met	Leu	Gln	Pro	Gly
				325					330					335	
Val	Ser	Lys	Tyr	Asp	Leu	Ala	Ala	Gly	Arg	Ser	His	Ile	Glu	Gly	Ala
			340					345					350		
Ser	Lys	Gln	Ser	Asp	Phe	Val	Gln	Ala	Gly	Tyr	Gln	Tyr	Gly	Phe	Asn
		355					360					365			
Asn	Leu	Leu	Thr	Leu	Tyr	Gly	Gly	Ser	Met	Val	Ala	Asn	Asn	Tyr	Tyr
	370					375					380				
Ala	Phe	Thr	Leu	Gly	Ala	Gly	Trp	Asn	Thr	Arg	Ile	Gly	Ala	Ile	Ser
385				390						395					400
Val	Asp	Ala	Thr	Lys	Ser	His	Ser	Lys	Gln	Asp	Asn	Gly	Asp	Val	Phe
				405					410					415	
Asp	Gly	Gln	Ser	Tyr	Gln	Ile	Ala	Tyr	Asn	Lys	Phe	Val	Ser	Gln	Thr
			420					425					430		
Ser	Thr	Arg	Phe	Gly	Leu	Ala	Ala	Trp	Arg	Tyr	Ser	Ser	Arg	Asp	Tyr
		435					440					445			
Arg	Thr	Phe	Asn	Asp	His	Val	Trp	Ala	Asn	Asn	Lys	Asp	Asn	Tyr	Arg
	450					455					460				
Arg	Asp	Glu	Asn	Asp	Val	Tyr	Asp	Ile	Ala	Asp	Tyr	Tyr	Gln	Asn	Asp
465				470						475					480
Phe	Gly	Arg	Lys	Asn	Ser	Phe	Ser	Ala	Asn	Met	Ser	Gln	Ser	Leu	Pro
				485					490					495	
Glu	Gly	Trp	Gly	Ser	Val	Ser	Leu	Ser	Thr	Leu	Trp	Arg	Asp	Tyr	Trp
			500					505					510		
Gly	Arg	Ser	Gly	Ser	Ser	Lys	Asp	Tyr	Gln	Leu	Ser	Tyr	Ser	Asn	Asn
		515					520					525			
Leu	Arg	Arg	Ile	Ser	Tyr	Thr	Leu	Ala	Ala	Ser	Gln	Ala	Tyr	Asp	Glu
	530					535					540				
Asn	His	His	Glu	Glu	Lys	Arg	Phe	Asn	Ile	Phe	Ile	Ser	Ile	Pro	Phe
545					550					555					560
Asp	Trp	Gly	Asp	Asp	Val	Ser	Thr	Pro	Arg	Arg	Gln	Ile	Tyr	Met	Ser
				565					570					575	
Asn	Ser	Thr	Thr	Phe	Asp	Asp	Gln	Gly	Phe	Ala	Ser	Asn	Asn	Thr	Gly
			580					585					590		
Leu	Ser	Gly	Thr	Val	Gly	Ser	Arg	Asp	Gln	Phe	Asn	Tyr	Gly	Val	Asn
		595					600					605			
Leu	Ser	His	Gln	His	Gln	Gly	Asn	Glu	Thr	Thr	Ala	Gly	Ala	Asn	Leu
	610					615					620				
Thr	Trp	Asn	Ala	Pro	Val	Ala	Thr	Val	Asn	Gly	Ser	Tyr	Ser	Gln	Ser
625					630					635					640
Ser	Thr	Tyr	Arg	Gln	Ala	Gly	Ala	Ser	Val	Ser	Gly	Gly	Ile	Val	Ala
				645					650					655	
Trp	Ser	Gly	Gly	Val	Asn	Leu</									

Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
 770 775 780
 Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
 785 790 795 800
 Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
 805 810 815
 Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln
 820 825

<210> 310
 <211> 239
 <212> PRT
 <213> Escherichia coli

<400> 310
 Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
 1 5 10 15
 Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
 20 25 30
 Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
 35 40 45
 Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
 50 55 60
 Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
 65 70 75 80
 Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
 85 90 95
 Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
 100 105 110
 Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
 115 120 125
 Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
 130 135 140
 Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
 145 150 155 160
 Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
 165 170 175
 Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
 180 185 190
 Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
 195 200 205
 Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His
 210 215 220
 Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
 225 230 235

<210> 311
 <211> 180
 <212> PRT
 <213> Escherichia coli

<400> 311
 Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
 1 5 10 15
 Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile

Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala
65 70 75 80
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val
85 90 95
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn
100 105 110
Tyr Asp Val Ile Leu Arg Phe
115

<210> 314
<211> 128
<212> PRT
<213> Escherichia coli

<400> 314
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln
1 5 10 15
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His
20 25 30
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn
35 40 45
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp
50 55 60
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala
65 70 75 80
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu
85 90 95
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu
100 105 110
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe
115 120 125

<210> 315
<211> 244
<212> PRT
<213> Escherichia coli

<400> 315
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu
1 5 10 15
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile
20 25 30
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly
35 40 45
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser
50 55 60
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser
65 70 75 80
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala
85 90 95
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val
100 105 110
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val
115 120 125
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln

130		135		140
Ile Met Ser Thr Phe Val	Pro Pro Glu Thr Pro Asp Val Gly Ser Ser			
145		150		155
Val Asn Phe Ala Ser Ser	Val Glu Asp Leu Val Thr Gln Thr Leu Glu			160
		165		170
Phe Thr Ile Glu Glu Val	Asn Ala Asp Arg Asn Val Ser Asn Asn Ala			175
		180		185
Lys Asn Arg Gln Ile Val	Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp			190
		195		200
Ile Lys Asp Ala Ile Asn	Gln Val Ala Asp Arg Leu Asn Ile Ser Lys			205
		210		215
His Thr Val Tyr Leu Tyr	Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln			220
225		230		235
Gly Gln Asp Lys				240

<210> 316
 <211> 84
 <212> PRT
 <213> Escherichia coli

<400> 316
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
1 5 10 15
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
20 25 30
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
35 40 45
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
50 55 60
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
65 70 75 80
Lys Ala Val Leu

<210> 317
 <211> 63
 <212> PRT
 <213> Escherichia coli

<400> 317
Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
1 5 10 15
Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
20 25 30
Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
35 40 45
Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
50 55 60

<210> 318
 <211> 136
 <212> PRT
 <213> Escherichia coli

<400> 318

Met	Leu	Gln	Pro	Lys	Arg	Thr	Lys	Phe	Arg	Lys	Met	His	Lys	Gly	Arg
1				5					10					15	
Asn	Arg	Gly	Leu	Ala	Gln	Gly	Thr	Asp	Val	Ser	Phe	Gly	Ser	Phe	Gly
		20						25					30		
Leu	Lys	Ala	Val	Gly	Arg	Gly	Arg	Leu	Thr	Ala	Arg	Gln	Ile	Glu	Ala
		35					40					45			
Ala	Arg	Arg	Ala	Met	Thr	Arg	Ala	Val	Lys	Arg	Gln	Gly	Lys	Ile	Trp
		50				55					60				
Ile	Arg	Val	Phe	Pro	Asp	Lys	Pro	Ile	Thr	Glu	Lys	Pro	Leu	Ala	Val
65					70					75				80	
Arg	Met	Gly	Lys	Gly	Lys	Gly	Asn	Val	Glu	Tyr	Trp	Val	Ala	Leu	Ile
				85					90					95	
Gln	Pro	Gly	Lys	Val	Leu	Tyr	Glu	Met	Asp	Gly	Val	Pro	Glu	Glu	Leu
		100						105					110		
Ala	Arg	Glu	Ala	Phe	Lys	Leu	Ala	Ala	Ala	Lys	Leu	Pro	Ile	Lys	Thr
		115					120					125			
Thr	Phe	Val	Thr	Lys	Thr	Val	Met								
		130				135									

<210> 319

<211> 233

<212> PRT

<213> Escherichia coli

<400> 319

Met	Gly	Gln	Lys	Val	His	Pro	Asn	Gly	Ile	Arg	Leu	Gly	Ile	Val	Lys
1				5					10					15	
Pro	Trp	Asn	Ser	Thr	Trp	Phe	Ala	Asn	Thr	Lys	Glu	Phe	Ala	Asp	Asn
		20						25					30		
Leu	Asp	Ser	Asp	Phe	Lys	Val	Arg	Gln	Tyr	Leu	Thr	Lys	Glu	Leu	Ala
		35					40					45			
Lys	Ala	Ser	Val	Ser	Arg	Ile	Val	Ile	Glu	Arg	Pro	Ala	Lys	Ser	Ile
		50				55				60					
Arg	Val	Thr	Ile	His	Thr	Ala	Arg	Pro	Gly	Ile	Val	Ile	Gly	Lys	Lys
65					70				75					80	
Gly	Glu	Asp	Val	Glu	Lys	Leu	Arg	Lys	Val	Val	Ala	Asp	Ile	Ala	Gly
			85					90					95		
Val	Pro	Ala	Gln	Ile	Asn	Ile	Ala	Glu	Val	Arg	Lys	Pro	Glu	Leu	Asp
		100					105					110			
Ala	Lys	Leu	Val	Ala	Asp	Ser	Ile	Thr	Ser	Gln	Leu	Glu	Arg	Arg	Val
		115					120					125			
Met	Phe	Arg	Arg	Ala	Met	Lys	Arg	Ala	Val	Gln	Asn	Ala	Met	Arg	Leu
		130				135				140					
Gly	Ala	Lys	Gly	Ile	Lys	Val	Glu	Val	Ser	Gly	Arg	Leu	Gly	Gly	Ala
145					150				155					160	
Glu	Ile	Ala	Arg	Thr	Glu	Trp	Tyr	Arg	Glu	Gly	Arg	Val	Pro	Leu	His
			165					170					175		
Thr	Leu	Arg	Ala	Asp	Ile	Asp	Tyr	Asn	Thr	Ser	Glu	Ala	His	Thr	Thr
		180					185					190			
Tyr	Gly	Val	Ile	Gly	Val	Lys	Val	Trp	Ile	Phe	Lys	Gly	Glu	Ile	Leu
		195				200					205				
Gly	Gly	Met	Ala	Ala	Val	Glu	Gln	Pro	Glu	Lys	Pro	Ala	Ala	Gln	Pro
		210				215					220				
Lys	Lys	Gln	Gln	Arg	Lys	Gly	Arg	Lys							

225

230

<210> 320

<211> 110

<212> PRT

<213> Escherichia coli

<400> 320

Met	Glu	Thr	Ile	Ala	Lys	His	Arg	His	Ala	Arg	Ser	Ser	Ala	Gln	Lys
1				5					10					15	
Val	Arg	Leu	Val	Ala	Asp	Leu	Ile	Arg	Gly	Lys	Lys	Val	Ser	Gln	Ala
		20					25					30			
Leu	Asp	Ile	Leu	Thr	Tyr	Thr	Asn	Lys	Lys	Ala	Ala	Val	Leu	Val	Lys
	35					40						45			
Lys	Val	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Ala	Glu	His	Asn	Asp	Gly	Ala
	50				55					60					
Asp	Ile	Asp	Asp	Leu	Lys	Val	Thr	Lys	Ile	Phe	Val	Asp	Glu	Gly	Pro
65				70					75						80
Ser	Met	Lys	Arg	Ile	Met	Pro	Arg	Ala	Lys	Gly	Arg	Ala	Asp	Arg	Ile
			85					90					95		
Leu	Lys	Arg	Thr	Ser	His	Ile	Thr	Val	Val	Val	Ser	Asp	Arg		
			100					105					110		

<210> 321

<211> 92

<212> PRT

<213> Escherichia coli

<400> 321

Met	Pro	Arg	Ser	Leu	Lys	Lys	Gly	Pro	Phe	Ile	Asp	Leu	His	Leu	Leu
1				5				10					15		
Lys	Lys	Val	Glu	Lys	Ala	Val	Glu	Ser	Gly	Asp	Lys	Lys	Pro	Leu	Arg
		20					25					30			
Thr	Trp	Ser	Arg	Arg	Ser	Thr	Ile	Phe	Pro	Asn	Met	Ile	Gly	Leu	Thr
	35					40						45			
Ile	Ala	Val	His	Asn	Gly	Arg	Gln	His	Val	Pro	Val	Phe	Val	Thr	Asp
	50				55					60					
Glu	Met	Val	Gly	His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr
65				70					75						80
Arg	Gly	His	Ala	Ala	Asp	Lys	Lys	Ala	Lys	Lys	Lys				
			85					90							

<210> 322

<211> 273

<212> PRT

<213> Escherichia coli

<400> 322

Met	Ala	Val	Val	Lys	Cys	Lys	Pro	Thr	Ser	Pro	Gly	Arg	Arg	His	Val
1				5				10						15	
Val	Lys	Val	Val	Asn	Pro	Glu	Leu	His	Lys	Gly	Lys	Pro	Phe	Ala	Pro
		20					25					30			
Leu	Leu	Glu	Lys	Asn	Ser	Lys	Ser	Gly	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35					40					45			

Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
 50 55 60
 Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
 65 70 75 80
 Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
 85 90 95
 Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
 100 105 110
 Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
 115 120 125
 Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
 130 135 140
 Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
 145 150 155 160
 Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
 165 170 175
 Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
 180 185 190
 Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
 195 200 205
 Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
 210 215 220
 Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
 225 230 235 240
 Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
 245 250 255
 Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
 260 265 270
 Lys

<210> 323
 <211> 100
 <212> PRT
 <213> Escherichia coli

<400> 323
 Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1 5 10 15
 Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
 20 25 30
 Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
 35 40 45
 Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
 50 55 60
 Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
 65 70 75 80
 Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
 85 90 95
 Gly Gly Ala Glu
 100

<210> 324
 <211> 201
 <212> PRT

[illegible]

Met	Glu	Leu	Val	Leu	Lys	Asp	Ala	Gln	Ser	Ala	Leu	Thr	Val	Ser	Glu
1				5					10					15	
Thr	Thr	Phe	Gly	Arg	Asp	Phe	Asn	Glu	Ala	Leu	Val	His	Gln	Val	Val
			20					25					30		
Val	Ala	Tyr	Ala	Ala	Gly	Ala	Arg	Gln	Gly	Thr	Arg	Ala	Gln	Lys	Thr
		35					40					45			
Arg	Ala	Glu	Val	Thr	Gly	Ser	Gly	Lys	Lys	Pro	Trp	Arg	Gln	Lys	Gly
	50					55					60				
Thr	Gly	Arg	Ala	Arg	Ser	Gly	Ser	Ile	Lys	Ser	Pro	Ile	Trp	Arg	Ser
65					70					75					80
Gly	Gly	Val	Thr	Phe	Ala	Ala	Arg	Pro	Gln	Asp	His	Ser	Gln	Lys	Val
				85					90					95	
Asn	Lys	Lys	Met	Tyr	Arg	Gly	Ala	Leu	Lys	Ser	Ile	Leu	Ser	Glu	Leu
			100					105						110	
Val	Arg	Gln	Asp	Arg	Leu	Ile	Val	Val	Glu	Lys	Phe	Ser	Val	Glu	Ala
			115					120					125		
Pro	Lys	Thr	Lys	Leu	Leu	Ala	Gln	Lys	Leu	Lys	Asp	Met	Ala	Leu	Glu
						135					140				
Asp	Val	Leu	Ile	Ile	Thr	Gly	Glu	Leu	Asp	Glu	Asn	Leu	Phe	Leu	Ala
145					150					155					160
Ala	Arg	Asn	Leu	His	Lys	Val	Asp	Val	Arg	Asp	Ala	Thr	Gly	Ile	Asp
				165					170					175	
Pro	Val	Ser	Leu	Ile	Ala	Phe	Asp	Lys	Val	Val	Met	Thr	Ala	Asp	Ala
			180					185						190	
Val	Lys	Gln	Val	Glu	Glu	Met	Leu	Ala							
		195					200								

<211> 209

<213> Escherichia coli

Met 1	Ile	Gly	Leu	Val 5	Gly	Lys	Lys	Val	Gly 10	Met	Thr	Arg	Ile	Phe 15	Thr
Glu	Asp	Gly	Val	Ser	Ile	Pro	Val	Thr	Val	Ile	Glu	Val	Glu	Ala	Asn
			20					25					30		
Arg	Val	Thr	Gln	Val	Lys	Asp	Leu	Ala	Asn	Asp	Gly	Tyr	Arg	Ala	Ile
		35					40					45			
Gln	Val	Thr	Thr	Gly	Ala	Lys	Lys	Ala	Asn	Arg	Val	Thr	Lys	Pro	Glu
	50					55					60				
Ala	Gly	His	Phe	Ala	Lys	Ala	Gly	Val	Glu	Ala	Gly	Arg	Gly	Leu	Trp
65				70					75					80	
Glu	Phe	Arg	Leu	Ala	Glu	Gly	Glu	Glu	Phe	Thr	Val	Gly	Gln	Ser	Ile
			85						90					95	
Ser	Val	Glu	Leu	Phe	Ala	Asp	Val	Lys	Lys	Val	Asp	Val	Thr	Gly	Thr
			100					105					110		
Ser	Lys	Gly	Lys	Gly	Phe	Ala	Gly	Thr	Val	Lys	Arg	Trp	Asn	Phe	Arg
		115					120					125			
Thr	Gln	Asp	Ala	Thr	His	Gly	Asn	Ser	Leu	Ser	His	Arg	Val	Pro	Gly
	130					135					140				
Ser	Ile	Gly	Gln	Asn	Gln	Thr	Pro	Gly	Lys	Val	Phe	Lys	Gly	Lys	Lys
145				150					155					160	

Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
165 170 175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
180 185 190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
195 200 205
Ala

<210> 326
<211> 103
<212> PRT
<213> Escherichia coli

<400> 326
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
1 5 10 15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
20 25 30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
35 40 45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
50 55 60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65 70 75 80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
85 90 95
Asp Val Gln Ile Ser Leu Gly
100

<210> 327
<211> 104
<212> PRT
<213> Escherichia coli

<400> 327
Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
1 5 10 15
Glu Tyr Gln Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
20 25 30
Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
35 40 45
Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
50 55 60
Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
65 70 75 80
Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
85 90 95
Leu Gln Glu Val Phe Tyr Leu Pro
100

<210> 328
<211> 287
<212> PRT

<213> Escherichia coli

<400> 328

Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
1 5 10 15
Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
20 25 30
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val
35 40 45
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys
50 55 60
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu
65 70 75 80
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys
85 90 95
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp
100 105 110
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala
115 120 125
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala
130 135 140
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu
145 150 155 160
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu
165 170 175
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala
180 185 190
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu
195 200 205
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His
210 215 220
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg
225 230 235 240
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu
245 250 255
Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
260 265 270
Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu
275 280 285

<210> 329

<211> 163

<212> PRT

<213> Escherichia coli

<400> 329

Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
1 5 10 15
Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
20 25 30
His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
35 40 45
Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
50 55 60
Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
65 70 75 80

Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
85 90 95
Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
100 105 110
Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
115 120 125
Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
130 135 140
Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu
145 150 155 160
Asp Asn Gly

<210> 330

<211> 648

<212> PRT

<213> Escherichia coli

<400> 330

Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
1 5 10 15
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
20 25 30
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
35 40 45
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
50 55 60
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
65 70 75 80
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
85 90 95
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
100 105 110
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
115 120 125
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
130 135 140
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
145 150 155 160
Ala Gly Gly Glu Trp Ile Val Ser Ala Gly Ala Leu Gly Ser Gly Ile
165 170 175
Phe Gly Phe Ile Asn Arg Leu Leu Ile Pro Thr Gly Leu His Gln Val
180 185 190
Leu Asn Thr Ile Ala Trp Phe Gln Ile Gly Glu Phe Thr Asn Ala Ala
195 200 205
Gly Thr Val Phe His Gly Asp Ile Asn Arg Phe Tyr Ala Gly Asp Gly
210 215 220
Thr Ala Gly Met Phe Met Ser Gly Phe Phe Pro Ile Met Met Phe Gly
225 230 235 240
Leu Pro Gly Ala Ala Leu Ala Met Tyr Phe Ala Ala Pro Lys Glu Arg
245 250 255
Arg Pro Met Val Gly Gly Met Leu Leu Ser Val Ala Val Thr Ala Phe
260 265 270
Leu Thr Gly Val Thr Glu Pro Leu Glu Phe Leu Phe Met Phe Leu Ala
275 280 285
Pro Leu Leu Tyr Leu Leu His Ala Leu Leu Thr Gly Ile Ser Leu Phe

Val 305	Ala 305	Thr 305	Leu 305	Leu 305	Gly 310	Ile 295	His 295	Ala 295	Gly 310	Phe 315	Ser 300	Phe 300	Ser 300	Ala 300	Gly 320
Ala 320	Ile 320	Asp 320	Tyr 320	Ala 325	Leu 325	Met 325	Tyr 325	Asn 325	Leu 330	Pro 315	Ala 330	Ala 330	Ser 330	Gln 335	Asn 320
Val 335	Trp 335	Met 335	Leu 340	Leu 340	Val 340	Met 340	Gly 340	Val 345	Ile 345	Phe 345	Phe 345	Ala 350	Ile 350	Tyr 350	Phe 340
Val 350	Val 355	Phe 355	Ser 355	Leu 355	Val 355	Ile 355	Arg 360	Met 360	Phe 360	Asn 365	Leu 365	Lys 365	Thr 365	Pro 365	Gly 350
Arg 370	Glu 370	Asp 370	Lys 370	Glu 370	Asp 375	Glu 375	Ile 375	Val 375	Thr 380	Glu 380	Glu 380	Ala 380	Asn 380	Ser 380	Asn 370
Thr 385	Glu 385	Glu 385	Gly 385	Leu 385	Thr 390	Gln 390	Leu 390	Ala 390	Thr 395	Asn 395	Tyr 395	Ile 395	Ala 400	Ala 400	Val 385
Gly 405	Gly 405	Thr 405	Asp 405	Asn 405	Leu 405	Lys 410	Ala 410	Ile 410	Asp 410	Ala 410	Cys 410	Ile 415	Thr 415	Arg 415	Leu 405
Arg 420	Leu 420	Thr 420	Val 420	Ala 420	Asp 425	Ser 425	Ala 425	Arg 425	Val 425	Asn 425	Asp 430	Thr 430	Met 430	Cys 430	Lys 420
Arg 435	Leu 435	Gly 435	Ala 435	Ser 435	Gly 440	Val 440	Val 440	Lys 440	Leu 445	Asn 445	Lys 445	Gln 445	Thr 445	Ile 445	Gln 435
Val 450	Ile 450	Val 450	Gly 450	Ala 450	Lys 455	Ala 455	Glu 455	Ser 455	Ile 460	Gly 460	Asp 460	Ala 460	Met 460	Lys 460	Lys 450
Val 465	Val 465	Ala 465	Arg 465	Gly 465	Pro 470	Val 470	Ala 470	Ala 470	Ala 475	Ser 475	Ala 475	Glu 475	Ala 475	Thr 475	Pro 465
Ala 480	Thr 480	Ala 480	Ala 480	Pro 485	Val 485	Ala 485	Lys 485	Pro 485	Gln 490	Ala 490	Val 490	Pro 490	Asn 490	Ala 490	Val 480
Ser 495	Ile 495	Ala 495	Glu 495	Leu 495	Val 500	Ser 500	Pro 500	Ile 505	Thr 505	Gly 505	Asp 510	Val 510	Val 510	Ala 510	Leu 495
Asp 515	Gln 515	Val 515	Pro 515	Asp 515	Glu 520	Ala 520	Phe 520	Ala 520	Ser 525	Lys 525	Ala 525	Val 525	Gly 525	Asp 525	Gly 515
Val 530	Ala 530	Val 530	Lys 530	Pro 530	Thr 535	Asp 535	Lys 535	Ile 535	Val 540	Val 540	Ser 540	Pro 540	Ala 540	Ala 540	Gly 530
Thr 545	Ile 545	Val 545	Lys 545	Ile 545	Phe 550	Asn 550	Thr 550	Asn 550	His 555	Ala 555	Phe 555	Cys 555	Leu 555	Glu 555	Thr 545
Glu 560	Lys 560	Gly 560	Ala 560	Glu 565	Ile 565	Val 565	Val 565	His 565	Met 570	Gly 570	Ile 570	Asp 570	Thr 570	Val 570	Ala 560
Leu 575	Glu 575	Gly 575	Lys 575	Gly 575	Phe 580	Lys 580	Arg 580	Leu 585	Val 585	Glu 585	Glu 585	Gly 585	Ala 585	Gln 585	Val 575
Ser 590	Ala 590	Gly 590	Gln 590	Pro 590	Ile 590	Leu 590	Glu 590	Met 590	Asp 590	Leu 590	Asp 590	Tyr 590	Leu 590	Asn 590	Ala 590
Asn 600	Ala 600	Arg 600	Ser 600	Met 600	Ile 600	Ser 600	Pro 600	Val 600	Val 600	Cys 600	Ser 600	Asn 600	Ile 600	Asp 600	Asp 600
Phe 605	Ser 605	Gly 605	Leu 605	Ile 605	Ile 610	Lys 610	Ala 610	Gln 610	Gly 610	His 610	Ile 610	Val 610	Ala 610	Gly 610	Gln 605
Thr 615	Pro 615	Leu 615	Tyr 615	Glu 615	Ile 615	Lys 615	Lys 615								615

```
<210> 331
<211> 412
<212> PRT
<213> Escherichia coli
```

```

<400> 331
Met  Lys  Thr  Ile  Phe  Arg  Tyr  Ile  Leu  Phe  Leu  Ala  Leu  Tyr  Ser  Cys
 1          5          10          15
Cys  Asn  Thr  Val  Ser  Ala  Tyr  Thr  Ser  Phe  Ile  Val  Gly  Asn  Asn  Ala
          20          25          30

```

Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
35 40 45
Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
50 55 60
Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
65 70 75 80
Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
85 90 95
Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
100 105 110
Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
115 120 125
Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
130 135 140
Gln Ser Pro Gly Ile Tyr Ile Gly Asp Pro Ser Asn Gln Glu Phe Phe
145 150 155 160
Phe Ser Val Thr Asp Ser Asp Leu Gln Thr Lys Gly Cys Asn Lys Ala
165 170 175
Asp Asp Tyr Asp Lys Phe Trp Ala Ile Gly Gly Ile Val His Asn Ile
180 185 190
Thr Val Glu Phe Tyr Thr Asp Thr Asn Phe Asp Pro Thr Leu Asn Gln
195 200 205
Gln Val Gln Leu Ser Ser Ser Ser Asn Tyr Leu Tyr Ser Phe Lys Ala
210 215 220
Tyr Ser Pro Gly Thr Lys Val Val Asp His Ser Asn His Ile Tyr Val
225 230 235 240
Asn Phe Thr Leu Asn Asn Val Lys Leu Thr Leu Pro Thr Cys Phe Thr
245 250 255
Ser Ile Leu Thr Gly Pro Ser Val Asn Gly Ser Thr Val Arg Met Gly
260 265 270
Glu Tyr Ser Ser Gly Thr Ile Lys Asn Gly Ala Ser Pro Val Pro Phe
275 280 285
Asp Ile Ser Leu Gln Asn Cys Ile Arg Val Arg Asn Ile Glu Thr Lys
290 295 300
Leu Val Thr Gly Lys Val Gly Thr Gln Asn Thr Gln Leu Leu Gly Asn
305 310 315 320
Thr Leu Thr Gly Ser Thr Ala Ala Lys Gly Val Gly Val Leu Ile Glu
325 330 335
Gly Leu Ala Thr Ser Lys Asn Pro Leu Met Thr Leu Lys Pro Asn Asp
340 345 350
Thr Asn Ser Val Tyr Ile Asp Tyr Glu Thr Glu Asp Asp Thr Ser Asp
355 360 365
Gly Val Tyr Pro Asn Gln Gly Asn Gly Thr Ser Gln Pro Leu His Phe
370 375 380
Gln Ala Thr Leu Lys Gln Asp Gly Asn Ile Ala Ile Glu Pro Gly Glu
385 390 395 400
Phe Lys Ala Thr Ser Thr Phe Gln Val Thr Tyr Pro
405 410

<210> 332

<211> 198

<212> PRT

<213> Escherichia coli

<400> 332

Met His Pro Thr Gln Arg Lys Leu Met Lys Arg Ile Ile Leu Phe Leu

Pro Ala Thr Phe Thr Val Thr Tyr Asn
 195 200

<210> 334
 <211> 203
 <212> PRT
 <213> Escherichia coli

<400> 334
 Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile
 1 5 10 15
 Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser
 20 25 30
 Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val
 35 40 45
 Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn
 50 55 60
 Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp
 65 70 75 80
 Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val
 85 90 95
 Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
 100 105 110
 Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
 115 120 125
 Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
 130 135 140
 Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
 145 150 155 160
 Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
 165 170 175
 Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
 180 185 190
 Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln
 195 200

<210> 335
 <211> 139
 <212> PRT
 <213> Escherichia coli

<400> 335
 Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
 1 5 10 15
 Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
 20 25 30
 Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
 35 40 45
 Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
 50 55 60
 Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
 65 70 75 80
 Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
 85 90 95
 Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp

100 105 110
 Val Asp Tyr Ala Gln Ala Ser Ala Glu Leu Ala Lys Ala Ile Ala Gln
 115 120 125
 Leu Arg Val Ile Glu Leu Thr Lys Lys Ala Met
 130 135

<210> 336
 <211> 460
 <212> PRT
 <213> Escherichia coli

<400> 336
 Met Ala Thr Gly Lys Ile Val Gln Val Ile Gly Ala Val Val Asp Val
 1 5 10 15
 Glu Phe Pro Gln Asp Ala Val Pro Arg Val Tyr Asp Ala Leu Glu Val
 20 25 30
 Gln Asn Gly Asn Glu Arg Leu Val Leu Glu Val Gln Gln Gln Leu Gly
 35 40 45
 Gly Gly Ile Val Arg Thr Ile Ala Met Gly Ser Ser Asp Gly Leu Arg
 50 55 60
 Arg Gly Leu Asp Val Lys Asp Leu Glu His Pro Ile Glu Val Pro Val
 65 70 75 80
 Gly Lys Ala Thr Leu Gly Arg Ile Met Asn Val Leu Gly Glu Pro Val
 85 90 95
 Asp Met Lys Gly Glu Ile Gly Glu Glu Arg Trp Ala Ile His Arg
 100 105 110
 Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu
 115 120 125
 Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly
 130 135 140
 Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met
 145 150 155 160
 Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val
 165 170 175
 Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His
 180 185 190
 Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly
 195 200 205
 Gln Met Asn Glu Pro Pro Gly Asn Arg Leu Arg Val Ala Leu Thr Gly
 210 215 220
 Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu
 225 230 235 240
 Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser
 245 250 255
 Ala Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu
 260 265 270
 Ala Glu Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Thr
 275 280 285
 Gly Ser Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu
 290 295 300
 Thr Asp Pro Ser Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Val
 305 310 315 320
 Val Leu Ser Arg Gln Ile Ala Ser Leu Gly Ile Tyr Pro Ala Val Asp
 325 330 335
 Pro Leu Asp Ser Thr Ser Arg Gln Leu Asp Pro Leu Val Val Gly Gln
 340 345 350

Glu	His	Tyr	Asp	Thr	Ala	Arg	Gly	Val	Gln	Ser	Ile	Leu	Gln	Arg	Tyr
	355						360					365			
Gln	Glu	Leu	Lys	Asp	Ile	Ile	Ala	Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser
	370					375					380				
Glu	Glu	Asp	Lys	Leu	Val	Val	Ala	Arg	Ala	Arg	Lys	Ile	Gln	Arg	Phe
385					390					395					400
Leu	Ser	Gln	Pro	Phe	Phe	Val	Ala	Glu	Val	Phe	Thr	Gly	Ser	Pro	Gly
				405					410					415	
Lys	Tyr	Val	Ser	Leu	Lys	Asp	Thr	Ile	Arg	Gly	Phe	Lys	Gly	Ile	Met
		420						425					430		
Glu	Gly	Glu	Tyr	Asp	His	Leu	Pro	Glu	Gln	Ala	Phe	Tyr	Met	Val	Gly
	435					440						445			
Ser	Ile	Glu	Glu	Ala	Val	Glu	Lys	Ala	Lys	Lys	Leu				
	450					455					460				

<210> 337

<211> 287

<212> PRT

<213> Escherichia coli

<400> 337

Met	Ala	Gly	Ala	Lys	Glu	Ile	Arg	Ser	Lys	Ile	Ala	Ser	Val	Gln	Asn
1				5				10					15		
Thr	Gln	Lys	Ile	Thr	Lys	Ala	Met	Glu	Met	Val	Ala	Ala	Ser	Lys	Met
		20						25					30		
Arg	Lys	Ser	Gln	Asp	Arg	Met	Ala	Ala	Ser	Arg	Pro	Tyr	Ala	Glu	Thr
	35					40						45			
Met	Arg	Lys	Val	Ile	Gly	His	Leu	Ala	His	Gly	Asn	Leu	Glu	Tyr	Lys
50					55					60					
His	Pro	Tyr	Leu	Glu	Asp	Arg	Asp	Val	Lys	Arg	Val	Gly	Tyr	Leu	Val
65				70					75					80	
Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Ile	Asn	Leu	Phe
			85					90					95		
Lys	Lys	Leu	Leu	Ala	Glu	Met	Lys	Thr	Trp	Thr	Asp	Lys	Gly	Val	Gln
		100						105					110		
Cys	Asp	Leu	Ala	Met	Ile	Gly	Ser	Lys	Gly	Val	Ser	Phe	Phe	Asn	Ser
	115					120						125			
Val	Gly	Gly	Asn	Val	Val	Ala	Gln	Val	Thr	Gly	Met	Gly	Asp	Asn	Pro
	130					135					140				
Ser	Leu	Ser	Glu	Leu	Ile	Gly	Pro	Val	Lys	Val	Met	Leu	Gln	Ala	Tyr
145				150						155					160
Asp	Glu	Gly	Arg	Leu	Asp	Lys	Leu	Tyr	Ile	Val	Ser	Asn	Lys	Phe	Ile
			165					170						175	
Asn	Thr	Met	Ser	Gln	Val	Pro	Thr	Ile	Ser	Gln	Leu	Leu	Pro	Leu	Pro
		180						185					190		
Ala	Ser	Asp	Asp	Asp	Asp	Leu	Lys	His	Lys	Ser	Trp	Asp	Tyr	Leu	Tyr
	195					200						205			
Glu	Pro	Asp	Pro	Lys	Ala	Leu	Leu	Asp	Thr	Leu	Leu	Arg	Arg	Tyr	Val
	210					215					220				
Glu	Ser	Gln	Val	Tyr	Gln	Gly	Val	Val	Glu	Asn	Leu	Ala	Ser	Glu	Gln
225					230					235					240
Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Gly	Gly	Ser
			245					250						255	
Leu	Ile	Lys	Glu	Leu	Gln	Leu	Val	Tyr	Asn	Lys	Ala	Arg	Gln	Ala	Ser
		260						265					270		
Ile	Thr	Gln	Glu	Leu	Thr	Glu	Ile	Val	Ser	Gly	Ala	Ala	Ala	Val	

275

280

285

<210> 338

<211> 513

<212> PRT

<213> Escherichia coli

<400> 338

```

Met Gln Leu Asn Ser Thr Glu Ile Ser Glu Leu Ile Lys Gln Arg Ile
 1           5           10           15
Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
 20           25           30
Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
 35           40           45
Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
 50           55           60
Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
 65           70           75           80
Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
 85           90           95
Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
100           105           110
Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
115           120           125
Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln
130           135           140
Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly
145           150           155           160
Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
165           170           175
Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys
180           185           190
Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val
195           200           205
Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val
210           215           220
Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr
225           230           235           240
Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala
245           250           255
Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln
260           265           270
Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly
275           280           285
Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val
290           295           300
Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys
305           310           315           320
Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp
325           330           335
Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
340           345           350
Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val
355           360           365
Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
370           375           380

```

Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr
 385 390 395 400
 Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala
 405 410 415
 Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys
 420 425 430
 Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu
 435 440 445
 Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile
 450 455 460
 Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala
 465 470 475 480
 Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile
 485 490 495
 Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser
 500 505 510
 Trp

<210> 339
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 339
 Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu
 20 25 30
 Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu
 35 40 45
 Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val
 50 55 60
 Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met
 65 70 75 80
 Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe
 85 90 95
 Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile
 100 105 110
 Ser Ala Ala Ala Leu Ser Glu Gln Leu Ala Lys Ile Ser Ala Ala
 115 120 125
 Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp
 130 135 140
 Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile
 145 150 155 160
 Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln
 165 170 175
 Ser

<210> 340
 <211> 156
 <212> PRT
 <213> Escherichia coli

<400> 340

```

Met Asn Leu Asn Ala Thr Ile Leu Gly Gln Ala Ile Ala Phe Val Leu
 1          5          10          15
Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala
 20          25          30
Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu
 35          40          45
Arg Ala His Lys Asp Leu Asp Leu Ala Lys Ala Ser Ala Thr Asp Gln
 50          55          60
Leu Lys Lys Ala Lys Ala Glu Ala Gln Val Ile Ile Glu Gln Ala Asn
 65          70          75          80
Lys Arg Arg Ser Gln Ile Leu Asp Glu Ala Lys Ala Glu Ala Glu Gln
 85          90          95
Glu Arg Thr Lys Ile Val Ala Gln Ala Gln Ala Glu Ile Glu Ala Glu
100          105          110
Arg Lys Arg Ala Arg Glu Glu Leu Arg Lys Gln Val Ala Ile Leu Ala
115          120          125
Val Ala Gly Ala Glu Lys Ile Ile Glu Arg Ser Val Asp Glu Ala Ala
130          135          140
Asn Ser Asp Ile Val Asp Lys Leu Val Ala Glu Leu
145          150          155

```

<210> 341

<211> 79

<212> PRT

<213> Escherichia coli

<400> 341

```

Met Glu Asn Leu Asn Met Asp Leu Leu Tyr Met Ala Ala Ala Val Met
 1          5          10          15
Met Gly Leu Ala Ala Ile Gly Ala Ala Ile Gly Ile Gly Ile Leu Gly
 20          25          30
Gly Lys Phe Leu Glu Gly Ala Ala Arg Gln Pro Asp Leu Ile Pro Leu
 35          40          45
Leu Arg Thr Gln Phe Phe Ile Val Met Gly Leu Val Asp Ala Ile Pro
 50          55          60
Met Ile Ala Val Gly Leu Gly Leu Tyr Val Met Phe Ala Val Ala
 65          70          75

```

<210> 342

<211> 271

<212> PRT

<213> Escherichia coli

<400> 342

```

Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
 1          5          10          15
Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
 20          25          30
Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
 35          40          45
Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
 50          55          60
Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
 65          70          75          80

```


[illegible]
$$\begin{array}{ll} \langle 210 \rangle & 345 \\ \langle 211 \rangle & 325 \end{array}$$

<212> PRT

<213> Escherichia coli

<400> 345

Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp
1 5 10 15
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met
20 25 30
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile
35 40 45
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala
50 55 60
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile
65 70 75 80
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys
85 90 95
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile
100 105 110
Asn Arg Tyr Thr Ala Asp Arg Arg Leu Arg His Asp Asp Ala Tyr Thr
115 120 125
Pro Asp Asn Val Ala Gly Lys Arg Pro Asp Arg Ala Thr Leu Val Tyr
130 135 140
Thr Gln Arg Cys Lys Glu Ala Trp Lys Asp Val Pro Val Ile Leu Gly
145 150 155 160
Gly Ile Glu Ala Ser Leu Arg Arg Thr Ala His Tyr Asp Tyr Trp Ser
165 170 175
Asp Thr Val Arg Arg Ser Val Leu Val Asp Ser Lys Ala Asp Met Leu
180 185 190
Met Phe Gly Asn Gly Glu Arg Pro Leu Val Glu Val Ala His Arg Leu
195 200 205
Ala Met Gly Glu Pro Ile Ser Glu Ile Arg Asp Val Arg Asn Thr Ala
210 215 220
Ile Ile Val Lys Glu Ala Leu Pro Gly Trp Ser Gly Val Asp Ser Thr
225 230 235 240
Arg Leu Asp Thr Pro Gly Lys Ile Asp Pro Ile Pro His Pro Tyr Gly
245 250 255
Glu Asp Leu Pro Cys Ala Asp Asn Lys Pro Val Ala Pro Lys Lys Gln
260 265 270
Glu Ala Lys Ala Val Thr Val Gln Pro Pro Arg Pro Lys Pro Trp Glu
275 280 285
Lys Thr Tyr Val Leu Leu Pro Ser Phe Glu Lys Val Lys Gly Asp Lys
290 295 300
Val Leu Tyr Ala His Ala Ser Arg Ile Leu His His Glu Thr Asn Pro
305 310 315 320
Ala Val Pro Ala His
325

<210> 346

<211> 226

<212> PRT

<213> Escherichia coli

<400> 346

Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile
1 5 10 15
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly

Pro	Ala	Met	Ser	Met	Val	Ser	Tyr	Ala	Ala	Gly	Thr	Arg	Tyr	Leu	Ser
		195					200					205			
Leu	Leu	Gly	Gly	Thr	Cys	Leu	Ser	Phe	Tyr	Asp	Trp	Tyr	Cys	Asp	Leu
		210				215					220				
Pro	Pro	Ala	Ser	Pro	Met	Thr	Trp	Gly	Glu	Gln	Thr	Asp	Val	Pro	Glu
225					230					235					240
Ser	Ala	Asp	Trp	Tyr	Asn	Ser	Ser	Tyr	Ile	Ile	Ala	Trp	Gly	Ser	Asn
				245					250					255	
Val	Pro	Gln	Thr	Arg	Thr	Pro	Asp	Ala	His	Phe	Phe	Thr	Glu	Val	Arg
			260					265					270		
Tyr	Lys	Gly	Thr	Lys	Thr	Ile	Ala	Ile	Thr	Pro	Asp	Tyr	Ser	Glu	Val
		275					280					285			
Ala	Lys	Leu	Cys	Asp	Gln	Trp	Leu	Ala	Pro	Lys	Gln	Gly	Thr	Asp	Ser
		290				295					300				
Ala	Leu	Ala	Met	Ala	Met	Gly	His	Val	Ile	Leu	Lys	Glu	Phe	His	Leu
305					310					315					320
Asp	Asn	Pro	Ser	Asp	Tyr	Phe	Ile	Asn	Tyr	Cys	Arg	Arg	Tyr	Ser	Asp
				325					330					335	
Met	Pro	Met	Leu	Val	Met	Leu	Glu	Pro	Arg	Asp	Asp	Gly	Ser	Tyr	Val
			340					345					350		
Pro	Gly	Arg	Met	Ile	Arg	Ala	Ser	Asp	Leu	Val	Asp	Gly	Leu	Gly	Glu
		355					360					365			
Ser	Asn	Asn	Pro	Gln	Trp	Lys	Thr	Val	Ala	Val	Asn	Thr	Ala	Gly	Glu
		370				375					380				
Leu	Val	Val	Pro	Asn	Gly	Ser	Ile	Gly	Phe	Arg	Trp	Gly	Glu	Lys	Gly
385					390					395					400
Lys	Trp	Asn	Leu	Glu	Ser	Ile	Ala	Ala	Gly	Thr	Glu	Thr	Glu	Leu	Ser
				405					410					415	
Leu	Thr	Leu	Leu	Gly	Gln	His	Asp	Ala	Val	Ala	Gly	Val	Ala	Phe	Pro
			420					425					430		
Tyr	Phe	Gly	Gly	Ile	Glu	Asn	Pro	His	Phe	Arg	Ser	Val	Lys	His	Asn
		435					440					445			
Pro	Val	Leu	Val	Arg	Gln	Leu	Pro	Val	Lys	Asn	Leu	Thr	Leu	Val	Asp
		450				455					460				
Gly	Asn	Thr	Cys	Pro	Val	Val	Ser	Val	Tyr	Asp	Leu	Val	Leu	Ala	Asn
465				470						475					480
Tyr	Gly	Leu	Asp	Arg	Gly	Leu	Glu	Asp	Glu	Asn	Ser	Ala	Lys	Asp	Tyr
			485						490					495	
Ala	Glu	Ile	Lys	Pro	Tyr	Thr	Pro	Ala	Trp	Gly	Glu	Gln	Ile	Thr	Gly
			500					505					510		
Val	Pro	Arg	Gln	Tyr	Ile	Glu	Thr	Ile	Ala	Arg	Glu	Phe	Ala	Asp	Thr
		515					520					525			
Ala	His	Lys	Thr	His	Gly	Arg	Ser	Met	Ile	Ile	Leu	Gly	Ala	Gly	Val
		530				535					540				
Asn	His														

[illegible]

```

Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser
1105          1110          1115          1120
Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu
          1125          1130          1135
Val Phe Asn Ala Asn Gly Ala Leu Thr Ala Arg Ala Val Val Ser Gln
          1140          1145          1150
Arg Val Pro Pro Gly Met Thr Met Met Tyr His Ala Gln Glu Arg Ile
          1155          1160          1165
Met Asn Ile Pro Gly Ser Glu Val Thr Gly Met Arg Gly Gly Ile His
          1170          1175          1180
Asn Ser Val Thr Arg Val Cys Pro Lys Pro Thr His Met Ile Gly Gly
1185          1190          1195          1200
Tyr Ala Gln Leu Ala Trp Gly Phe Asn Tyr Tyr Gly Thr Val Gly Ser
          1205          1210          1215
Asn Arg Asp Glu Phe Ile Met Ile Arg Lys Met Lys Asn Val Asn Trp
          1220          1225          1230
Leu Asp Asp Glu Gly Arg Asp Gln Val Gln Glu Ala Lys Lys
          1235          1240          1245

```

```

<210> 350
<211> 165
<212> PRT
<213> Escherichia coli

```

```

<400> 350
Met Asp Leu Ser Gln Leu Thr Pro Arg Arg Pro Tyr Leu Leu Arg Ala
 1          5          10          15
Phe Tyr Glu Trp Leu Leu Asp Asn Gln Leu Thr Pro His Leu Val Val
          20          25          30
Asp Val Thr Leu Pro Gly Val Gln Val Pro Met Glu Tyr Ala Arg Asp
          35          40          45
Gly Gln Ile Val Leu Asn Ile Ala Pro Arg Ala Val Gly Asn Leu Glu
          50          55          60
Leu Ala Asn Asp Glu Val Arg Phe Asn Ala Arg Phe Gly Gly Ile Pro
65          70          75          80
Arg Gln Val Ser Val Pro Leu Ala Ala Val Leu Ala Ile Tyr Ala Arg
          85          90          95
Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu
          100          105          110
Asp Thr Ser Ile Met Asn Asp Glu Glu Ala Ser Ala Asp Asn Glu Thr
          115          120          125
Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr
          130          135          140
His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala
145          150          155          160
Leu Arg Val Val Lys
          165

```

```

<210> 351
<211> 212
<212> PRT
<213> Escherichia coli

```

```

<400> 351
Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly

```



```

1           5           10           15
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys
20           25           30
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln
35           40           45
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp
50           55           60
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp
65           70           75           80
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg
85           90           95
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr
100          105          110
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala
115          120          125
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly
130          135          140
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr
145          150          155          160
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser
165          170          175
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu
180          185          190
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg
195          200          205
Leu Gly Arg Ser
210

```

<210> 352

<211> 505

<212> PRT

<213> Escherichia coli

<400> 352

```

Met Ser Glu Gln His Ala Gln Gly Ala Asp Ala Val Val Asp Leu Asn
1           5           10           15
Asn Glu Leu Lys Thr Arg Arg Glu Lys Leu Ala Asn Leu Arg Glu Gln
20           25           30
Gly Ile Ala Phe Pro Asn Asp Phe Arg Arg Asp His Thr Ser Asp Gln
35           40           45
Leu His Ala Glu Phe Asp Gly Lys Glu Asn Glu Glu Leu Glu Ala Leu
50           55           60
Asn Ile Glu Val Ala Val Ala Gly Arg Met Met Thr Arg Arg Ile Met
65           70           75           80
Gly Lys Ala Ser Phe Val Thr Leu Gln Asp Val Gly Gly Arg Ile Gln
85           90           95
Leu Tyr Val Ala Arg Asp Asp Leu Pro Glu Gly Val Tyr Asn Glu Gln
100          105          110
Phe Lys Lys Trp Asp Leu Gly Asp Ile Leu Gly Ala Lys Gly Lys Leu
115          120          125
Phe Lys Thr Lys Thr Gly Glu Leu Ser Ile His Cys Thr Glu Leu Arg
130          135          140
Leu Leu Thr Lys Ala Leu Arg Pro Leu Pro Asp Lys Phe His Gly Leu
145          150          155          160
Gln Asp Gln Glu Ala Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Ser
165          170          175

```

Asn	Asp	Glu	Ser	Arg	Asn	Thr	Phe	Lys	Val	Arg	Ser	Gln	Ile	Leu	Ser
			180					185					190		
Gly	Ile	Arg	Gln	Phe	Met	Val	Asn	Arg	Gly	Phe	Met	Glu	Val	Glu	Thr
		195					200					205			
Pro	Met	Met	Gln	Val	Ile	Pro	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Ile
		210				215					220				
Thr	His	His	Asn	Ala	Leu	Asp	Leu	Asp	Met	Tyr	Leu	Arg	Ile	Ala	Pro
225					230					235					240
Glu	Leu	Tyr	Leu	Lys	Arg	Leu	Val	Val	Gly	Gly	Phe	Glu	Arg	Val	Phe
				245					250					255	
Glu	Ile	Asn	Arg	Asn	Phe	Arg	Asn	Glu	Gly	Ile	Ser	Val	Arg	His	Asn
			260					265					270		
Pro	Glu	Phe	Thr	Met	Met	Glu	Leu	Tyr	Met	Ala	Tyr	Ala	Asp	Tyr	Lys
		275					280					285			
Asp	Leu	Ile	Glu	Leu	Thr	Glu	Ser	Leu	Phe	Arg	Thr	Leu	Ala	Gln	Asp
		290				295					300				
Ile	Leu	Gly	Lys	Thr	Glu	Val	Thr	Tyr	Gly	Asp	Val	Thr	Leu	Asp	Phe
305					310					315					320
Gly	Lys	Pro	Phe	Glu	Lys	Leu	Thr	Met	Arg	Glu	Ala	Ile	Lys	Lys	Tyr
				325					330					335	
Arg	Pro	Glu	Thr	Asp	Met	Ala	Asp	Leu	Asp	Asn	Phe	Asp	Ser	Ala	Lys
			340				345						350		
Ala	Ile	Ala	Glu	Ser	Ile	Gly	Ile	His	Val	Glu	Lys	Ser	Trp	Gly	Leu
		355					360					365			
Gly	Arg	Ile	Val	Thr	Glu	Ile	Phe	Glu	Glu	Val	Ala	Glu	Ala	His	Leu
		370				375					380				
Ile	Gln	Pro	Thr	Phe	Ile	Thr	Glu	Tyr	Pro	Ala	Glu	Val	Ser	Pro	Leu
385					390					395					400
Ala	Arg	Arg	Asn	Asp	Val	Asn	Pro	Glu	Ile	Thr	Asp	Arg	Phe	Glu	Phe
				405					410					415	
Phe	Ile	Gly	Gly	Arg	Glu	Ile	Gly	Asn	Gly	Phe	Ser	Glu	Leu	Asn	Asp
			420					425					430		
Ala	Glu	Asp	Gln	Ala	Gln	Arg	Phe	Leu	Asp	Gln	Val	Ala	Ala	Lys	Asp
		435					440					445			
Ala	Gly	Asp	Asp	Glu	Ala	Met	Phe	Tyr	Asp	Glu	Asp	Tyr	Val	Thr	Ala
		450				455					460				
Leu	Glu	His	Gly	Leu	Pro	Pro	Thr	Ala	Gly	Leu	Gly	Ile	Gly	Ile	Asp
465					470					475					480
Arg	Met	Val	Met	Leu	Phe	Thr	Asn	Ser	His	Thr	Ile	Arg	Asp	Val	Ile
				485					490					495	
Leu	Phe	Pro	Ala	Met	Arg	Pro	Val	Lys							
			500					505							

```
<210> 353
<211> 365
<212> PRT
<213> Escherichia coli
```

<400> 353

Met	Phe	Glu	Ile	Asn	Pro	Val	Asn	Asn	Arg	Ile	Gln	Asp	Leu	Thr	Glu
1				5					10					15	
Arg	Ser	Asp	Val	Leu	Arg	Gly	Tyr	Leu	Asp	Tyr	Asp	Ala	Lys	Lys	Glu
			20					25					30		
Arg	Leu	Glu	Glu	Val	Asn	Ala	Glu	Leu	Glu	Gln	Pro	Asp	Val	Trp	Asn
		35					40					45			
Glu	Pro	Glu	Arg	Ala	Gln	Ala	Leu	Gly	Lys	Glu	Arg	Ser	Ser	Leu	Glu

	50					55					60				
Ala 65	Val	Val	Asp	Thr	Leu 70	Asp	Gln	Met	Lys	Gln 75	Gly	Leu	Glu	Asp	Val 80
Ser	Gly	Leu	Leu	Glu 85	Leu	Ala	Val	Glu	Ala 90	Asp	Asp	Glu	Glu	Thr 95	Phe
Asn	Glu	Ala	Val	Ala 100	Glu	Leu	Asp	Ala 105	Leu	Glu	Glu	Lys	Leu	Ala 110	Gln
Leu	Glu	Phe	Arg	Arg 115	Met	Phe	Ser	Gly 120	Glu	Tyr	Asp	Ser	Ala	Asp 125	Cys
Tyr	Leu	Asp	Ile	Gln 130	Ala	Gly 135	Ser	Gly 135	Gly	Thr	Glu 140	Ala	Gln	Asp 145	Trp
Ala 145	Ser	Met	Leu	Glu 150	Arg	Met	Tyr	Leu	Arg	Trp 155	Ala	Glu	Ser	Arg 160	Gly
Phe	Lys	Thr	Glu	Ile 165	Ile	Glu	Glu	Ser	Glu 170	Gly	Glu	Val	Ala	Gly 175	Ile
Lys	Ser	Val	Thr 180	Ile	Lys	Ile	Ser	Gly 185	Asp	Tyr	Ala	Tyr	Gly 190	Trp	Leu
Arg	Thr	Glu 195	Thr	Gly	Val	His	Arg 200	Leu	Val	Arg	Lys	Ser 205	Pro	Phe	Asp
Ser	Gly 210	Gly	Arg	Arg	His	Thr 215	Ser	Phe	Ser	Ser	Ala 220	Phe	Val	Tyr	Pro
Glu 225	Val	Asp	Asp	Asp 230	Ile	Asp	Ile	Glu	Ile	Asn 235	Pro	Ala	Asp	Leu	Arg 240
Ile	Asp	Val	Tyr	Arg 245	Thr	Ser	Gly	Ala	Gly 250	Gly	Gln	His	Val	Asn 255	Arg
Thr	Glu	Ser	Ala 260	Val	Arg	Ile	Thr	His 265	Ile	Pro	Thr	Gly	Ile 270	Val	Thr
Gln	Cys	Gln 275	Asn	Asp	Arg	Ser	Gln 280	His	Lys	Asn	Lys	Asp 285	Gln	Ala	Met
Lys	Gln 290	Met	Lys	Ala	Lys	Leu 295	Tyr	Glu	Leu	Glu	Met 300	Gln	Lys	Lys	Asn
Ala 305	Glu	Lys	Gln	Ala 310	Met	Glu	Asp	Asn	Lys	Ser 315	Asp	Ile	Gly	Trp	Gly 320
Ser	Gln	Ile	Arg	Ser 325	Tyr	Val	Leu	Asp	Asp 330	Ser	Arg	Ile	Lys	Asp 335	Leu
Arg	Thr	Gly	Val 340	Glu	Thr	Arg	Asn	Thr 345	Gln	Ala	Val	Leu	Asp 350	Gly	Ser
Leu	Asp	Gln 355	Phe	Ile	Glu	Ala	Ser 360	Leu	Lys	Ala	Gly	Leu			

```
<210> 354
<211> 577
<212> PRT
<213> Escherichia coli
```

<400> 354															
Met	Lys	Gln	Gln	Ile	Gln	Leu	Arg	Arg	Arg	Glu	Val	Asp	Glu	Thr	Ala
1				5					10					15	
Asp	Leu	Pro	Ala	Glu	Leu	Pro	Pro	Leu	Leu	Arg	Arg	Leu	Tyr	Ala	Ser
			20					25					30		
Arg	Gly	Val	Arg	Ser	Ala	Gln	Glu	Leu	Glu	Arg	Ser	Val	Lys	Gly	Met
		35					40					45			
Leu	Pro	Trp	Gln	Gln	Leu	Ser	Gly	Val	Glu	Lys	Ala	Val	Glu	Ile	Leu
	50					55					60				
Tyr	Asn	Ala	Phe	Arg	Glu	Gly	Thr	Arg	Ile	Ile	Val	Val	Gly	Asp	Phe
65					70					75					80

Asp Ala Asp Gly Ala Thr Ser Thr Ala Leu Ser Val Leu Ala Met Arg
 85 90 95
 Ser Leu Gly Cys Ser Asn Ile Asp Tyr Leu Val Pro Asn Arg Phe Glu
 100 105 110
 Asp Gly Tyr Gly Leu Ser Pro Glu Val Val Asp Gln Ala His Ala Arg
 115 120 125
 Gly Ala Gln Leu Ile Val Thr Val Asp Asn Gly Ile Ser Ser His Ala
 130 135 140
 Gly Val Glu His Ala Arg Ser Leu Gly Ile Pro Val Ile Val Thr Asp
 145 150 155 160
 His His Leu Pro Gly Asp Thr Leu Pro Ala Ala Glu Ala Ile Ile Asn
 165 170 175
 Pro Asn Leu Arg Asp Cys Asn Phe Pro Ser Lys Ser Leu Ala Gly Val
 180 185 190
 Gly Val Ala Phe Tyr Leu Met Leu Ala Leu Arg Thr Phe Leu Arg Asp
 195 200 205
 Gln Gly Trp Phe Asp Glu Arg Asn Ile Ala Ile Pro Asn Leu Ala Glu
 210 215 220
 Leu Leu Asp Leu Val Ala Leu Gly Thr Val Ala Asp Val Val Pro Leu
 225 230 235 240
 Asp Ala Asn Asn Arg Ile Leu Thr Trp Gln Gly Met Ser Arg Ile Arg
 245 250 255
 Ala Gly Lys Cys Arg Pro Gly Ile Lys Ala Leu Leu Glu Val Ala Asn
 260 265 270
 Arg Asp Ala Gln Lys Leu Ala Ala Ser Asp Leu Gly Phe Ala Leu Gly
 275 280 285
 Pro Arg Leu Asn Ala Ala Gly Arg Leu Asp Asp Met Ser Val Gly Val
 290 295 300
 Ala Leu Leu Leu Cys Asp Asn Ile Gly Glu Ala Arg Val Leu Ala Asn
 305 310 315 320
 Glu Leu Asp Ala Leu Asn Gln Thr Arg Lys Glu Ile Glu Gln Gly Met
 325 330 335
 Gln Ile Glu Ala Leu Thr Leu Cys Glu Lys Leu Glu Arg Ser Arg Asp
 340 345 350
 Thr Leu Pro Gly Gly Leu Ala Met Tyr His Pro Glu Trp His Gln Gly
 355 360 365
 Val Val Gly Ile Leu Ala Ser Arg Ile Lys Glu Arg Phe His Arg Pro
 370 375 380
 Val Ile Ala Phe Ala Pro Ala Gly Asp Gly Thr Leu Lys Gly Ser Gly
 385 390 395 400
 Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp
 405 410 415
 Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala
 420 425 430
 Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg
 435 440 445
 Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly
 450 455 460
 Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu
 465 470 475 480
 Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro
 485 490 495
 Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val
 500 505 510
 Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro
 515 520 525
 Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp

530 535 540
 Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu
 545 550 555 560
 Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro
 565 570 575
 Ile

<210> 355
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 355
 Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
 1 5 10 15
 Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
 20 25 30
 Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
 35 40 45
 Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 50 55 60
 His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 65 70 75 80
 Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 85 90 95
 Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 100 105 110
 Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125
 Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140
 Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160
 Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 225 230 235

<210> 356
 <211> 298
 <212> PRT
 <213> Escherichia coli

<400> 356
 Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1 5 10 15
 Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
 20 25 30

```

Leu Ser Met Met Val Glu Trp Leu His His Arg Gly Leu Thr Leu Ala
 35                                40                                45
Thr Ala Gln Ser Asp Asp Leu Gln Ala Leu Leu Ala Glu Arg Leu Glu
 50                                55                                60
Gly Gly Tyr Lys Ala Thr Ser Ser Ala Arg Leu Leu Ser Ala Val Arg
 65                                70                                75                                80
Arg Leu Phe Gln Tyr Leu Tyr Arg Glu Lys Phe Arg Glu Asp Asp Pro
      85                                90                                95
Ser Ala His Leu Ala Ser Pro Lys Leu Pro Gln Arg Leu Pro Lys Asp
      100                                105                                110
Leu Ser Glu Ala Gln Val Glu Arg Leu Leu Gln Ala Pro Leu Ile Asp
      115                                120                                125
Gln Pro Leu Glu Leu Arg Asp Lys Ala Met Leu Glu Val Leu Tyr Ala
      130                                135                                140
Thr Gly Leu Arg Val Ser Glu Leu Val Gly Leu Thr Met Ser Asp Ile
 145                                150                                155                                160
Ser Leu Arg Gln Gly Val Val Arg Val Ile Gly Lys Gly Asn Lys Glu
      165                                170                                175
Arg Leu Val Pro Leu Gly Glu Glu Ala Val Tyr Trp Leu Glu Thr Tyr
      180                                185                                190
Leu Glu His Gly Arg Pro Trp Leu Leu Asn Gly Val Ser Ile Asp Val
      195                                200                                205
Leu Phe Pro Ser Gln Arg Ala Gln Gln Met Thr Arg Gln Thr Phe Trp
      210                                215                                220
His Arg Ile Lys His Tyr Ala Val Leu Ala Gly Ile Asp Ser Glu Lys
 225                                230                                235                                240
Leu Ser Pro His Val Leu Arg His Ala Phe Ala Thr His Leu Leu Asn
      245                                250                                255
His Gly Ala Asp Leu Arg Val Val Gln Met Leu Leu Gly His Ser Asp
      260                                265                                270
Leu Ser Thr Thr Gln Ile Tyr Thr His Val Ala Thr Glu Arg Leu Arg
      275                                280                                285
Gln Leu His Gln Gln His His Pro Arg Ala
      290                                295

```

<210> 357

<211> 367

<212> PRT

<213> Escherichia coli

<400> 357

```

Met Ser Asp Ser Gln Thr Leu Val Val Lys Leu Gly Thr Ser Val Leu
 1                                5                                10                                15
Thr Gly Gly Ser Arg Arg Leu Asn Arg Ala His Ile Val Glu Leu Val
      20                                25                                30
Arg Gln Cys Ala Gln Leu His Ala Ala Gly His Arg Ile Val Ile Val
      35                                40                                45
Thr Ser Gly Ala Ile Ala Ala Gly Arg Glu His Leu Gly Tyr Pro Glu
 50                                55                                60
Leu Pro Ala Thr Ile Ala Ser Lys Gln Leu Leu Ala Ala Val Gly Gln
 65                                70                                75                                80
Ser Arg Leu Ile Gln Leu Trp Glu Gln Leu Phe Ser Ile Tyr Gly Ile
      85                                90                                95
His Val Gly Gln Met Leu Leu Thr Arg Ala Asp Met Glu Asp Arg Glu
      100                                105                                110
Arg Phe Leu Asn Ala Arg Asp Thr Leu Arg Ala Leu Leu Asp Asn Asn

```

```

      115              120              125
Ile Val Pro Val Ile Asn Glu Asn Asp Ala Val Ala Thr Ala Glu Ile
 130              135              140
Lys Val Gly Asp Asn Asp Asn Leu Ser Ala Leu Ala Ala Ile Leu Ala
 145              150              155              160
Gly Ala Asp Lys Leu Leu Leu Thr Asp Gln Lys Gly Leu Tyr Thr
      165              170              175
Ala Asp Pro Arg Ser Asn Pro Gln Ala Glu Leu Ile Lys Asp Val Tyr
      180              185              190
Gly Ile Asp Asp Ala Leu Arg Ala Ile Ala Gly Asp Ser Val Ser Gly
      195              200              205
Leu Gly Thr Gly Gly Met Ser Thr Lys Leu Gln Ala Ala Asp Val Ala
      210              215              220
Cys Arg Ala Gly Ile Asp Thr Ile Ile Ala Ala Gly Ser Lys Pro Gly
 225              230              235              240
Val Ile Gly Asp Val Met Glu Gly Ile Ser Val Gly Thr Leu Phe His
      245              250              255
Ala Gln Ala Thr Pro Leu Glu Asn Arg Lys Arg Trp Ile Phe Gly Ala
      260              265              270
Pro Pro Ala Gly Glu Ile Thr Val Asp Glu Gly Ala Thr Ala Ala Ile
      275              280              285
Leu Glu Arg Gly Ser Ser Leu Leu Pro Lys Gly Ile Lys Ser Val Thr
      290              295              300
Gly Asn Phe Ser Arg Gly Glu Val Ile Arg Ile Cys Asn Leu Glu Gly
 305              310              315              320
Arg Asp Ile Ala His Gly Val Ser Arg Tyr Asn Ser Asp Ala Leu Arg
      325              330              335
Arg Ile Ala Gly His His Ser Gln Glu Ile Asp Ala Ile Leu Gly Tyr
      340              345              350
Glu Tyr Gly Pro Val Ala Val His Arg Asp Asp Met Ile Thr Arg
      355              360              365

```

<210> 358

<211> 417

<212> PRT

<213> Escherichia coli

<400> 358

```

Met Leu Glu Gln Met Gly Ile Ala Ala Lys Gln Ala Ser Tyr Lys Leu
 1              5              10              15
Ala Gln Leu Ser Arg Glu Lys Asn Arg Val Leu Glu Lys Ile Ala
      20              25              30
Asp Glu Leu Glu Ala Gln Ser Glu Ile Ile Leu Asn Ala Asn Ala Gln
      35              40              45
Asp Val Ala Asp Ala Arg Ala Asn Gly Leu Ser Glu Ala Met Leu Asp
      50              55              60
Arg Leu Ala Leu Thr Pro Ala Arg Leu Lys Gly Ile Ala Asp Asp Val
      65              70              75              80
Arg Gln Val Cys Asn Leu Ala Asp Pro Val Gly Gln Val Ile Asp Gly
      85              90              95
Gly Val Leu Asp Ser Gly Leu Arg Leu Glu Arg Arg Arg Val Pro Leu
      100              105              110
Gly Val Ile Gly Val Ile Tyr Glu Ala Arg Pro Asn Val Thr Val Asp
      115              120              125
Val Ala Ser Leu Cys Leu Lys Thr Gly Asn Ala Val Ile Leu Arg Gly
      130              135              140

```

Gly Lys Glu Thr Cys Arg Thr Asn Ala Ala Thr Val Ala Val Ile Gln
145 150 155 160
Asp Ala Leu Lys Ser Cys Gly Leu Pro Ala Gly Ala Val Gln Ala Ile
165 170 175
Asp Asn Pro Asp Arg Ala Leu Val Ser Glu Met Leu Arg Met Asp Lys
180 185 190
Tyr Ile Asp Met Leu Ile Pro Arg Gly Gly Ala Gly Leu His Lys Leu
195 200 205
Cys Arg Glu Gln Ser Thr Ile Pro Val Ile Thr Gly Gly Ile Gly Val
210 215 220
Cys His Ile Tyr Val Asp Glu Ser Val Glu Ile Ala Glu Ala Leu Lys
225 230 235 240
Val Ile Val Asn Ala Lys Thr Gln Arg Pro Ser Thr Cys Asn Thr Val
245 250 255
Glu Thr Leu Leu Val Asn Lys Asn Ile Ala Asp Ser Phe Leu Pro Ala
260 265 270
Leu Ser Lys Gln Met Ala Glu Ser Gly Val Thr Leu His Ala Asp Ala
275 280 285
Ala Ala Leu Ala Gln Leu Gln Ala Gly Pro Ala Lys Val Val Ala Val
290 295 300
Lys Ala Glu Glu Tyr Asp Asp Glu Phe Leu Ser Leu Asp Leu Asn Val
305 310 315 320
Lys Ile Val Ser Asp Leu Asp Asp Ala Ile Ala His Ile Arg Glu His
325 330 335
Gly Thr Gln His Ser Asp Ala Ile Leu Thr Arg Asp Met Arg Asn Ala
340 345 350
Gln Arg Phe Val Asn Glu Val Asp Ser Ser Ala Val Tyr Val Asn Ala
355 360 365
Ser Thr Arg Phe Thr Asp Gly Gly Gln Phe Gly Leu Gly Ala Glu Val
370 375 380
Ala Val Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Gly Leu Glu
385 390 395 400
Ala Leu Thr Thr Tyr Lys Trp Ile Gly Ile Gly Asp Tyr Thr Ile Arg
405 410 415
Ala

<210> 359

<211> 186

<212> PRT

<213> Escherichia coli

<400> 359

Met Met Thr Arg Gln Ala Ser Met Lys Gly Phe Pro Ile Ala His Ile
1 5 10 15
Phe His Pro Ser Ile Pro Pro Met His Ala Val Val Asn Asn His Asn
20 25 30
Arg Asn Ile Asp Tyr Trp Thr Val Lys Arg Lys Phe Ala Glu Ile Val
35 40 45
Ser Thr Asn Asp Val Asn Lys Ile Tyr Ser Ile Ser Asn Glu Leu Arg
50 55 60
Arg Val Leu Ser Ala Ile Thr Ala Leu Asn Phe Tyr His Gly Asp Val
65 70 75 80
Pro Ser Val Met Ile Arg Ile Gln Pro Glu Asn Met Ser Pro Phe Ile
85 90 95
Ile Asp Ile Ser Thr Gly Glu His Asp Asp Tyr Ile Ile Gln Thr Leu

[illegible]

<400>	360														
Met	Phe	Pro	Val	Ser	Ser	Ile	Gly	Asn	Asp	Ile	Ser	Ser	Asp	Leu	Val
1				5					10					15	
Arg	Arg	Lys	Met	Asn	Asp	Leu	Pro	Glu	Ser	Pro	Thr	Gly	Asn	Asn	Leu
			20					25					30		
Glu	Ala	Leu	Ala	Pro	Gly	Ile	Glu	Lys	Leu	Lys	Gln	Thr	Ser	Ile	Glu
		35					40					45			
Met	Val	Thr	Leu	Leu	Asn	Thr	Leu	Gln	Pro	Gly	Gly	Lys	Cys	Ile	Ile
	50					55					60				
Thr	Gly	Asp	Phe	Gln	Lys	Glu	Leu	Ala	Tyr	Leu	Gln	Asn	Val	Ile	Leu
65					70					75				80	
Tyr	Asn	Val	Ser	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Gly	Tyr	Asn	Ala	Gln
				85					90					95	
Ile	Ile	Gln	Arg	Ser	Asp	Asn	Thr	Cys	Glu	Leu	Thr	Ile	Asn	Glu	Pro
			100					105					110		
Leu	Lys	Asn	Gln	Glu	Ile	Ser	Thr	Gly	Asn	Ile	Asn	Ile	Asn	Cys	Pro
		115					120					125			
Leu	Lys	Asp	Ile	Tyr	Asn	Glu	Ile	Arg	Arg	Leu	Asn	Val	Ile	Phe	Ser
	130					135					140				
Cys	Gly	Thr	Gly	Asp	Ile	Val	Asp	Leu	Ser	Ser	Leu	Asp	Leu	Arg	Asn
145					150					155				160	
Val	Asp	Leu	Asp	Tyr	Tyr	Asp	Phe	Thr	Asp	Lys	His	Met	Ala	Asn	Thr
				165					170					175	
Ile	Leu	Asn	Pro	Phe	Lys	Leu	Asn	Ser	Thr	Asn	Phe	Thr	Asn	Ala	Asn
			180					185					190		
Met	Phe	Gln	Val	Asn	Phe	Val	Ser	Ser	Thr	Gln	Asn	Ala	Thr	Ile	Ser
		195					200					205			
Trp	Asp	Tyr	Leu	Leu	Lys	Ile	Thr	Pro	Val	Leu	Ile	Ser	Ile	Ser	Asp
	210					215					220				
Met	Tyr	Ser	Glu	Glu	Lys	Ile	Lys	Phe	Val	Glu	Ser	Cys	Leu	Asn	Glu
225					230					235				240	
Pro	Gly	Asp	Ile	Thr	Glu	Glu	Gln	Leu	Lys	Ile	Met	Arg	Phe	Ala	Ile
				245					250					255	
Ile	Lys	Ser	Ile	Pro	Arg	Ala	Thr	Leu	Thr	Asp	Lys	Leu	Glu	Asn	Glu
			260					265					270		
Leu	Thr	Lys	Glu	Ile	Tyr	Lys	Ser	Ser	Ser	Lys	Ile	Ile	Asn	Cys	Leu
	275						280					285			
Asn	Arg	Ile	Lys	Leu	Thr	Glu	Met	Lys	Glu	Phe	Ser	Ser	Glu	Lys	Ile
	290					295					300				

Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu
 305 310 315 320
 Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn
 325 330 335
 Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu
 340 345 350
 Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn
 355 360 365
 Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp
 370 375 380
 Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile
 385 390 395

<210> 361

<211> 315

<212> PRT

<213> Escherichia coli

<400> 361

Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe
 1 5 10 15
 Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr
 20 25 30
 Leu Ile Pro Leu Arg Gln Gln Ala Leu Lys Val Ile Asn Gln Leu
 35 40 45
 Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu
 50 55 60
 Ala Phe Leu Asp Asn Leu Ala Ser Asn Leu Leu Ala Ile Leu His Tyr
 65 70 75 80
 Ser Ala Val Ser Ile Thr Val Ile Leu Leu Cys Asn Ile Ala Ala Leu
 85 90 95
 Met Trp Leu Glu Arg Gly Leu Pro Trp Arg Asn His His Gln Gln Glu
 100 105 110
 Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys
 115 120 125
 Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe
 130 135 140
 Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu
 145 150 155 160
 Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln
 165 170 175
 Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val
 180 185 190
 Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro
 195 200 205
 Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu
 210 215 220
 Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala
 225 230 235 240
 Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile
 245 250 255
 Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly
 260 265 270
 Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly
 275 280 285
 Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu

290 295 300
 Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala
 305 310 315

<210> 362
 <211> 96
 <212> PRT
 <213> Escherichia coli

<400> 362
 Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
 1 5 10 15
 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
 20 25 30
 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
 35 40 45
 Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
 50 55 60
 Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
 65 70 75 80
 Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
 85 90 95

<210> 363
 <211> 562
 <212> PRT
 <213> Escherichia coli

<400> 363
 Met Ala Ser Ser Gly Thr Thr Ser Thr Arg Lys Arg Phe Thr Gly Ala
 1 5 10 15
 Glu Phe Ile Val His Phe Leu Glu Gln Gln Gly Ile Lys Ile Val Thr
 20 25 30
 Gly Ile Pro Gly Gly Ser Ile Leu Pro Val Tyr Asp Ala Leu Ser Gln
 35 40 45
 Ser Thr Gln Ile Arg His Ile Leu Ala Arg His Glu Gln Gly Ala Gly
 50 55 60
 Phe Ile Ala Gln Gly Met Ala Arg Thr Asp Gly Lys Pro Ala Val Cys
 65 70 75 80
 Met Ala Cys Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Ala Ile Ala
 85 90 95
 Asp Ala Arg Leu Asp Ser Ile Pro Leu Ile Cys Ile Thr Gly Gln Val
 100 105 110
 Pro Ala Ser Met Ile Gly Thr Asp Ala Phe Gln Glu Val Asp Thr Tyr
 115 120 125
 Gly Ile Ser Ile Pro Ile Thr Lys His Asn Tyr Leu Val Arg His Ile
 130 135 140
 Glu Glu Leu Pro Gln Val Met Ser Asp Ala Phe Arg Ile Ala Gln Ser
 145 150 155 160
 Gly Arg Pro Gly Pro Val Trp Ile Asp Ile Pro Lys Asp Val Gln Thr
 165 170 175
 Ala Val Phe Glu Ile Glu Thr Gln Pro Ala Met Ala Glu Lys Ala Ala
 180 185 190
 Ala Pro Ala Phe Ser Glu Glu Ser Ile Arg Asp Ala Ala Ala Met Ile
 195 200 205

Asn	Ala	Ala	Lys	Arg	Pro	Val	Leu	Tyr	Leu	Gly	Gly	Gly	Val	Ile	Asn
210						215					220				
Ala	Pro	Ala	Arg	Val	Arg	Glu	Leu	Ala	Glu	Lys	Ala	Gln	Leu	Pro	Thr
225					230					235					240
Thr	Met	Thr	Leu	Met	Ala	Leu	Gly	Met	Leu	Pro	Lys	Ala	His	Pro	Leu
				245					250					255	
Ser	Leu	Gly	Met	Leu	Gly	Met	His	Gly	Val	Arg	Ser	Thr	Asn	Tyr	Ile
		260				265							270		
Leu	Gln	Glu	Ala	Asp	Leu	Leu	Ile	Val	Leu	Gly	Ala	Arg	Phe	Asp	Asp
		275				280						285			
Arg	Ala	Ile	Gly	Lys	Thr	Glu	Gln	Phe	Cys	Pro	Asn	Ala	Lys	Ile	Ile
	290					295					300				
His	Val	Asp	Ile	Asp	Arg	Ala	Glu	Leu	Gly	Lys	Ile	Lys	Gln	Pro	His
305					310					315					320
Val	Ala	Ile	Gln	Ala	Asp	Val	Asp	Asp	Val	Leu	Ala	Gln	Leu	Ile	Pro
			325						330					335	
Leu	Val	Glu	Ala	Gln	Pro	Arg	Ala	Glu	Trp	His	Gln	Leu	Val	Ala	Asp
		340						345					350		
Leu	Gln	Arg	Glu	Phe	Pro	Cys	Pro	Ile	Pro	Lys	Ala	Cys	Asp	Pro	Leu
		355				360						365			
Ser	His	Tyr	Gly	Leu	Ile	Asn	Ala	Val	Ala	Ala	Cys	Val	Asp	Asp	Asn
	370					375					380				
Ala	Ile	Ile	Thr	Thr	Asp	Val	Gly	Gln	His	Gln	Met	Trp	Thr	Ala	Gln
385					390					395					400
Ala	Tyr	Pro	Leu	Asn	Arg	Pro	Arg	Gln	Trp	Leu	Thr	Ser	Gly	Gly	Leu
			405					410						415	
Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Ile	Gly	Ala	Ala	Leu	Ala
		420						425					430		
Asn	Pro	Asp	Arg	Lys	Val	Leu	Cys	Phe	Ser	Gly	Asp	Gly	Ser	Leu	Met
		435					440					445			
Met	Asn	Ile	Gln	Glu	Met	Ala	Thr	Ala	Ser	Glu	Asn	Gln	Leu	Asp	Val
	450					455					460				
Lys	Ile	Ile	Leu	Met	Asn	Asn	Glu	Ala	Leu	Gly	Leu	Val	His	Gln	Gln
465					470					475					480
Gln	Ser	Leu	Phe	Tyr	Glu	Gln	Gly	Val	Phe	Ala	Ala	Thr	Tyr	Pro	Gly
			485					490						495	
Lys	Ile	Asn	Phe	Met	Gln	Ile	Ala	Ala	Gly	Phe	Gly	Leu	Glu	Thr	Cys
		500						505					510		
Asp	Leu	Asn	Asn	Glu	Ala	Asp	Pro	Gln	Ala	Ser	Leu	Gln	Glu	Ile	Ile
		515					520					525			
Asn	Arg	Pro	Gly	Pro	Ala	Leu	Ile	His	Val	Arg	Ile	Asp	Ala	Glu	Glu
	530					535					540				
Lys	Val	Tyr	Pro	Met	Val	Pro	Pro	Gly	Ala	Ala	Asn	Thr	Glu	Met	Val
545					550					555					5

<210> 364

<211> 32

<212> PRT

<213> Escherichia coli

<400> 364

Met Thr Thr Ser Met Leu Asn Ala Lys Leu Leu Pro Thr Ala Pro Ser
1 5 10 15

Ala Ala Val Val Val Val Arg Val Val Val Val Val Gly Asn Ala Pro

20

25

30

<210> 365

<211> 338

<212> PRT

<213> Escherichia coli

<400> 365

Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
 245 250 255
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
 260 265 270
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
 275 280 285
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
 290 295 300
 Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 366

<211> 157

<212> PRT
 <213> Escherichia coli

<400> 366

Met	Val	Tyr	Ile	Ile	Ile	Val	Ser	His	Gly	His	Glu	Asp	Tyr	Ile	Lys
1				5					10					15	
Lys	Leu	Leu	Glu	Asn	Leu	Asn	Ala	Asp	Asp	Glu	His	Tyr	Lys	Ile	Ile
			20					25					30		
Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His
		35				40						45			
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His
	50					55					60				
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala
65					70					75					80
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His
				85					90					95	
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala
		100						105					110		
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp
		115					120					125			
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe
	130					135					140				
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile			
145					150					155					

<210> 367
 <211> 372
 <212> PRT
 <213> Escherichia coli

<400> 367

Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly
1				5					10					15	
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys
			20					25					30		
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys
		35				40						45			
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly
	50					55					60				
Ser	Trp	Leu	Lys	Arg	Leu	His	Phe	Glu	Tyr	Val	Val	Cys	Lys	Lys	Leu
65					70					75					80
Ser	Lys	Glu	Leu	Asn	Ala	Thr	His	Trp	Ile	Cys	Leu	His	Asp	Ile	Thr
				85					90					95	
Ala	Asn	Val	Val	Thr	Lys	Lys	Arg	Tyr	Val	Tyr	Cys	His	Asn	Pro	Ala
		100						105					110		
Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser
		115					120					125			
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile
	130					135					140				
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys
145					150					155				160	
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu
				165					170					175	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe
		180						185					190		
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg

195 200 205
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
210 215 220
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
225 230 235 240
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
245 250 255
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
260 265 270
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
275 280 285
Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
290 295 300
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
305 310 315 320
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
325 330 335
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
340 345 350
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
355 360 365
Thr Glu Glu His
370

<210> 368
<211> 196
<212> PRT
<213> Escherichia coli

<400> 368
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
1 5 10 15
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
20 25 30
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
35 40 45
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
50 55 60
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
65 70 75 80
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
85 90 95
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
100 105 110
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
115 120 125
Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
130 135 140
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
145 150 155 160
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
165 170 175
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
180 185 190
Trp Glu Lys Ala
195

<210> 369
 <211> 330
 <212> PRT
 <213> Escherichia coli

<400> 369

Met	Tyr	Phe	Leu	Asn	Asp	Leu	Asn	Phe	Ser	Arg	Arg	Asp	Ala	Gly	Phe
1				5					10					15	
Lys	Ala	Arg	Lys	Asp	Ala	Leu	Asp	Ile	Ala	Ser	Asp	Tyr	Glu	Asn	Ile
			20					25					30		
Ser	Val	Val	Asn	Ile	Pro	Leu	Trp	Gly	Gly	Val	Val	Gln	Arg	Ile	Ile
		35					40					45			
Ser	Ser	Val	Lys	Leu	Ser	Thr	Phe	Leu	Cys	Gly	Leu	Glu	Asn	Lys	Asp
	50					55					60				
Val	Leu	Ile	Phe	Asn	Phe	Pro	Met	Ala	Lys	Pro	Phe	Trp	His	Ile	Leu
65					70					75					80
Ser	Phe	Phe	His	Arg	Leu	Leu	Lys	Phe	Arg	Ile	Val	Pro	Leu	Ile	His
				85					90					95	
Asp	Ile	Asp	Glu	Leu	Arg	Gly	Gly	Gly	Gly	Ser	Asp	Ser	Val	Arg	Leu
			100					105					110		
Ala	Thr	Cys	Asp	Met	Val	Ile	Ser	His	Asn	Pro	Gln	Met	Thr	Lys	Tyr
		115					120					125			
Leu	Ser	Lys	Tyr	Met	Ser	Gln	Asp	Lys	Ile	Lys	Asp	Ile	Lys	Ile	Phe
	130					135					140				
Asp	Tyr	Leu	Val	Ser	Ser	Asp	Val	Glu	His	Arg	Asp	Val	Thr	Asp	Lys
145					150					155					160
Gln	Arg	Gly	Val	Ile	Tyr	Ala	Gly	Asn	Leu	Ser	Arg	His	Lys	Cys	Ser
				165				170						175	
Phe	Ile	Tyr	Thr	Glu	Gly	Cys	Asp	Phe	Thr	Leu	Phe	Gly	Val	Asn	Tyr
			180					185					190		
Glu	Asn	Lys	Asp	Asn	Pro	Lys	Tyr	Leu	Gly	Ser	Phe	Asp	Ala	Gln	Ser
		195					200					205			
Pro	Glu	Lys	Ile	Asn	Leu	Pro	Gly	Met	Gln	Phe	Gly	Leu	Ile	Trp	Asp
	210				215						220				
Gly	Asp	Ser	Val	Glu	Thr	Cys	Ser	Gly	Ala	Phe	Gly	Asp	Tyr	Leu	Lys
225					230					235					240
Phe	Asn	Asn	Pro	His	Lys	Thr	Ser	Leu	Tyr	Leu	Ser	Met	Glu	Leu	Pro
				245					250					255	
Val	Phe	Ile	Trp	Asp	Lys	Ala	Ala	Leu	Ala	Asp	Phe	Ile	Val	Asp	Asn
			260					265					270		
Arg	Ile	Gly	Tyr	Ala	Val	Gly	Ser	Ile	Lys	Glu	Met	Gln	Glu	Ile	Val
		275					280					285			
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys
	290					295					300				
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu
305				310						315					320
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg						
				325					330						

<210> 370
 <211> 388
 <212> PRT
 <213> Escherichia coli

<400> 370

```

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1           5           10           15
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
 20           25           30
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
 35           40           45
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
 50           55           60
Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
 65           70           75           80
Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
 85           90           95
Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
100           105           110
Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
115           120           125
Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
130           135           140
Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
145           150           155           160
Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
165           170           175
Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
180           185           190
Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
195           200           205
Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
210           215           220
Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
225           230           235           240
Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
245           250           255
Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
260           265           270
Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
275           280           285
Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
290           295           300
Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
305           310           315           320
Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
325           330           335
Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
340           345           350
Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
355           360           365
Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
370           375           380
Gln Lys Ile Lys
385

```

<210> 371

<211> 367

<212> PRT

<213> Escherichia coli

[illegible]

```
<210> 372
<211> 230
<212> PRT
<213> Escherichia coli
```

Met Thr Ser Ser Ile Thr Asn Glu Ile Met Gln Leu Tyr Thr Asp Arg

145		150		155		160
Cys	Gln	Leu	Tyr	Gln	Arg	Ser
				165		170
Asn	Ile	Ala	Ser	Tyr	Ala	Leu
						175
Asp	Leu	Glu	Val	Gly	Asp	Phe
						185
Tyr	Ser	Asn	His	Met	Asp	Gln
						190
Arg	Pro	Leu	Pro	Lys	Leu	Ile
						200
Asp	Tyr	Arg	Phe	Glu	Asp	Phe
						210
Gly	Ile	Lys	Ala	Pro	Val	Ala
						260

<210> 375
 <211> 291
 <212> PRT
 <213> Escherichia coli

<400> 375
Met Thr Ser Ser Tyr Leu His Phe Pro Glu Phe Asp Pro Val Ile Phe
1 5 10 15
Ser Ile Gly Pro Val Ala Leu His Trp Tyr Gly Leu Met Tyr Leu Val
20 25 30
Gly Phe Ile Phe Ala Met Trp Leu Ala Thr Arg Arg Ala Asn Arg Pro
35 40 45
Gly Ser Gly Trp Thr Lys Asn Glu Val Glu Asn Leu Tyr Ala Gly
50 55 60
Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr
65 70 75 80
Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp
85 90 95
Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val
100 105 110
Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser
115 120 125
Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu
130 135 140
Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe
145 150 155 160
Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu
165 170 175
Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val
180 185 190
Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val
195 200 205
Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met
210 215 220
Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile
225 230 235 240
Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp
245 250 255
Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val
260 265 270

Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln
 275 280 285
 His Val Ser
 290

<210> 376
 <211> 241
 <212> PRT
 <213> Escherichia coli

<400> 376
 Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
 1 5 10 15
 Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
 20 25 30
 Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
 35 40 45
 Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
 50 55 60
 Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
 65 70 75 80
 Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
 85 90 95
 Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
 100 105 110
 Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
 115 120 125
 Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
 130 135 140
 Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
 145 150 155 160
 Asp Lys Lys Val Asp Gln Glu Tyr Glu Gly Ile Val Arg Gln Leu Met
 165 170 175
 Thr Tyr Met Met Glu Asp Ser Arg Thr Ile Pro Ser Val Leu Thr Ala
 180 185 190
 Leu Phe Cys Ala Arg Ser Ile Glu Arg Ile Gly Asp Arg Cys Gln Asn
 195 200 205
 Ile Cys Glu Phe Ile Phe Tyr Tyr Val Lys Gly Gln Asp Phe Arg His
 210 215 220
 Val Gly Gly Asp Glu Leu Asp Lys Leu Leu Ala Gly Lys Asp Ser Asp
 225 230 235 240
 Lys

<210> 377
 <211> 257
 <212> PRT
 <213> Escherichia coli

<400> 377
 Met Ser Met Val Glu Thr Ala Pro Ser Lys Ile Gln Val Arg Asn Leu
 1 5 10 15
 Asn Phe Tyr Tyr Gly Lys Phe His Ala Leu Lys Asn Ile Asn Leu Asp
 20 25 30
 Ile Ala Lys Asn Gln Val Thr Ala Phe Ile Gly Pro Ser Gly Cys Gly

```

      35              40              45
Lys Ser Thr Leu Leu Arg Thr Phe Asn Lys Met Phe Glu Leu Tyr Pro
  50              55              60
Glu Gln Arg Ala Glu Gly Glu Ile Leu Leu Asp Gly Asp Asn Ile Leu
  65              70              75              80
Thr Asn Ser Gln Asp Ile Ala Leu Leu Arg Ala Lys Val Gly Met Val
      85              90              95
Phe Gln Lys Pro Thr Pro Phe Pro Met Ser Ile Tyr Asp Asn Ile Ala
      100              105              110
Phe Gly Val Arg Leu Phe Glu Lys Leu Ser Arg Ala Asp Met Asp Glu
      115              120              125
Arg Val Gln Trp Ala Leu Thr Lys Ala Ala Leu Trp Asn Glu Thr Lys
      130              135              140
Asp Lys Leu His Gln Ser Gly Tyr Ser Leu Ser Gly Gly Gln Gln Gln
  145              150              155              160
Arg Leu Cys Ile Ala Arg Gly Ile Ala Ile Arg Pro Glu Val Leu Leu
      165              170              175
Leu Asp Glu Pro Cys Ser Ala Leu Asp Pro Ile Ser Thr Gly Arg Ile
      180              185              190
Glu Glu Leu Ile Thr Glu Leu Lys Gln Asp Tyr Thr Val Val Ile Val
      195              200              205
Thr His Asn Met Gln Gln Ala Ala Arg Cys Ser Asp His Thr Ala Phe
  210              215              220
Met Tyr Leu Gly Glu Leu Ile Glu Phe Ser Asn Thr Asp Asp Leu Phe
  225              230              235              240
Thr Lys Pro Ala Lys Lys Gln Thr Glu Asp Tyr Ile Thr Gly Arg Tyr
      245              250              255
Gly

```

<210> 378
 <211> 296
 <212> PRT
 <213> Escherichia coli

```

<400> 378
Met Ala Met Val Glu Met Gln Thr Thr Ala Ala Leu Ala Glu Ser Arg
  1              5              10              15
Arg Lys Met Gln Ala Arg Arg Arg Leu Lys Asn Arg Ile Ala Leu Thr
      20              25              30
Leu Ser Met Ala Thr Met Ala Phe Gly Leu Phe Trp Leu Ile Trp Ile
      35              40              45
Leu Met Ser Thr Ile Thr Arg Gly Ile Asp Gly Met Ser Leu Ala Leu
  50              55              60
Phe Thr Glu Met Thr Pro Pro Pro Asn Thr Glu Gly Gly Gly Leu Ala
  65              70              75              80
Asn Ala Leu Ala Gly Ser Gly Leu Leu Ile Leu Trp Ala Thr Val Phe
      85              90              95
Gly Thr Pro Leu Gly Ile Met Ala Gly Ile Tyr Leu Ala Glu Tyr Gly
      100              105              110
Arg Lys Ser Trp Leu Ala Glu Val Ile Arg Phe Ile Asn Asp Ile Leu
      115              120              125
Leu Ser Ala Pro Ser Ile Val Val Gly Leu Phe Val Tyr Thr Ile Val
      130              135              140
Val Ala Gln Met Glu His Phe Ser Gly Trp Ala Gly Val Ile Ala Leu
  145              150              155              160

```


Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn
 325 330 335
 Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr
 340 345

<210> 381
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 381
 Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu
 1 5 10 15
 Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr
 20 25 30
 Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
 35 40 45
 Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
 50 55 60
 Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
 65 70 75 80
 Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
 85 90 95
 Leu Asp Arg Tyr Ile Asp Arg Phe Ala Ala Lys His Glu Ala Gln Leu
 100 105 110
 Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
 115 120 125
 Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe
 130 135 140
 Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala
 145 150 155 160
 Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln
 165 170 175
 Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp
 180 185 190
 Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser
 195 200 205
 Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala
 210 215 220
 Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys
 225 230 235

<210> 382
 <211> 181
 <212> PRT
 <213> Escherichia coli

<400> 382
 Met Gln Ala Lys Ile Ala Ala Ser Asn Thr Gly Glu Leu Asp Ala Leu
 1 5 10 15
 Gln Gln Leu Gly Phe Ser Leu Val Glu Gly Glu Val Asp Leu Ala Leu
 20 25 30
 Pro Val Asn Asn Ala Ser Asp Ser Gly Ala Val Val Ala Gln Glu Thr
 35 40 45
 Asp Ile Pro Ala Leu Arg Gln Leu Ala Ser Ala Ala Phe Ala Gln Ser

50	55	60
Arg Phe Arg Ala Pro Trp Tyr Ala Pro Asp Ala Ser Ser Arg Phe Tyr		
65	70	75
Ala Gln Trp Ile Glu Asn Ala Val Arg Gly Thr Phe Asp His Gln Cys		80
	85	90
Leu Ile Leu Arg Ala Ala Ser Gly Asp Ile Arg Gly Tyr Val Ser Leu		95
	100	105
Arg Glu Leu Asn Ala Thr Asp Ala Arg Ile Gly Leu Leu Ala Gly Arg		110
	115	120
Gly Ala Gly Ala Glu Leu Met Gln Thr Ala Leu Asn Trp Ala Tyr Arg		125
	130	135
Arg Gly Lys Thr Thr Leu Arg Val Ala Thr Gln Met Gly Asn Thr Ala		140
145	150	155
Ala Leu Lys Arg Tyr Ile Gln Ser Gly Ala Asn Val Glu Ser Thr Ala		160
	165	170
Tyr Trp Leu Tyr Arg		175
	180	

<210> 383

<211> 376

<212> PRT

<213> Escherichia coli

<400> 383

Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr		
1	5	10
Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe		15
	20	25
Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys		30
	35	40
Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu		45
	50	55
Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr		60
65	70	75
Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val		80
	85	90
Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile		95
	100	105
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr		110
	115	120
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys		125
	130	135
His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr		140
145	150	155
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser		160
	165	170
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr		175
	180	185
Leu Ile Asn Asp Lys Ala Leu Ile Glu Arg Ala Glu Ile Ile Arg Glu		190
	195	200
Lys Gly Thr Asn Arg Ser Gln Phe Phe Arg Gly Gln Val Asp Lys Tyr		205
	210	215
Thr Trp Arg Asp Ile Gly Ser Ser Tyr Leu Met Ser Asp Leu Gln Ala		220
225	230	235
Ala Tyr Leu Trp Ala Gln Leu Glu Ala Ala Asp Arg Ile Asn Gln Gln		240
	245	250
		255

Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala
 260 265 270
 Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln
 275 280 285
 Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser
 290 295 300
 Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His
 305 310 315 320
 Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe
 325 330 335
 His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg
 340 345 350
 Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile
 355 360 365
 Ala Thr Leu Leu Asn Tyr Phe Ser
 370 375

<210> 384
 <211> 416
 <212> PRT
 <213> Escherichia coli

<400> 384
 Met Ser Leu Ala Lys Ala Ser Leu Trp Thr Ala Ala Ser Thr Leu Val
 1 5 10 15
 Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
 20 25 30
 Gly Pro Ala Gly Leu Gly Leu Ala Asn Phe Arg Gln Leu Ile Thr
 35 40 45
 Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
 50 55 60
 Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
 65 70 75 80
 Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
 85 90 95
 Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
 100 105 110
 Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
 115 120 125
 Ile Ala Trp Gly Asn Leu Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
 130 135 140
 Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
 145 150 155 160
 Leu Ala Tyr Tyr Val Ser Tyr Arg Leu Gly Gly Tyr Glu Gly Ala Leu
 165 170 175
 Leu Gly Leu Ala Leu Ile Pro Ala Leu Val Val Ile Pro Ala Ala Ile
 180 185 190
 Met Leu Ile Lys Arg Gly Val Ile Pro Leu Ser Tyr Leu Lys Pro Ser
 195 200 205
 Trp Asp Asn Gly Leu Ala Gly Gln Leu Ser Lys Phe Thr Leu Met Ala
 210 215 220
 Leu Ile Thr Ser Val Thr Leu Pro Val Ala Tyr Ile Met Met Arg Lys
 225 230 235 240
 Leu Leu Ala Ala Gln Tyr Ser Trp Asp Glu Val Gly Ile Trp Gln Gly
 245 250 255
 Val Ser Ser Ile Ser Asp Ala Tyr Leu Gln Phe Ile Thr Ala Ser Phe

Year	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

<211> 450

<213> Escherichia coli

225 230 235 240

				165						170					175				
Met	Arg	Asp	Cys	Arg	Leu	Val	His	Pro	Asp	Ala	Leu	Tyr	Met	Gly	Val				
			180						185					190					
Gly	Gly	Thr	Tyr	Asp	Val	Phe	Thr	Gly	His	Val	Lys	Arg	Ala	Pro	Lys				
		195					200					205							
Ile	Trp	Gln	Thr	Leu	Gly	Leu	Glu	Trp	Leu	Tyr	Arg	Leu	Leu	Ser	Gln				
	210				215					220									
Pro	Ser	Arg	Ile	Lys	Arg	Gln	Leu	Arg	Leu	Leu	Arg	Tyr	Leu	Arg	Trp				
	225				230					235					240				
His	Tyr	Thr	Gly	Asn	Leu														
				245															

<210> 387
 <211> 74
 <212> PRT
 <213> Escherichia coli

<400> 387

Met	Thr	Val	Leu	Ile	His	Val	Leu	Gly	Ser	Asp	Ile	Pro	His	His	Asn				
1				5				10						15					
Arg	Thr	Val	Leu	Arg	Phe	Phe	Asn	Asp	Ala	Leu	Ala	Ala	Thr	Ser	Glu				
		20					25					30							
His	Ala	Arg	Glu	Phe	Met	Val	Val	Gly	Lys	Asp	Asp	Gly	Leu	Ser	Asp				
	35					40					45								
Ser	Cys	Pro	Ala	Leu	Ser	Val	Gln	Phe	Phe	Pro	Trp	Glu	Lys	Ile	Ala				
	50					55					60								
Gly	Gly	Ser	Gly	His	Arg	Glu	Ser	Lys	Ser										
65					70														

<210> 388
 <211> 204
 <212> PRT
 <213> Escherichia coli

<400> 388

Met	Arg	Gly	Glu	Leu	Leu	Phe	Phe	Pro	Thr	Arg	Met	Asp	Pro	Ser	Leu				
1				5				10						15					
Asn	Thr	Met	Ala	Asn	Asp	Arg	Gln	Arg	Glu	Gly	Lys	Met	Thr	Ile	Leu				
		20					25					30							
Val	Gly	Asn	Ser	Gly	Asp	Arg	Ser	Asn	Glu	His	Ile	Ala	Ala	Leu	Arg				
	35					40					45								
Ala	Val	His	Gln	Gln	Phe	Gly	Asp	Thr	Val	Lys	Val	Val	Val	Pro	Met				
	50					55				60									
Gly	Tyr	Pro	Pro	Asn	Asn	Glu	Ala	Tyr	Ile	Glu	Glu	Val	Arg	Gln	Ala				
65				70				75						80					
Gly	Leu	Glu	Leu	Phe	Ser	Glu	Glu	Asn	Leu	Gln	Ile	Leu	Ser	Glu	Lys				
			85					90					95						
Leu	Glu	Phe	Asp	Ala	Tyr	Leu	Ala	Leu	Leu	Arg	Gln	Cys	Asp	Leu	Gly				
		100					105					110							
Tyr	Phe	Ile	Phe	Ala	Arg	Gln	Gln	Gly	Ile	Gly	Thr	Leu	Cys	Leu	Leu				
	115					120					125								
Ile	Gln	Ala	Gly	Ile	Pro	Cys	Val	Leu	Asn	Arg	Glu	Asn	Pro	Phe	Trp				
	130				135					140									
Gln	Asp	Met	Thr	Glu	Gln	His	Leu	Pro	Val	Leu	Phe	Thr	Thr	Asp	Asp				
145					150					155					160				

Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
165 170 175
Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp
180 185 190
Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala
195 200

<210> 389
<211> 182
<212> PRT
<213> Escherichia coli

<400> 389
Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
1 5 10 15
Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
20 25 30
Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
35 40 45
Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
50 55 60
Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
65 70 75 80
Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
85 90 95
Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
100 105 110
Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
115 120 125
Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
130 135 140
Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
145 150 155 160
Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
165 170 175
Ser Lys Val Trp Glu Trp
180

<210> 390
<211> 91
<212> PRT
<213> Escherichia coli

<400> 390
Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
1 5 10 15
Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
20 25 30
Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
35 40 45
Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
50 55 60
Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu
65 70 75 80
Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg

<210> 391
 <211> 702
 <212> PRT
 <213> Escherichia coli

<400> 391

```

Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro
 1           5           10           15
Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp
      20           25           30
Ala His Glu Gly Gln Thr Arg Ser Gly Glu Pro Tyr Ile Thr His
      35           40           45
Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu
      50           55           60
Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala
      65           70           75           80
Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu
      85           90           95
Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys
      100           105           110
Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln
      115           120           125
Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met
      130           135           140
Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg
      145           150           155           160
Glu Thr Leu Glu Ile Tyr Ser Pro Leu Ala His Arg Leu Gly Ile His
      165           170           175
His Ile Lys Thr Glu Leu Glu Glu Leu Gly Phe Glu Ala Leu Tyr Pro
      180           185           190
Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn
      195           200           205
Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu
      210           215           220
Gln Glu Ala Gly Ile Pro Cys Arg Val Ser Gly Arg Glu Lys His Leu
      225           230           235           240
Tyr Ser Ile Tyr Cys Lys Met Val Leu Lys Glu Gln Arg Phe His Ser
      245           250           255
Ile Met Asp Ile Tyr Ala Phe Arg Val Ile Val Asn Asp Ser Asp Thr
      260           265           270
Cys Tyr Arg Val Leu Gly Gln Met His Ser Leu Tyr Lys Pro Arg Pro
      275           280           285
Gly Arg Val Lys Asp Tyr Ile Ala Ile Pro Lys Ala Asn Gly Tyr Gln
      290           295           300
Ser Leu His Thr Ser Met Ile Gly Pro His Gly Val Pro Val Glu Val
      305           310           315           320
Gln Ile Arg Thr Glu Asp Met Asp Gln Met Ala Glu Met Gly Val Ala
      325           330           335
Ala His Trp Ala Tyr Lys Glu His Gly Glu Thr Ser Thr Thr Ala Gln
      340           345           350
Ile Arg Ala Gln Arg Trp Met Gln Ser Leu Leu Glu Leu Gln Gln Ser
      355           360           365
Ala Gly Ser Ser Phe Glu Phe Ile Glu Ser Val Lys Ser Asp Leu Phe
      370           375           380

```


65		70		75		80									
Asp	Ala	Val	Ala	His	Leu	Lys	Gly	Gln	Gly	Met	Gln	Ile	Leu	Ala	Thr
			85						90					95	
His	Leu	Ser	Asp	Asn	Ala	Val	Asp	Phe	Arg	Glu	Ile	Asp	Tyr	Thr	Arg
			100					105					110		
Pro	Thr	Cys	Ile	Leu	Met	Gly	Gln	Glu	Lys	Thr	Gly	Ile	Thr	Gln	Glu
		115					120					125			
Ala	Leu	Ala	Leu	Ala	Asp	Gln	Asp	Ile	Ile	Ile	Pro	Met	Ile	Gly	Met
		130				135					140				
Val	Gln	Ser	Leu	Asn	Val	Ser	Val	Ala	Ser	Ala	Leu	Ile	Leu	Tyr	Glu
145				150					155						160
Ala	Gln	Arg	Gln	Arg	Gln	Asn	Ala	Gly	Met	Tyr	Leu	Arg	Glu	Asn	Ser
			165					170					175		
Met	Leu	Pro	Glu	Ala	Glu	Gln	Gln	Arg	Leu	Leu	Phe	Glu	Gly	Gly	Tyr
		180					185					190			
Pro	Val	Leu	Ala	Lys	Val	Ala	Lys	Arg	Lys	Gly	Leu	Pro	Tyr	Pro	His
		195				200					205				
Val	Asn	Gln	Gln	Gly	Glu	Ile	Glu	Ala	Asp	Ala	Asp	Trp	Trp	Ala	Thr
	210				215				220						
Met	Gln	Ala	Ala	Gly											
225															

<210> 393

<211> 693

<212> PRT

<213> Escherichia coli

<400> 393

Met	Lys	Gly	Arg	Leu	Leu	Asp	Ala	Val	Pro	Leu	Ser	Ser	Leu	Thr	Gly
1				5					10				15		
Val	Gly	Ala	Ala	Leu	Ser	Asn	Lys	Leu	Ala	Lys	Ile	Asn	Leu	His	Thr
		20					25					30			
Val	Gln	Asp	Leu	Leu	Leu	His	Leu	Pro	Leu	Arg	Tyr	Glu	Asp	Arg	Thr
		35				40					45				
His	Leu	Tyr	Pro	Ile	Gly	Glu	Leu	Leu	Pro	Gly	Val	Tyr	Ala	Thr	Val
	50				55				60						
Glu	Gly	Glu	Val	Leu	Asn	Cys	Asn	Ile	Ser	Phe	Gly	Gly	Arg	Arg	Met
65				70				75					80		
Met	Thr	Cys	Gln	Ile	Ser	Asp	Gly	Ser	Gly	Ile	Leu	Thr	Met	Arg	Phe
			85					90					95		
Phe	Asn	Phe	Ser	Ala	Ala	Met	Lys	Asn	Ser	Leu	Ala	Ala	Gly	Arg	Arg
			100				105						110		
Val	Leu	Ala	Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Lys	Tyr	Gly	Ala	Glu	Met
		115					120					125			
Ile	His	Pro	Glu	Tyr	Arg	Val	Gln	Gly	Asp	Leu	Ser	Thr	Pro	Glu	Leu
	130					135					140				
Gln	Glu	Thr	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Val	Lys	Gln
145				150					155						160
Ala	Thr	Leu	Arg	Lys	Leu	Thr	Asp	Gln	Ala	Leu	Asp	Leu	Leu	Asp	Thr
			165					170					175		
Cys	Ala	Ile	Glu	Glu	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Gln	Gly	Met	Met
		180					185					190			
Thr	Leu	Pro	Glu	Ala	Leu	Arg	Thr	Leu	His	Arg	Pro	Pro	Pro	Thr	Leu
	195					200					205				
Gln	Leu	Ser	Asp	Leu	Glu	Thr	Gly	Gln	His	Pro	Ala	Gln	Arg	Arg	Leu
	210				215					220					

675
Arg Tyr Ser Asn Ala
690

680

685

<210> 394
<211> 428
<212> PRT
<213> Escherichia coli

<400> 394

Met	Lys	Thr	Ser	Leu	Phe	Lys	Ser	Leu	Tyr	Phe	Gln	Val	Leu	Thr	Ala
1				5					10					15	
Ile	Ala	Ile	Gly	Ile	Leu	Leu	Gly	His	Phe	Tyr	Pro	Glu	Ile	Gly	Glu
	20							25					30		
Gln	Met	Lys	Pro	Leu	Gly	Asp	Gly	Phe	Val	Lys	Leu	Ile	Lys	Met	Ile
	35						40					45			
Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met
	50					55					60				
Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr
65					70					75					80
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val
			85						90					95	
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu
			100					105						110	
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly
		115						120					125		
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala
	130					135						140			
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe
145					150					155					160
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn
				165					170					175	
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile
			180					185						190	
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile
	195						200						205		
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile
	210					215						220			
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser
225					230					235					240
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile
				245						250				255	
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu	Gly	Thr	Ser	Ser	Ser	Glu	Ser	Ala
			260					265						270	
Leu	Pro	Arg	Met	Leu	Asp	Lys	Met	Glu	Lys	Leu	Gly	Cys	Arg	Lys	Ser
		275					280						285		
Val	Val	Gly	Leu	Val	Ile	Pro	Thr	Gly	Tyr	Ser	Phe	Asn	Leu	Asp	Gly
	290					295						300			
Thr	Ser	Ile	Tyr	Leu	Thr	Met	Ala	Ala	Val	Phe	Ile	Ala	Gln	Ala	Thr
305					310					315					320
Asn	Ser	Gln	Met	Asp	Ile	Val	His	Gln	Ile	Thr	Leu	Leu	Ile	Val	Leu
				325					330					335	
Leu	Leu	Ser	Ser	Lys	Gly	Ala	Ala	Gly	Val	Thr	Gly	Ser	Gly	Phe	Ile
			340					345					350		
Val	Leu	Ala	Ala	Thr	Leu	Ser	Ala	Val	Gly	His	Leu	Pro	Val	Ala	Gly
		355					360								365

Leu Ala Leu Ile Leu Gly Ile Asp Arg Phe Met Ser Glu Ala Arg Ala
 370 375 380
 Leu Thr Asn Leu Val Gly Asn Gly Val Ala Thr Ile Val Val Ala Lys
 385 390 395 400
 Trp Val Lys Glu Leu Asp His Lys Lys Leu Asp Asp Val Leu Asn Asn
 405 410 415
 Arg Ala Pro Asp Gly Lys Thr His Glu Leu Ser Ser
 420 425

<210> 395

<211> 396

<212> PRT

<213> Escherichia coli

<400> 395

Met Thr Thr Arg Gln His Ser Ser Phe Ala Ile Val Phe Ile Leu Gly
 1 5 10 15
 Leu Leu Ala Met Leu Met Pro Leu Ser Ile Asp Met Tyr Leu Pro Ala
 20 25 30
 Leu Pro Val Ile Ser Ala Gln Phe Gly Val Pro Ala Gly Ser Thr Gln
 35 40 45
 Met Thr Leu Ser Thr Tyr Ile Leu Gly Phe Ala Leu Gly Gln Leu Ile
 50 55 60
 Tyr Gly Pro Met Ala Asp Ser Phe Gly Arg Lys Pro Val Val Leu Gly
 65 70 75 80
 Gly Thr Leu Val Phe Ala Ala Ala Val Ala Cys Ala Leu Ala Asn
 85 90 95
 Thr Ile Asp Gln Leu Ile Val Met Arg Phe Phe His Gly Leu Ala Ala
 100 105 110
 Ala Ala Ala Ser Val Val Ile Asn Ala Leu Met Arg Asp Ile Tyr Pro
 115 120 125
 Lys Glu Glu Phe Ser Arg Met Met Ser Phe Val Met Leu Val Thr Thr
 130 135 140
 Ile Ala Pro Leu Met Ala Pro Ile Val Gly Gly Trp Val Leu Val Trp
 145 150 155 160
 Leu Ser Trp His Tyr Ile Phe Trp Ile Leu Ala Leu Ala Ala Ile Leu
 165 170 175
 Ala Ser Ala Met Ile Phe Phe Leu Ile Lys Glu Thr Leu Pro Pro Glu
 180 185 190
 Arg Arg Gln Pro Phe His Ile Arg Thr Thr Ile Gly Asn Phe Ala Ala
 195 200 205
 Leu Phe Arg His Lys Arg Val Leu Ser Tyr Met Leu Ala Ser Gly Phe
 210 215 220
 Ser Phe Ala Gly Met Phe Ser Phe Leu Ser Ala Gly Pro Phe Val Tyr
 225 230 235 240
 Ile Glu Ile Asn His Val Ala Pro Glu Asn Phe Gly Tyr Tyr Phe Ala
 245 250 255
 Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
 260 265 270
 Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
 275 280 285
 Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
 290 295 300
 Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
 305 310 315 320
 Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro

325 330 335
 His Met Ala Gly Thr Ala Ser Ser Leu Ala Gly Thr Phe Arg Phe Gly
 340 345 350
 Ile Gly Ala Ile Val Gly Ala Leu Leu Ser Leu Ala Thr Phe Asn Ser
 355 360 365
 Ala Trp Pro Met Ile Trp Ser Ile Ala Phe Cys Ala Thr Ser Ser Ile
 370 375 380
 Leu Phe Cys Leu Tyr Ala Ser Arg Pro Lys Lys Arg
 385 390 395

<210> 396
 <211> 231
 <212> PRT
 <213> Escherichia coli

<400> 396
 Met Arg Leu Asp Lys Phe Ile Ala Gln Gln Leu Gly Val Ser Arg Ala
 1 5 10 15
 Ile Ala Gly Arg Glu Ile Arg Gly Asn Arg Val Thr Val Asp Gly Glu
 20 25 30
 Ile Val Arg Asn Ala Ala Phe Lys Leu Leu Pro Glu His Asp Val Ala
 35 40 45
 Tyr Asp Gly Asn Pro Leu Ala Gln Gln His Gly Pro Arg Tyr Phe Met
 50 55 60
 Leu Asn Lys Pro Gln Gly Tyr Val Cys Ser Thr Asp Asp Pro Asp His
 65 70 75 80
 Pro Thr Val Leu Tyr Phe Leu Asp Glu Pro Val Ala Trp Lys Leu His
 85 90 95
 Ala Ala Gly Arg Leu Asp Ile Asp Thr Thr Gly Leu Val Leu Met Thr
 100 105 110
 Asp Asp Gly Gln Trp Ser His Arg Ile Thr Ser Pro Arg His His Cys
 115 120 125
 Glu Lys Thr Tyr Leu Val Thr Leu Glu Ser Pro Val Ala Asp Asp Thr
 130 135 140
 Ala Glu Gln Phe Ala Lys Gly Val Gln Leu His Asn Glu Lys Asp Leu
 145 150 155 160
 Thr Lys Pro Ala Val Leu Glu Val Ile Thr Pro Thr Gln Val Arg Leu
 165 170 175
 Thr Ile Ser Glu Gly Arg Tyr His Gln Val Lys Arg Met Phe Ala Ala
 180 185 190
 Val Gly Asn His Val Val Glu Leu His Arg Glu Arg Ile Gly Gly Ile
 195 200 205
 Thr Leu Asp Ala Asp Leu Ala Pro Gly Glu Tyr Arg Pro Leu Thr Glu
 210 215 220
 Glu Glu Ile Ala Ser Val Val
 225 230

<210> 397
 <211> 442
 <212> PRT
 <213> Escherichia coli

<400> 397
 Met Lys Lys Ile Glu Cys Ala Cys Asn Phe Leu Met Asp Lys Asp Ala
 1 5 10 15

<211> 238
 <212> PRT
 <213> Escherichia coli

<400> 398

```

Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp
 1           5           10           15
Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala
      20           25           30
Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys
      35           40           45
Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile
      50           55           60
Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val
      65           70           75           80
Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala
      85           90           95
Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr
      100          105          110
Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser
      115          120          125
Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro
      130          135          140
Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp
      145          150          155          160
Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp
      165          170          175
Leu His Lys Gly Ile Ala Ala Leu Lys Ala Ala Gly Ile Thr Glu Phe
      180          185          190
Ser Thr Thr Glu Leu Glu Met Ile Ala Gln Ser Glu Val Glu Leu Ser
      195          200          205
Pro Glu Asp Leu Glu Ile Phe Glu Gly Leu Val Asp Ala Leu Glu Asp
      210          215          220
Asp Asp Asp Val Gln Lys Val Tyr His Asn Val Ala Asn Leu
      225          230          235

```

<210> 399
 <211> 261
 <212> PRT
 <213> Escherichia coli

<400> 399

```

Met Val Leu Met Ser Glu Thr Lys Asn Glu Leu Glu Asp Leu Leu Glu
 1           5           10           15
Lys Ala Ala Thr Glu Pro Ala His Arg Pro Ala Phe Phe Arg Thr Leu
      20           25           30
Leu Glu Ser Thr Val Trp Val Pro Gly Thr Ala Ala Gln Gly Glu Ala
      35           40           45
Val Val Glu Asp Ser Ala Leu Asp Leu Gln His Trp Glu Lys Glu Asp
      50           55           60
Gly Thr Ser Val Ile Pro Phe Phe Thr Ser Leu Glu Ala Leu Gln Gln
      65           70           75           80
Ala Val Glu Asp Glu Gln Ala Phe Val Val Met Pro Val Arg Thr Leu
      85           90           95
Phe Glu Met Thr Leu Gly Glu Thr Leu Phe Leu Asn Ala Lys Leu Pro
      100          105          110

```

Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu
 115 120 125
 Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser
 130 135 140
 Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser
 145 150 155 160
 Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile
 165 170 175
 Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly
 180 185 190
 Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser
 195 200 205
 Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln
 210 215 220
 Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile
 225 230 235 240
 Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys
 245 250 255
 Gln Asn Arg Ile Ile
 260

<210> 400
 <211> 421
 <212> PRT
 <213> Escherichia coli

<400> 400
 Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys
 1 5 10 15
 Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile
 20 25 30
 Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala
 35 40 45
 Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile
 50 55 60
 Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu
 65 70 75 80
 Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr
 85 90 95
 Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met
 100 105 110
 Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser
 115 120 125
 Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile
 130 135 140
 Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe
 145 150 155 160
 Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu
 165 170 175
 Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys
 180 185 190
 Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys
 195 200 205
 Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile
 210 215 220
 Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe

Gly	Asp	Ile	Lys	Pro	Leu	Gln	Gln	Ala	Gly	Val	Tyr	Leu	Ala	Val	Met
			260					265					270		
Asn	Gln	Ala	Gly	Arg	Tyr	Asp	Tyr	Ser	Asn	Pro	Ala	Thr	Leu	Phe	Thr
		275					280					285			
Leu	Ser	Asp	Ile	Gly	Val	Ser	Ala	His	Arg	Tyr	His	Asn	Arg	Leu	Asp
	290					295					300				
Ile	Phe	Thr	Gln	Ser	Leu	Glu	Asn	Gly	Ala	Ala	Gln	Gln	Gly	Ile	Glu
305					310					315					320
Val	Ser	Leu	Leu	Asn	Glu	Lys	Gly	Gln	Thr	Leu	Thr	Gln	Ala	Thr	Ser
				325					330					335	
Asp	Ala	Gln	Gly	His	Val	Gln	Leu	Glu	Asn	Asp	Lys	Asn	Ala	Ala	Leu
			340					345					350		
Leu	Leu	Ala	Arg	Lys	Asp	Gly	Gln	Thr	Thr	Leu	Leu	Asp	Leu	Lys	Leu
		355					360					365			
Pro	Ala	Leu	Asp	Leu	Ala	Glu	Phe	Asn	Ile	Ala	Gly	Ala	Pro	Gly	Tyr
		370				375					380				
Ser	Lys	Gln	Phe	Phe	Met	Phe	Gly	Pro	Arg	Asp	Leu	Tyr	Arg	Pro	Gly
385					390					395					400
Glu	Thr	Val	Ile	Leu	Asn	Gly	Leu	Leu	Arg	Asp	Ala	Asp	Gly	Lys	Ala
				405					410					415	
Leu	Pro	Asn	Gln	Pro	Ile	Lys	Leu	Asp	Val	Ile	Lys	Pro	Asp	Gly	Gln
			420					425					430		
Val	Leu	Arg	Ser	Val	Val	Ser	Gln	Pro	Glu	Asn	Gly	Leu	Tyr	His	Phe
		435					440					445			
Thr	Trp	Pro	Leu	Asp	Ser	Asn	Ala	Ala	Thr	Gly	Met	Trp	His	Ile	Arg
	450					455					460				
Ala	Asn	Thr	Gly	Asp	Asn	Gln	Tyr	Arg	Met	Trp	Asp	Phe	His	Val	Glu
465					470					475					480
Asp	Phe	Met	Pro	Glu	Arg	Met	Ala	Leu	Asn	Leu	Thr	Gly	Glu	Lys	Thr
				485					490					495	
Pro	Leu	Thr	Pro	Lys	Asp	Glu	Val	Lys	Phe	Ser	Val	Val	Gly	Tyr	Tyr
			500					505					510		
Leu	Tyr	Gly	Ala	Pro	Ala	Asn	Gly	Asn	Thr	Leu	Gln	Gly	Gln	Leu	Phe
		515					520					525			
Leu	Arg	Pro	Leu	Arg	Glu	Ala	Val	Ser	Ala	Leu	Pro	Gly	Phe	Glu	Phe
	530					535					540				
Gly	Asp	Ile	Ala	Ala	Glu	Asn	Leu	Ser	Arg	Thr	Leu	Asp	Glu	Val	Gln
545					550					555					560
Leu	Thr	Leu	Asp	Asp	Lys	Gly	Arg	Gly	Glu	Val	Ser	Thr	Glu	Ser	Gln
				565					570					575	
Trp	Lys	Glu	Thr	His	Ser	Pro	Leu	Gln	Val	Ile	Phe	Gln	Gly	Ser	Leu
			580					585					590		
Leu	Glu	Ser	Gly	Gly	Arg	Pro	Val	Thr	Arg	Arg	Ala	Glu	Gln	Ala	Ile
		595					600					605			
Trp	Pro	Ala	Asp	Ala	Leu	Pro	Gly	Ile	Arg	Pro	Gln	Phe	Ala	Ser	Lys
	610					615					620				
Ser	Val	Tyr	Asp	Tyr	Arg	Thr	Asp	Ser	Thr	Val	Lys	Gln	Pro	Ile	Val
625					630					635					640
Asp	Glu	Gly	Ser	Asn	Ala	Ala	Phe	Asp	Ile	Val	Tyr	Ser	Asp	Ala	Gln
				645					650					655	
Gly	Val	Lys	Lys	Ala	Val	Ser	Gly	Leu	Gln	Val	Arg	Leu	Ile	Arg	Glu
			660					665					670		
Arg	Arg	Asp	Tyr	Tyr	Trp	Asn	Trp	Ser	Glu	Asp	Glu	Gly	Trp	Gln	Ser
		675					680					685			
Gln	Phe	Asp	Gln	Lys	Asp	Leu	Ile	Glu	Asn	Glu	Gln	Thr	Leu	Asp	Leu
	690					695					700				
Lys	Ala	Asp	Glu	Thr	Gly	Lys	Val	Ser	Phe	Pro	Val	Glu	Trp	Gly	Ala

705					710					715				720
Tyr	Arg	Leu	Glu	Val	Lys	Ala	Pro	Asn	Glu	Ala	Val	Ser	Ser	Val
					725					730				735
Phe	Trp	Ala	Gly	Tyr	Ser	Trp	Gln	Asp	Asn	Ser	Asp	Gly	Ser	Gly
					740					745				750
Val	Arg	Pro	Asp	Arg	Val	Thr	Leu	Lys	Leu	Asp	Lys	Ala	Ser	Tyr
					755					760				765
Pro	Gly	Asp	Thr	Ile	Lys	Leu	His	Ile	Ala	Ala	Pro	Thr	Ala	Gly
					770					775				780
Gly	Tyr	Ala	Met	Val	Glu	Ser	Ser	Glu	Gly	Pro	Leu	Trp	Trp	Gln
					785					790				800
Ile	Asp	Val	Arg	Ala	Gln	Gly	Leu	Asp	Leu	Thr	Ile	Pro	Val	Asp
					805					810				815
Thr	Trp	Asn	Arg	His	Asp	Leu	Tyr	Leu	Ser	Thr	Leu	Val	Val	Arg
					820					825				830
Gly	Asp	Lys	Ser	Arg	Ser	Ala	Thr	Pro	Lys	Arg	Ala	Val	Gly	Val
					835					840				845
His	Leu	Pro	Leu	Gly	Asp	Glu	Asn	Arg	Arg	Leu	Asp	Leu	Ala	Leu
					850					855				860
Thr	Pro	Ala	Lys	Met	Arg	Pro	Asn	Gln	Pro	Leu	Thr	Val	Lys	Ile
					865					870				875
Ala	Ser	Thr	Lys	Asn	Gly	Glu	Lys	Pro	Lys	Gln	Val	Asn	Val	Leu
					885					890				895
Ser	Ala	Val	Asp	Ser	Gly	Val	Leu	Asn	Ile	Thr	Asp	Tyr	Val	Thr
					900					905				910
Asp	Pro	Trp	Gln	Ala	Phe	Phe	Gly	Gln	Lys	Arg	Tyr	Gly	Ala	Asp
					915					920				925
Tyr	Asp	Ile	Tyr	Gly	Gln	Val	Ile	Glu	Gly	Gln	Gly	Arg	Leu	Ala
					930					935				940
Leu	Arg	Phe	Gly	Gly	Asp	Gly	Asp	Glu	Leu	Lys	Arg	Gly	Gly	Lys
					945					950				955
Pro	Val	Asn	His	Val	Asn	Ile	Val	Val	Gln	Gln	Ala	Leu	Pro	Val
					965					970				975
Leu	Asn	Glu	Gln	Gly	Glu	Gly	Ser	Val	Thr	Leu	Pro	Ile	Gly	Asp
					980					985				990
Asn	Gly	Glu	Leu	Arg	Val	Met	Ala	Gln	Ala	Trp	Thr	Ala	Asp	Asp
					995					1000				1005
Gly	Ser	Asn	Glu	Ser	Lys	Val	Ile	Val	Ala	Ala	Pro	Val	Ile	Ala
					1010					1015				1020
Leu	Asn	Met	Pro	Arg	Phe	Met	Ala	Ser	Gly	Asp	Thr	Ser	Arg	Leu
					1025					1030				1035
Leu	Asp	Ile	Thr	Asn	Leu	Thr	Asp	Lys	Pro	Gln	Lys	Leu	Asn	Val
					1040					1045				1050
Leu	Thr	Ala	Ser	Gly	Leu	Leu	Glu	Leu	Val	Ser	Asp	Ser	Pro	Ala
					1055					1060				1065
Val	Glu	Leu	Ala	Pro	Gly	Val	Arg	Thr	Thr	Leu	Phe	Ile	Pro	Val
					1070					1075				1080
Ala	Leu	Pro	Gly	Tyr	Gly	Asp	Gly	Glu	Ile	Gln	Ala	Thr	Ile	Ser
					1085					1090				1095
Leu	Ala	Leu	Pro	Gly	Glu	Thr	Val	Ala	Asp	Gln	His	Lys	Gln	Trp
					1100					1105				1110
Ile	Gly	Val	Arg	Pro	Ala	Phe	Pro	Ala	Gln	Thr	Val	Asn	Tyr	Gly
					1115					1120				1125
Ala	Leu	Gln	Pro	Gly	Glu	Thr	Trp	Ala	Ile	Pro	Ala	Asp	Gly	Leu
					1130					1135				1140
Asn	Phe	Ser	Pro	Val	Thr	Leu	Glu	Gly	Gln	Leu	Leu	Leu	Ser	Gly
					1145					1150				1155
					1160					1165				

465		470		475		480					
Asn	Pro	Gly	Leu	Asp	Phe	Ser	Asp	Glu	Val	Val	Arg
		485						490			

<210> 407
 <211> 344
 <212> PRT
 <213> Escherichia coli

<400> 407

Met	Met	Val	Ile	Arg	Pro	Val	Glu	Arg	Ser	Asp	Val	Ser	Ala	Leu	Met
1				5					10					15	
Gln	Leu	Ala	Ser	Lys	Thr	Gly	Gly	Gly	Leu	Thr	Ser	Leu	Pro	Ala	Asn
			20					25					30		
Glu	Ala	Thr	Leu	Ser	Ala	Arg	Ile	Glu	Arg	Ala	Ile	Lys	Thr	Trp	Gln
		35					40					45			
Gly	Glu	Leu	Pro	Lys	Ser	Glu	Gln	Gly	Tyr	Val	Phe	Val	Leu	Glu	Asp
	50					55					60				
Ser	Glu	Thr	Gly	Thr	Val	Ala	Gly	Ile	Cys	Ala	Ile	Glu	Val	Ala	Val
65					70				75						80
Gly	Leu	Asn	Asp	Pro	Trp	Tyr	Asn	Tyr	Arg	Val	Gly	Thr	Leu	Val	His
			85					90					95		
Ala	Ser	Lys	Glu	Leu	Asn	Val	Tyr	Asn	Ala	Leu	Pro	Thr	Leu	Phe	Leu
			100					105					110		
Ser	Asn	Asp	His	Thr	Gly	Ser	Ser	Glu	Leu	Cys	Thr	Leu	Phe	Leu	Asp
		115					120					125			
Pro	Asp	Trp	Arg	Lys	Glu	Gly	Asn	Gly	Tyr	Leu	Leu	Ser	Lys	Ser	Arg
	130					135					140				
Phe	Met	Phe	Met	Ala	Ala	Phe	Arg	Asp	Lys	Phe	Asn	Asp	Lys	Val	Val
145					150					155					160
Ala	Glu	Met	Arg	Gly	Val	Ile	Asp	Glu	His	Gly	Tyr	Ser	Pro	Phe	Trp
				165					170					175	
Gln	Ser	Leu	Gly	Lys	Arg	Phe	Phe	Ser	Met	Asp	Phe	Ser	Arg	Ala	Asp
			180					185					190		
Phe	Leu	Cys	Gly	Thr	Gly	Gln	Lys	Ala	Phe	Ile	Ala	Glu	Leu	Met	Pro
		195					200					205			
Lys	His	Pro	Ile	Tyr	Thr	His	Phe	Leu	Ser	Gln	Glu	Ala	Gln	Asp	Val
	210					215					220				
Ile	Gly	Gln	Val	His	Pro	Gln	Thr	Ala	Pro	Ala	Arg	Ala	Val	Leu	Glu
225					230					235				240	
Lys	Glu	Gly	Phe	Arg	Tyr	Arg	Asn	Tyr	Ile	Asp	Ile	Phe	Asp	Gly	Gly
			245					250					255		
Pro	Thr	Leu	Glu	Cys	Asp	Ile	Asp	Arg	Val	Arg	Ala	Ile	Arg	Lys	Ser
		260					265						270		
Arg	Leu	Val	Glu	Val	Ala	Glu	Gly	Gln	Pro	Ala	Gln	Gly	Asp	Phe	Pro
		275					280					285			
Ala	Cys	Leu	Val	Ala	Asn	Glu	Asn	Tyr	His	His	Phe	Arg	Val	Val	Leu
	290					295					300				
Val	Arg	Thr	Asp	Pro	Ala	Thr	Glu	Arg	Leu	Ile	Leu	Thr	Ala	Ala	Gln
305					310					315					320
Leu	Asp	Ala	Leu	Lys	Cys	His	Ala	Gly	Asp	Arg	Val	Arg	Leu	Val	Arg
			325					330					335		
Leu	Cys	Ala	Glu	Lys	Thr	Ala									
			340												

<210> 408
 <211> 406
 <212> PRT
 <213> Escherichia coli

<400> 408

Met	Ser	Gln	Pro	Ile	Thr	Arg	Glu	Asn	Phe	Asp	Glu	Trp	Met	Ile	Pro
1				5					10					15	
Val	Tyr	Ala	Pro	Ala	Pro	Phe	Ile	Pro	Val	Arg	Gly	Glu	Gly	Ser	Arg
			20					25					30		
Leu	Trp	Asp	Gln	Gln	Gly	Lys	Glu	Tyr	Ile	Asp	Phe	Ala	Gly	Gly	Ile
		35					40					45			
Ala	Val	Asn	Ala	Leu	Gly	His	Ala	His	Pro	Glu	Leu	Arg	Glu	Ala	Leu
	50					55				60					
Asn	Glu	Gln	Ala	Ser	Lys	Phe	Trp	His	Thr	Gly	Asn	Gly	Tyr	Thr	Asn
65					70					75					80
Glu	Pro	Val	Leu	Arg	Leu	Ala	Lys	Lys	Leu	Ile	Asp	Ala	Thr	Phe	Ala
				85					90					95	
Asp	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu	Ala	Asn	Glu	Ala	Ala
			100					105					110		
Leu	Lys	Leu	Ala	Arg	Lys	Phe	Ala	His	Asp	Arg	Tyr	Gly	Ser	His	Lys
		115					120					125			
Ser	Gly	Ile	Val	Ala	Phe	Lys	Asn	Ala	Phe	His	Gly	Arg	Thr	Leu	Phe
	130					135					140				
Thr	Val	Ser	Ala	Gly	Gly	Gln	Pro	Ala	Tyr	Ser	Gln	Asp	Phe	Ala	Pro
145				150					155						160
Leu	Pro	Ala	Asp	Ile	Arg	His	Ala	Ala	Tyr	Asn	Asp	Ile	Asn	Ser	Ala
			165						170					175	
Ser	Ala	Leu	Ile	Asp	Asp	Ser	Thr	Cys	Ala	Val	Ile	Val	Glu	Pro	Ile
		180						185					190		
Gln	Gly	Glu	Gly	Gly	Val	Val	Pro	Ala	Ser	Asn	Ala	Phe	Leu	Gln	Gly
		195					200					205			
Leu	Arg	Glu	Leu	Cys	Asn	Arg	His	Asn	Ala	Leu	Leu	Ile	Phe	Asp	Glu
	210					215					220				
Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Glu	Leu	Tyr	Ala	Tyr	Met	His
225					230					235					240
Tyr	Gly	Val	Thr	Pro	Asp	Leu	Leu	Thr	Thr	Ala	Lys	Ala	Leu	Gly	Gly
				245					250					255	
Gly	Phe	Pro	Val	Gly	Ala	Leu	Leu	Ala	Thr	Glu	Glu	Cys	Ala	Arg	Val
		260						265					270		
Met	Thr	Val	Gly	Thr	His	Gly	Thr	Thr	Tyr	Gly	Gly	Asn	Pro	Leu	Ala
	275						280					285			
Ser	Ala	Val	Ala	Gly	Lys	Val	Leu	Glu	Leu	Ile	Asn	Thr	Pro	Glu	Met
	290					295					300				
Leu	Asn	Gly	Val	Lys	Gln	Arg	His	Asp	Trp	Phe	Val	Glu	Arg	Leu	Asn
305				310						315					320
Thr	Ile	Asn	His	Arg	Tyr	Gly	Leu	Phe	Ser	Glu	Val	Arg	Gly	Leu	Gly
			325						330					335	
Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Ala	Asp	Tyr	Ala	Gly	Gln	Ala	Lys
		340						345					350		
Gln	Ile	Ser	Gln	Glu	Ala	Ala	Lys	Ala	Gly	Val	Met	Val	Leu	Ile	Ala
	355						360					365			
Gly	Gly	Asn	Val	Val	Arg	Phe	Ala	Pro	Ala	Leu	Asn	Val	Ser	Glu	Glu
	370					375					380				
Glu	Val	Thr	Thr	Gly	Leu	Asp	Arg	Phe	Ala	Ala	Ala	Cys	Glu	His	Phe
385					390					395					400
Val	Ser	Arg	Gly	Ser	Ser										

<210> 409
 <211> 1048
 <212> PRT
 <213> Escherichia coli

<400> 409

Met	Lys	Ile	Leu	Ser	Leu	Arg	Leu	Lys	Asn	Leu	Asn	Ser	Leu	Lys	Gly
1				5					10					15	
Glu	Trp	Lys	Ile	Asp	Phe	Thr	Arg	Glu	Pro	Phe	Ala	Ser	Asn	Gly	Leu
			20					25					30		
Phe	Ala	Ile	Thr	Gly	Pro	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Asp
		35					40					45			
Ala	Ile	Cys	Leu	Ala	Leu	Tyr	His	Glu	Thr	Pro	Arg	Leu	Ser	Asn	Val
	50					55				60					
Ser	Gln	Ser	Gln	Asn	Asp	Leu	Met	Thr	Arg	Asp	Thr	Ala	Glu	Cys	Leu
65				70					75					80	
Ala	Glu	Val	Glu	Phe	Glu	Val	Lys	Gly	Glu	Ala	Tyr	Arg	Ala	Phe	Trp
				85				90						95	
Ser	Gln	Asn	Arg	Ala	Arg	Asn	Gln	Pro	Asp	Gly	Asn	Leu	Gln	Val	Pro
			100					105					110		
Arg	Val	Glu	Leu	Ala	Arg	Cys	Ala	Asp	Gly	Lys	Ile	Leu	Ala	Asp	Lys
		115					120					125			
Val	Lys	Asp	Lys	Leu	Glu	Leu	Thr	Ala	Thr	Leu	Thr	Gly	Leu	Asp	Tyr
	130				135					140					
Gly	Arg	Phe	Thr	Arg	Ser	Met	Leu	Leu	Ser	Gln	Gly	Gln	Phe	Ala	Ala
145					150				155						160
Phe	Leu	Asn	Ala	Lys	Pro	Lys	Glu	Arg	Ala	Glu	Leu	Leu	Glu	Glu	Leu
				165				170						175	
Thr	Gly	Thr	Glu	Ile	Tyr	Gly	Gln	Ile	Ser	Ala	Met	Val	Phe	Glu	Gln
			180					185					190		
His	Lys	Ser	Ala	Arg	Thr	Glu	Leu	Glu	Lys	Leu	Gln	Ala	Gln	Ala	Ser
		195					200					205			
Gly	Val	Thr	Leu	Leu	Thr	Pro	Glu	Gln	Val	Gln	Ser	Leu	Thr	Ala	Ser
	210					215				220					
Leu	Gln	Val	Leu	Thr	Asp	Glu	Glu	Lys	Gln	Leu	Ile	Thr	Ala	Gln	Gln
225					230					235					240
Gln	Glu	Gln	Gln	Ser	Leu	Asn	Trp	Leu	Thr	Arg	Gln	Asp	Glu	Leu	Gln
				245				250						255	
Gln	Glu	Ala	Ser	Arg	Arg	Gln	Gln	Ala	Leu	Gln	Gln	Ala	Leu	Ala	Glu
		260						265					270		
Glu	Glu	Lys	Ala	Gln	Pro	Gln	Leu	Ala	Ala	Leu	Ser	Leu	Ala	Gln	Pro
		275					280					285			
Ala	Arg	Asn	Leu	Arg	Pro	His	Trp	Glu	Arg	Ile	Ala	Glu	His	Ser	Ala
	290					295					300				
Ala	Leu	Ala	His	Ile	Arg	Gln	Gln	Ile	Glu	Glu	Val	Asn	Thr	Arg	Leu
305				310					315						320
Gln	Ser	Thr	Met	Ala	Leu	Arg	Ala	Ser	Ile	Arg	His	His	Ala	Ala	Lys
			325					330					335		
Gln	Ser	Ala	Glu	Leu	Gln	Gln	Gln	Gln	Gln	Ser	Leu	Asn	Thr	Trp	Leu
		340					345					350			
Gln	Glu	His	Asp	Arg	Phe	Arg	Gln	Trp	Asn	Asn	Glu	Pro	Ala	Gly	Trp
	355					360					365				
Arg	Ala	Gln	Phe	Ser	Gln	Gln	Thr	Ser	Asp	Arg	Glu	His	Leu	Arg	Gln
	370					375					380				

Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe
 305 310 315 320
 Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala
 325 330 335
 Ala Lys Val Gln Leu Val Phe
 340

<210> 413
 <211> 548
 <212> PRT
 <213> Escherichia coli

<400> 413

Met Asp Ser Gln Arg Asn Leu Leu Val Ile Ala Leu Leu Phe Val Ser
 1 5 10 15
 Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln
 20 25 30
 Ala Gln Gln Thr Thr Gln Thr Thr Thr Thr Ala Ala Gly Ser Ala Ala
 35 40 45
 Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys
 50 55 60
 Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu
 65 70 75 80
 Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro
 85 90 95
 Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser
 100 105 110
 Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg
 115 120 125
 Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln
 130 135 140
 Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr
 145 150 155 160
 Phe Thr Lys Thr Phe Val Leu Lys Arg Gly Asp Tyr Ala Val Asn Val
 165 170 175
 Asn Tyr Asn Val Gln Asn Ala Gly Glu Lys Pro Leu Glu Ile Ser Ser
 180 185 190
 Phe Gly Gln Leu Lys Gln Ser Ile Thr Leu Pro Pro His Leu Asp Thr
 195 200 205
 Gly Ser Ser Asn Phe Ala Leu His Thr Phe Arg Gly Ala Ala Tyr Ser
 210 215 220
 Thr Pro Asp Glu Lys Tyr Glu Lys Tyr Lys Phe Asp Thr Ile Ala Asp
 225 230 235 240
 Asn Glu Asn Leu Asn Ile Ser Ser Lys Gly Gly Trp Val Ala Met Leu
 245 250 255
 Gln Gln Tyr Phe Ala Thr Ala Trp Ile Pro His Asn Asp Gly Thr Asn
 260 265 270
 Asn Phe Tyr Thr Ala Asn Leu Gly Asn Gly Ile Ala Ala Ile Gly Tyr
 275 280 285
 Lys Ser Gln Pro Val Leu Val Gln Pro Gly Gln Thr Gly Ala Met Asn
 290 295 300
 Ser Thr Leu Trp Val Gly Pro Glu Ile Gln Asp Lys Met Ala Ala Val
 305 310 315 320
 Ala Pro His Leu Asp Leu Thr Val Asp Tyr Gly Trp Leu Trp Phe Ile
 325 330 335
 Ser Gln Pro Leu Phe Lys Leu Leu Lys Trp Ile His Ser Phe Val Gly

```

      340      345      350
Asn Trp Gly Phe Ser Ile Ile Ile Ile Thr Phe Ile Val Arg Gly Ile
      355      360      365
Met Tyr Pro Leu Thr Lys Ala Gln Tyr Thr Ser Met Ala Lys Met Arg
      370      375      380
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp
      385      390      395      400
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys
      405      410      415
Val Asn Pro Leu Gly Gly Cys Phe Pro Leu Leu Ile Gln Met Pro Ile
      420      425      430
Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln
      435      440      445
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr
      450      455      460
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys
      465      470      475      480
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr
      485      490      495
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly
      500      505      510
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln
      515      520      525
Gln Leu Ile Tyr Arg Gly Leu Glu Lys Arg Gly Leu His Ser Arg Glu
      530      535      540
Lys Lys Lys Ser
      545

```

```

<210> 414
<211> 542
<212> PRT
<213> Escherichia coli

```

```

<400> 414
Met Lys Thr Arg Asp Ser Gln Ser Ser Asp Val Ile Ile Ile Gly Gly
  1      5      10      15
Gly Ala Thr Gly Ala Gly Ile Ala Arg Asp Cys Ala Leu Arg Gly Leu
      20      25      30
Arg Val Ile Leu Val Glu Arg His Asp Ile Ala Thr Gly Ala Thr Gly
      35      40      45
Arg Asn His Gly Leu Leu His Ser Gly Ala Arg Tyr Ala Val Thr Asp
      50      55      60
Ala Glu Ser Ala Arg Glu Cys Ile Ser Glu Asn Gln Ile Leu Lys Arg
      65      70      75      80
Ile Ala Arg His Cys Val Glu Pro Thr Asn Gly Leu Phe Ile Thr Leu
      85      90      95
Pro Glu Asp Asp Leu Ser Phe Gln Ala Thr Phe Ile Arg Ala Cys Glu
      100      105      110
Glu Ala Gly Ile Ser Ala Glu Ala Ile Asp Pro Gln Gln Ala Arg Ile
      115      120      125
Ile Glu Pro Ala Val Asn Pro Ala Leu Ile Gly Ala Val Lys Val Pro
      130      135      140
Asp Gly Thr Val Asp Pro Phe Arg Leu Thr Ala Ala Asn Met Leu Asp
      145      150      155      160
Ala Lys Glu His Gly Ala Val Ile Leu Thr Ala His Glu Val Thr Gly
      165      170      175

```

Leu Ile Arg Glu Gly Ala Thr Val Cys Gly Val Arg Val Arg Asn His
 180 185 190
 Leu Thr Gly Glu Thr Gln Ala Leu His Ala Pro Val Val Val Asn Ala
 195 200 205
 Ala Gly Ile Trp Gly Gln His Ile Ala Glu Tyr Ala Asp Leu Arg Ile
 210 215 220
 Arg Met Phe Pro Ala Lys Gly Ser Leu Leu Ile Met Asp His Arg Ile
 225 230 235 240
 Asn Gln His Val Ile Asn Arg Cys Arg Lys Pro Ser Asp Ala Asp Ile
 245 250 255
 Leu Val Pro Gly Asp Thr Ile Ser Leu Ile Gly Thr Thr Ser Leu Arg
 260 265 270
 Ile Asp Tyr Asn Glu Ile Asp Asp Asn Arg Val Thr Ala Glu Glu Val
 275 280 285
 Asp Ile Leu Leu Arg Glu Gly Glu Lys Leu Ala Pro Val Met Ala Lys
 290 295 300
 Thr Arg Ile Leu Arg Ala Tyr Ser Gly Val Arg Pro Leu Val Ala Ser
 305 310 315 320
 Asp Asp Asp Pro Ser Gly Arg Asn Val Ser Arg Gly Ile Val Leu Leu
 325 330 335
 Asp His Ala Glu Arg Asp Gly Leu Asp Gly Phe Ile Thr Ile Thr Gly
 340 345 350
 Gly Lys Leu Met Thr Tyr Arg Leu Met Ala Glu Trp Ala Thr Asp Ala
 355 360 365
 Val Cys Arg Lys Leu Gly Asn Thr Arg Pro Cys Thr Thr Ala Asp Leu
 370 375 380
 Ala Leu Pro Gly Ser Gln Glu Pro Ala Glu Val Thr Leu Arg Lys Val
 385 390 395 400
 Ile Ser Leu Pro Ala Pro Leu Arg Gly Ser Ala Val Tyr Arg His Gly
 405 410 415
 Asp Arg Thr Pro Ala Trp Leu Ser Glu Gly Arg Leu His Arg Ser Leu
 420 425 430
 Val Cys Glu Cys Glu Ala Val Thr Ala Gly Glu Val Gln Tyr Ala Val
 435 440 445
 Glu Asn Leu Asn Val Asn Ser Leu Leu Asp Leu Arg Arg Arg Thr Arg
 450 455 460
 Val Gly Met Gly Thr Cys Gln Gly Glu Leu Cys Ala Cys Arg Ala Ala
 465 470 475 480
 Gly Leu Leu Gln Arg Phe Asn Val Thr Thr Ser Ala Gln Ser Ile Glu
 485 490 495
 Gln Leu Ser Thr Phe Leu Asn Glu Arg Trp Lys Gly Val Gln Pro Ile
 500 505 510
 Ala Trp Gly Asp Ala Leu Arg Glu Ser Glu Phe Thr Arg Trp Val Tyr
 515 520 525
 Gln Gly Leu Cys Gly Leu Glu Lys Glu Gln Lys Asp Ala Leu
 530 535 540

<210> 415

<211> 419

<212> PRT

<213> Escherichia coli

<400> 415

Met Arg Phe Asp Thr Val Ile Met Gly Gly Gly Leu Ala Gly Leu Leu
 1 5 10 15
 Cys Gly Leu Gln Leu Gln Lys His Gly Leu Arg Cys Ala Ile Val Thr

[illegible]

```
<210> 416
<211> 396
<212> PRT
<213> Escherichia coli
```

[illegible]

<210> 417

<212> PRT

<213> Escherichia coli

<400> 417

Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
1 5 10 15
Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
20 25 30
Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
35 40 45
Ser Ser Val Pro Phe Ser Tyr Asp Asn Gln Gln Lys Val Val Gly
50 55 60
Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
65 70 75 80
Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln
85 90 95
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly
100 105 110
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp
115 120 125
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp
130 135 140
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser
145 150 155 160
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys
165 170 175
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg
180 185 190
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu
195 200 205
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile
210 215 220
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys
225 230 235 240
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val
245 250 255
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn
260 265 270
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu
275 280 285
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn
290 295 300

<210> 418

<211> 328

<212> PRT

<213> Escherichia coli

<400> 418

Met Asn Asn Ser Ala Phe Thr Phe Gln Thr Leu His Pro Asp Thr Ile
1 5 10 15
Met Asp Ala Leu Phe Glu His Gly Ile Arg Val Asp Ser Gly Leu Thr
20 25 30
Pro Leu Asn Ser Tyr Glu Asn Arg Val Tyr Gln Phe Gln Asp Glu Asp
35 40 45
Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala
50 55 60

```

Asp Gln Ile Leu Glu Glu His Gln Phe Ala Leu Gln Leu Val Asn Asp
65          70          75          80
Glu Val Pro Val Ala Ala Pro Val Ala Phe Asn Gly Gln Thr Leu Leu
      85          90          95
Asn His Gln Gly Phe Tyr Phe Ala Val Phe Pro Ser Val Gly Gly Arg
      100          105          110
Gln Phe Glu Ala Asp Asn Ile Asp Gln Met Glu Ala Val Gly Arg Tyr
      115          120          125
Leu Gly Arg Met His Gln Thr Gly Arg Lys Gln Leu Phe Ile His Arg
      130          135          140
Pro Thr Ile Gly Leu Asn Glu Tyr Leu Ile Glu Pro Arg Lys Leu Phe
145          150          155          160
Glu Asp Ala Thr Leu Ile Pro Ser Gly Leu Lys Ala Ala Phe Leu Lys
      165          170          175
Ala Thr Asp Glu Leu Ile Ala Ala Val Thr Ala His Trp Arg Glu Asp
      180          185          190
Phe Thr Val Leu Arg Leu His Gly Asp Cys His Ala Gly Asn Ile Leu
      195          200          205
Trp Arg Asp Gly Pro Met Phe Val Asp Leu Asp Asp Ala Arg Asn Gly
      210          215          220
Pro Ala Val Gln Asp Leu Trp Met Leu Leu Asn Gly Asp Lys Ala Glu
225          230          235          240
Gln Arg Met Gln Leu Glu Thr Ile Ile Glu Ala Tyr Glu Glu Phe Ser
      245          250          255
Glu Phe Asp Thr Ala Glu Ile Gly Leu Ile Glu Pro Leu Arg Ala Met
      260          265          270
Arg Leu Val Tyr Tyr Leu Ala Trp Leu Met Arg Arg Trp Ala Asp Pro
      275          280          285
Ala Phe Pro Lys Asn Phe Pro Trp Leu Thr Gly Glu Asp Tyr Trp Leu
      290          295          300
Arg Gln Thr Ala Thr Phe Ile Glu Gln Ala Lys Val Leu Gln Glu Pro
305          310          315          320
Pro Leu Gln Leu Thr Pro Met Tyr
      325

```

```

<210> 419
<211> 208
<212> PRT
<213> Escherichia coli

```

```

<400> 419
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
 1          5          10          15
Ala Ser Ala Ala Gln Tyr Glu Asp Gly Lys Gln Tyr Thr Thr Leu Glu
      20          25          30
Lys Pro Val Ala Gly Ala Pro Gln Val Leu Glu Phe Phe Ser Phe Phe
      35          40          45
Cys Pro His Cys Tyr Gln Phe Glu Glu Val Leu His Ile Ser Asp Asn
      50          55          60
Val Lys Lys Lys Leu Pro Glu Gly Val Lys Met Thr Lys Tyr His Val
65          70          75          80
Asn Phe Met Gly Gly Asp Leu Gly Lys Asp Leu Thr Gln Ala Trp Ala
      85          90          95
Val Ala Met Ala Leu Gly Val Glu Asp Lys Val Thr Val Pro Leu Phe
      100          105          110
Glu Gly Val Gln Lys Thr Gln Thr Ile Arg Ser Ala Ser Asp Ile Arg

```

```

      115              120              125
Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala
  130              135              140
Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala
 145              150              155              160
Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly
      165              170              175
Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val
      180              185              190
Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys
      195              200              205

```

```

<210> 420
<211> 112
<212> PRT
<213> Escherichia coli

```

```

<400> 420
Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
  1              5              10              15
Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
      20              25              30
Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
      35              40              45
Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
      50              55              60
Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
      65              70              75              80
Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
      85              90              95
Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
      100              105              110

```

```

<210> 421
<211> 346
<212> PRT
<213> Escherichia coli

```

```

<400> 421
Met Lys Ser Val Val Asn Asp Thr Asp Gly Ile Val Arg Val Ala Glu
  1              5              10              15
Ser Val Ile Pro Glu Ile Lys His Gln Asp Glu Val Arg Val Lys Ile
      20              25              30
Ala Ser Ser Gly Leu Cys Gly Ser Asp Leu Pro Arg Ile Phe Lys Asn
      35              40              45
Gly Ala His Tyr Tyr Pro Ile Thr Leu Gly His Glu Phe Ser Gly Tyr
      50              55              60
Ile Asp Ala Val Gly Ser Gly Val Asp Asp Leu His Pro Gly Asp Ala
      65              70              75              80
Val Ala Cys Val Pro Leu Leu Pro Cys Phe Thr Cys Pro Glu Cys Leu
      85              90              95
Lys Gly Phe Tyr Ser Gln Cys Ala Lys Tyr Asp Phe Ile Gly Ser Arg
      100              105              110
Arg Asp Gly Gly Phe Ala Glu Tyr Ile Val Val Lys Arg Lys Asn Val
      115              120              125

```

```

Phe Ala Leu Pro Thr Asp Met Pro Ile Glu Asp Gly Ala Phe Ile Glu
130      135      140
Pro Ile Thr Val Gly Leu His Ala Phe His Leu Ala Gln Gly Cys Glu
145      150      155      160
Asn Lys Asn Val Ile Ile Ile Gly Ala Gly Thr Ile Gly Leu Leu Ala
      165      170      175
Ile Gln Cys Ala Val Ala Leu Gly Ala Lys Ser Val Thr Ala Ile Asp
      180      185      190
Ile Ser Ser Glu Lys Leu Ala Leu Ala Lys Ser Phe Gly Ala Met Gln
      195      200      205
Thr Phe Asn Ser Ser Glu Met Ser Ala Pro Gln Met Gln Ser Val Leu
      210      215      220
Arg Glu Leu Arg Phe Asn Gln Leu Ile Leu Glu Thr Ala Gly Val Pro
      225      230      235      240
Gln Thr Val Glu Leu Ala Val Glu Ile Ala Gly Pro His Ala Gln Leu
      245      250      255
Ala Leu Val Gly Thr Leu His Gln Asp Leu His Leu Thr Ser Ala Thr
      260      265      270
Phe Gly Lys Ile Leu Arg Lys Glu Leu Thr Val Ile Gly Ser Trp Met
      275      280      285
Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
      290      295      300
Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
      305      310      315      320
Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
      325      330      335
Ala Met Pro Gly Lys Val Leu Leu Ile Pro
      340      345

```

<210> 422

<211> 451

<212> PRT

<213> Escherichia coli

<400> 422

```

Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
1      5      10      15
Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
      20      25      30
Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
      35      40      45
Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
      50      55      60
Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
      65      70      75      80
Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
      85      90      95
Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
      100      105      110
Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His
      115      120      125
Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met
      130      135      140
Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu
      145      150      155      160
Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly

```

```

      165      170      175
Ile Ala Ile Pro His Gly Thr Ser Ala Tyr Met Gly Pro Ile Ala Val
      180      185      190
Leu Val Asp Ala Ile Ile Glu Lys Ile Pro Gly Val Asn Arg Ile Lys
      195      200      205
Phe Ser Ala Asp Asp Ile Gln Arg Lys Phe Gly Pro Phe Gly Glu Pro
      210      215      220
Val Thr Val Gly Phe Val Met Gly Leu Ile Ile Gly Ile Leu Ala Gly
      225      230      235      240
Tyr Asp Val Lys Gly Val Leu Gln Leu Ala Val Lys Thr Ala Ala Val
      245      250      255
Met Leu Leu Met Pro Arg Val Ile Lys Pro Ile Met Asp Gly Leu Thr
      260      265      270
Pro Ile Ala Lys Gln Ala Arg Ser Arg Leu Gln Ala Lys Phe Gly Gly
      275      280      285
Gln Glu Phe Leu Ile Gly Leu Asp Pro Ala Leu Leu Leu Gly His Thr
      290      295      300
Ala Val Val Ser Ala Ser Leu Ile Phe Ile Pro Leu Thr Ile Leu Ile
      305      310      315      320
Ala Val Cys Val Pro Gly Asn Gln Val Leu Pro Phe Gly Asp Leu Ala
      325      330      335
Thr Ile Gly Phe Phe Val Ala Met Ala Val Ala Val His Arg Gly Asn
      340      345      350
Leu Phe Arg Thr Leu Ile Ser Gly Val Ile Ile Met Ser Ile Thr Leu
      355      360      365
Trp Ile Ala Thr Gln Thr Ile Gly Leu His Thr Gln Leu Ala Ala Asn
      370      375      380
Ala Gly Ala Leu Lys Ala Gly Gly Met Val Ala Ser Met Asp Gln Gly
      385      390      395      400
Gly Ser Pro Ile Thr Trp Leu Leu Ile Gln Val Phe Ser Pro Gln Asn
      405      410      415
Ile Pro Gly Phe Ile Ile Ile Gly Ala Ile Tyr Leu Thr Gly Ile Phe
      420      425      430
Met Thr Trp Arg Arg Ala Arg Gly Phe Ile Lys Gln Glu Lys Val Val
      435      440      445
Leu Ala Glu
      450

```

<210> 423
 <211> 94
 <212> PRT
 <213> Escherichia coli

```

<400> 423
Met Lys Arg Lys Ile Ile Val Ala Cys Gly Gly Ala Val Ala Thr Ser
 1      5      10      15
Thr Met Ala Ala Glu Glu Ile Lys Glu Leu Cys Gln Asn His Asn Ile
      20      25      30
Pro Val Glu Leu Ile Gln Cys Arg Val Asn Glu Ile Glu Thr Tyr Met
      35      40      45
Asp Gly Val His Leu Ile Cys Thr Thr Ala Lys Val Asp Arg Ser Phe
      50      55      60
Gly Asp Ile Pro Leu Val His Gly Met Pro Phe Ile Ser Gly Ile Gly
      65      70      75      80
Ile Glu Ala Leu Gln Asn Lys Ile Leu Thr Ile Leu Gln Gly
      85      90

```

<210> 424
 <211> 150
 <212> PRT
 <213> Escherichia coli

<400> 424

```

Met Thr Asn Leu Phe Val Arg Ser Gly Ile Ser Phe Val Asp Arg Ser
 1           5           10           15
Glu Val Leu Thr His Ile Gly Asn Glu Met Leu Ala Lys Gly Val Val
      20           25           30
His Asp Thr Trp Pro Gln Ala Leu Ile Ala Arg Glu Ala Glu Phe Pro
      35           40           45
Thr Gly Ile Met Leu Glu Gln His Ala Ile Ala Ile Pro His Cys Glu
      50           55           60
Ala Ile His Ala Lys Ser Ser Ala Ile Tyr Leu Leu Arg Pro Thr Asn
      65           70           75           80
Lys Val His Phe Gln Gln Ala Asp Asp Asp Asn Asp Val Ala Val Ser
      85           90           95
Leu Val Ile Ala Leu Ile Val Glu Asn Pro Gln Gln Gln Leu Lys Leu
      100          105          110
Leu Arg Cys Leu Phe Gly Lys Leu Gln Gln Pro Asp Ile Val Glu Thr
      115          120          125
Leu Ile Thr Leu Pro Glu Thr Gln Leu Lys Glu Tyr Phe Thr Lys Tyr
      130          135          140
Val Leu Asp Ser Asp Glu
      145          150

```

<210> 425
 <211> 420
 <212> PRT
 <213> Escherichia coli

<400> 425

```

Met Lys Thr Leu Ile Ala Arg His Lys Ala Gly Glu His Ile Gly Ile
 1           5           10           15
Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
      20           25           30
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
      35           40           45
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
      50           55           60
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
      65           70           75           80
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
      85           90           95
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
      100          105          110
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
      115          120          125
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
      130          135          140
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
      145          150          155          160
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly

```


Phe	Asp	Val	Ser	Val	Glu	Ala	Glu	Leu	Gly	Gln	Leu	Gly	Gly	Gln	Glu
130						135					140				
Asp	Asp	Val	Gln	Val	Asn	Glu	Ala	Asp	Ala	Leu	Tyr	Thr	Asn	Pro	Ala
145					150					155					160
Gln	Ala	Arg	Glu	Phe	Ala	Glu	Ala	Thr	Gly	Ile	Asp	Ser	Leu	Ala	Val
				165					170						175
Ala	Ile	Gly	Thr	Ala	His	Gly	Met	Tyr	Ala	Ser	Ala	Pro	Ala	Leu	Asp
			180					185					190		
Phe	Ser	Arg	Leu	Glu	Asn	Ile	Arg	Gln	Trp	Val	Asn	Leu	Pro	Leu	Val
		195					200					205			
Leu	His	Gly	Ala	Ser	Gly	Leu	Ser	Thr	Lys	Asp	Ile	Gln	Gln	Thr	Ile
	210					215					220				
Lys	Leu	Gly	Ile	Cys	Lys	Ile	Asn	Val	Ala	Thr	Glu	Leu	Lys	Asn	Ala
225					230					235					240
Phe	Ser	Gln	Ala	Leu	Lys	Asn	Tyr	Leu	Thr	Glu	His	Pro	Glu	Ala	Thr
				245					250						255
Asp	Pro	Arg	Asp	Tyr	Leu	Gln	Ser	Ala	Lys	Ser	Ala	Met	Arg	Asp	Val
			260					265					270		
Val	Ser	Lys	Val	Ile	Ala	Asp	Cys	Gly	Cys	Glu	Gly	Arg	Ala		
		275					280						285		

<210> 427
 <211> 157
 <212> PRT
 <213> Escherichia coli

<400> 427															
Met	Ser	Gln	Asn	Asp	Ile	Ile	Ile	Arg	Thr	His	Tyr	Lys	Ser	Pro	His
1				5					10					15	
Arg	Leu	His	Ile	Asp	Ser	Asp	Ile	Pro	Thr	Pro	Ser	Ser	Glu	Pro	Ile
			20					25					30		
Asn	Gln	Phe	Ala	Arg	Gln	Leu	Ile	Thr	Leu	Leu	Asp	Thr	Ser	Asp	Leu
		35				40					45				
Ser	Ser	Met	Leu	Ser	Tyr	Cys	Val	Thr	Gln	Glu	Phe	Thr	Ala	Asn	Cys
	50					55					60				
Arg	Lys	Ile	Ser	Gln	Asn	Cys	Tyr	Ser	Thr	Ala	Leu	Phe	Thr	Ile	Asn
65				70					75						80
Phe	Ala	Thr	Ser	Pro	Ile	His	Thr	Glu	Asn	Ile	Leu	Ile	Thr	Leu	His
			85					90						95	
Tyr	Lys	Lys	Glu	Ile	Ile	Ser	Leu	Leu	Leu	Glu	Thr	Thr	Pro	Ile	Lys
		100					105						110		
Ala	Asn	His	Leu	Arg	Ser	Ile	Leu	Asp	Tyr	Ile	Glu	Gln	Glu	Gln	Leu
		115					120					125			
Thr	Ala	Glu	Asp	Arg	Asn	His	Cys	Met	Lys	Leu	Ser	Lys	Lys	Ile	His
	130					135					140				
Arg	Glu	Lys	Asn	Tyr	Thr	Pro	Asn	Ser	Lys	Ser	Gln	Trp			
145					150							155			

<210> 428
 <211> 471
 <212> PRT
 <213> Escherichia coli

<400> 428
 Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln

Asp Glu Ile Lys Thr Tyr Leu
465 470

<210> 429
<211> 128
<212> PRT
<213> Escherichia coli

<400> 429
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

<210> 430
<211> 398
<212> PRT
<213> Escherichia coli

<400> 430
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30
Asp Ala Ile Ile Pro Ala Tyr Asn Glu Gly Pro Cys Leu Ala Gln Ser
35 40 45
Leu Asp Asn Leu Leu Arg Asn Pro Tyr Phe Cys Arg Val Ile Cys Val
50 55 60
Asn Asp Gly Ser Thr Asp Asn Thr Glu Ala Val Met Ala Glu Val Lys
65 70 75 80
Arg Lys Trp Gly Asp Arg Phe Val Ala Val Thr Gln Lys Asn Thr Gly
85 90 95
Lys Gly Gly Ala Leu Met Asn Gly Leu Asn Tyr Ala Thr Cys Asp Gln
100 105 110
Val Phe Leu Ser Asp Ala Asp Thr Tyr Val Pro Pro Asp Gln Asp Gly
115 120 125
Met Gly Tyr Met Leu Ala Glu Ile Glu Arg Gly Ala Asp Ala Val Gly
130 135 140
Gly Ile Pro Ser Thr Ala Leu Lys Gly Ala Gly Leu Leu Pro His Ile
145 150 155 160
Arg Ala Thr Val Lys Leu Pro Met Ile Val Met Lys Arg Thr Leu Gln
165 170 175
Gln Leu Leu Gly Gly Ala Pro Phe Ile Ile Ser Gly Ala Cys Gly Met

180 185 190
 Phe Arg Thr Asp Val Leu Arg Lys Phe Gly Phe Ser Asp Arg Thr Lys
 195 200 205
 Val Glu Asp Leu Asp Leu Thr Trp Thr Leu Val Ala Asn Gly Tyr Arg
 210 215 220
 Ile Arg Gln Ala Asn Arg Cys Ile Val Tyr Pro Gln Glu Cys Asn Ser
 225 230 235 240
 Pro Arg Glu Glu Trp Arg Arg Trp Arg Trp Ile Val Gly Tyr Ala
 245 250 255
 Val Cys Met Arg Leu His Lys Arg Leu Leu Phe Ser Arg Phe Gly Ile
 260 265 270
 Phe Ser Ile Phe Pro Met Leu Leu Val Val Leu Tyr Gly Val Gly Ile
 275 280 285
 Tyr Leu Thr Thr Trp Phe Asn Glu Phe Ile Thr Thr Gly Pro His Gly
 290 295 300
 Val Val Leu Ala Met Phe Pro Leu Ile Trp Val Gly Val Val Cys Val
 305 310 315 320
 Ile Gly Ala Phe Ser Ala Trp Phe His Arg Cys Trp Leu Leu Val Pro
 325 330 335
 Leu Ala Pro Leu Ser Val Val Tyr Val Leu Leu Ala Tyr Ala Ile Trp
 340 345 350
 Ile Ile Tyr Gly Leu Ile Ala Phe Phe Thr Gly Arg Glu Pro Gln Arg
 355 360 365
 Asp Lys Pro Thr Arg Tyr Ser Ala Leu Val Glu Ala Ser Thr Ala Tyr
 370 375 380
 Ser Gln Pro Ser Val Thr Gly Thr Glu Lys Leu Ser Glu Ala
 385 390 395

<210> 431

<211> 552

<212> PRT

<213> Escherichia coli

<400> 431

Met Ile Leu Glu Arg Val Glu Ile Val Gly Phe Arg Gly Ile Asn Arg
 1 5 10 15
 Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala
 20 25 30
 Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Ser Pro
 35 40 45
 Glu Ser Asp Leu Tyr His Phe Glu Arg Asp Asp Phe Trp Phe Pro Pro
 50 55 60
 Gly Asp Ile Asn Gly Arg Glu His His Leu His Ile Ile Leu Thr Phe
 65 70 75 80
 Arg Glu Ser Leu Pro Gly Arg His Arg Val Arg Arg Tyr Arg Pro Leu
 85 90 95
 Glu Ala Cys Trp Thr Pro Cys Thr Asp Gly Tyr His Arg Ile Phe Tyr
 100 105 110
 Arg Leu Glu Gly Glu Ser Ala Glu Asp Gly Ser Val Met Thr Leu Arg
 115 120 125
 Ser Phe Leu Asp Lys Asp Gly His Pro Ile Asp Val Glu Asp Ile Asn
 130 135 140
 Asp Gln Ala Arg His Leu Val Arg Leu Met Pro Val Leu Arg Leu Arg
 145 150 155 160
 Asp Ala Arg Phe Met Arg Arg Ile Arg Asn Gly Thr Val Pro Asn Val
 165 170 175

Pro Asn Val Glu Val Thr Ala Arg Gln Leu Asp Phe Leu Ala Arg Glu
180 185 190
Leu Ser Ser His Pro Gln Asn Leu Ser Asp Gly Gln Ile Arg Gln Gly
195 200 205
Leu Ser Ala Met Val Gln Leu Leu Glu His Tyr Phe Ser Glu Gln Gly
210 215 220
Ala Gly Gln Ala Arg Tyr Arg Leu Met Arg Arg Ala Ser Asn Glu
225 230 235 240
Gln Arg Ser Trp Arg Tyr Leu Asp Ile Ile Asn Arg Met Ile Asp Arg
245 250 255
Pro Gly Gly Arg Ser Tyr Arg Val Ile Leu Leu Gly Leu Phe Ala Thr
260 265 270
Leu Leu Gln Ala Lys Gly Thr Leu Arg Leu Asp Lys Asp Ala Arg Pro
275 280 285
Leu Leu Leu Ile Glu Asp Pro Glu Thr Arg Leu His Pro Ile Met Leu
290 295 300
Ser Val Ala Trp His Leu Leu Asn Leu Leu Pro Leu Gln Arg Ile Ala
305 310 315 320
Thr Thr Asn Ser Gly Glu Leu Leu Ser Leu Thr Pro Val Glu His Val
325 330 335
Cys Arg Leu Val Arg Glu Ser Ser Arg Val Ala Ala Trp Arg Leu Gly
340 345 350
Pro Ser Gly Leu Ser Thr Glu Asp Ser Arg Arg Ile Ser Phe His Ile
355 360 365
Arg Phe Asn Arg Pro Ser Ser Leu Phe Ala Arg Cys Trp Leu Leu Val
370 375 380
Glu Gly Glu Thr Glu Thr Trp Val Ile Asn Glu Leu Ala Arg Gln Cys
385 390 395 400
Gly His His Phe Asp Ala Glu Gly Ile Lys Val Ile Glu Phe Ala Gln
405 410 415
Ser Gly Leu Lys Pro Leu Val Lys Phe Ala Arg Arg Met Gly Ile Glu
420 425 430
Trp His Val Leu Val Asp Gly Asp Glu Ala Gly Lys Lys Tyr Ala Ala
435 440 445
Thr Val Arg Ser Leu Leu Asn Asn Asp Arg Glu Ala Glu Arg Glu His
450 455 460
Leu Thr Ala Leu Pro Ala Leu Asp Met Glu His Phe Met Tyr Arg Gln
465 470 475 480
Gly Phe Ser Asp Val Phe His Arg Met Ala Gln Ile Pro Glu Asn Val
485 490 495
Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser
500 505 510
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly
515 520 525
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu
530 535 540
Trp Leu Ala Arg Gly Arg Ala Asp
545 550

<210> 432

<211> 352

<212> PRT

<213> Escherichia coli

<400> 432

Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu

1 5 10 15
 Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu
 20 25 30
 Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys
 35 40 45
 His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro
 50 55 60
 Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp
 65 70 75 80
 Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro
 85 90 95
 Ile Glu Leu Pro Ala Asn Tyr Lys Asp Lys Glu Leu Val Arg Thr Ile
 100 105 110
 Ile Asn Asp Asn Ile Val Glu Lys Thr His Asp Ile Asn Asn Lys Glu
 115 120 125
 Met Ile Phe Ser Ala Leu Lys Glu Ile Tyr Asp Gly Asp Pro Gly Phe
 130 135 140
 Ile Phe Asp Lys Ile Ser His Lys Leu Arg His Thr Val Thr Glu Phe
 145 150 155 160
 Asp Glu Ser Gly Lys Ser Glu Pro Thr Asp Leu Phe Thr Trp Tyr Gly
 165 170 175
 Lys Asp Lys Lys Gly Asp Ser Leu Ala Ile Val Ile Lys Asn Lys Asn
 180 185 190
 Gly Asn Asp Tyr Leu Ser Leu Gly Tyr Tyr Asp Gln Asp Asp Tyr His
 195 200 205
 Ile Gln Arg Gly Ile Arg Ile Asn Gly Asp Ser Leu Thr Gln Tyr Cys
 210 215 220
 Ser Glu Asn Ala Arg Ser Ala Ser Ala Trp Phe Glu Ser Ser Lys Ala
 225 230 235 240
 Ile Met Ala Glu Ser Phe Ala Thr Gly Ser Asp His Gln Val Val Asn
 245 250 255
 Glu Leu Asn Gly Glu Arg Leu Arg Glu Pro Asn Asp Val Phe Lys Arg
 260 265 270
 Tyr Gly Arg Ala Ile Arg Tyr Asp Phe Gln Val Asp Asp Ala Lys Tyr
 275 280 285
 Lys Cys Asp His Leu Lys Glu Ile Val Ser Thr Leu Val Gly Asn Lys
 290 295 300
 Ile Asn Val Gly His Ser Gln Lys Ile Tyr Lys His Phe Lys Asp Leu
 305 310 315 320
 Glu Gly Lys Ile Glu Glu Arg Leu Gln Asn Arg Gln Ala Glu Tyr Gln
 325 330 335
 Asn Glu Ile Asn Gln Pro Ser Ala Pro Gly Val Asn Phe Asp Asp Ile
 340 345 350

<210> 433
 <211> 375
 <212> PRT
 <213> Escherichia coli

<400> 433
 Met Met Arg His Leu Arg Asn Ile Phe Asn Leu Gly Ile Lys Glu Leu
 1 5 10 15
 Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser
 20 25 30
 Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu
 35 40 45

Asn	Leu	Ala	Pro	Ile	Ala	Ile	Ala	Asp	Met	Asp	Gln	Ser	Gln	Leu	Ser
50						55					60				
Asn	Arg	Ile	Val	Asn	Ser	Phe	Tyr	Arg	Pro	Trp	Phe	Leu	Pro	Pro	Glu
65					70					75					80
Met	Ile	Thr	Ala	Asp	Glu	Met	Asp	Ala	Gly	Leu	Asp	Ala	Gly	Arg	Tyr
				85					90					95	
Thr	Phe	Ala	Ile	Asn	Ile	Pro	Pro	Asn	Phe	Gln	Arg	Asp	Val	Leu	Ala
			100					105					110		
Gly	Arg	Gln	Pro	Asp	Ile	Gln	Val	Asn	Val	Asp	Ala	Thr	Arg	Met	Ser
		115					120					125			
Gln	Ala	Phe	Thr	Gly	Asn	Gly	Tyr	Ile	Gln	Asn	Ile	Ile	Asn	Gly	Glu
		130				135					140				
Val	Asn	Ser	Phe	Val	Ala	Arg	Tyr	Arg	Asp	Asn	Ser	Glu	Pro	Leu	Val
145					150					155					160
Ser	Leu	Glu	Thr	Arg	Met	Arg	Phe	Asn	Pro	Asn	Leu	Asp	Pro	Ala	Trp
				165					170					175	
Phe	Gly	Gly	Val	Met	Ala	Ile	Ile	Asn	Asn	Ile	Thr	Met	Leu	Ala	Ile
			180					185					190		
Val	Leu	Thr	Gly	Ser	Ala	Leu	Ile	Arg	Glu	Arg	Glu	His	Gly	Thr	Val
		195					200					205			
Glu	His	Leu	Leu	Val	Met	Pro	Ile	Thr	Pro	Phe	Glu	Ile	Met	Met	Ala
		210				215					220				
Lys	Ile	Trp	Ser	Met	Gly	Leu	Val	Val	Leu	Val	Val	Ser	Gly	Leu	Ser
225					230					235					240
Leu	Val	Leu	Met	Val	Lys	Gly	Val	Leu	Gly	Val	Pro	Ile	Glu	Gly	Ser
				245					250					255	
Ile	Pro	Leu	Phe	Met	Leu	Gly	Val	Ala	Leu	Ser	Leu	Phe	Ala	Thr	Thr
			260					265					270		
Ser	Ile	Gly	Ile	Phe	Met	Gly	Thr	Ile	Ala	Arg	Ser	Met	Pro	Gln	Leu
		275					280					285			
Gly	Leu	Leu	Val	Ile	Leu	Val	Leu	Leu	Pro	Leu	Gln	Met	Leu	Ser	Gly
		290				295					300				
Gly	Ser	Thr	Pro	Arg	Glu	Ser	Met	Pro	Gln	Met	Val	Gln	Asp	Ile	Met
305					310					315					320
Leu	Thr	Met	Pro	Thr	Thr	His	Phe	Val	Ser	Leu	Ala	Gln	Ala	Ile	Leu
				325					330					335	
Tyr	Arg	Gly	Ala	Gly	Phe	Glu	Ile	Val	Trp	Pro	Gln	Phe	Leu	Thr	Leu
			340					345					350		
Met	Ala	Ile	Gly	Gly	Ala	Phe	Phe	Thr	Ile	Ala	Leu	Leu	Arg	Phe	Arg
		355					360					365			
Lys	Thr	Ile	Gly	Thr	Met	Ala									
		370				375									

<210> 434

<211> 894

<212> PRT

<213> Escherichia coli

<400> 434

Met	Ser	Gln	His	Tyr	Gly	Lys	Thr	Val	Ala	Leu	Asn	Asn	Ile	Thr	Leu
1				5					10				15		
Asp	Ile	Pro	Ala	Arg	Cys	Met	Val	Gly	Leu	Ile	Gly	Pro	Asp	Gly	Val
		20						25				30			
Gly	Lys	Ser	Ser	Leu	Leu	Ser	Leu	Ile	Ser	Gly	Ala	Arg	Val	Ile	Glu
		35				40						45			
Gln	Gly	Asn	Val	Met	Val	Leu	Gly	Gly	Asp	Met	Arg	Asp	Pro	Lys	His

Thr	Thr	His	Ala	Pro	Arg	Gln	Gly	Phe	Ser	Leu	Arg	Arg	Leu	Phe	Ser
		515					520					525			
Tyr	Ser	Arg	Arg	Glu	Ala	Leu	Glu	Leu	Arg	Arg	Asp	Pro	Val	Arg	Ser
	530					535					540				
Thr	Leu	Ala	Leu	Met	Gly	Thr	Val	Ile	Leu	Met	Leu	Ile	Met	Gly	Tyr
545					550					555					560
Gly	Ile	Ser	Met	Asp	Val	Glu	Asn	Leu	Arg	Phe	Ala	Val	Leu	Asp	Arg
				565						570				575	
Asp	Gln	Thr	Val	Ser	Ser	Gln	Ala	Trp	Thr	Leu	Asn	Leu	Ser	Gly	Ser
			580					585					590		
Arg	Tyr	Phe	Ile	Glu	Gln	Pro	Pro	Leu	Thr	Ser	Tyr	Asp	Glu	Leu	Asp
		595					600					605			
Arg	Arg	Met	Arg	Ala	Gly	Asp	Ile	Thr	Val	Ala	Ile	Glu	Ile	Pro	Pro
		610				615					620				
Asn	Phe	Gly	Arg	Asp	Ile	Ala	Arg	Gly	Thr	Pro	Val	Glu	Leu	Gly	Val
625					630						635				640
Trp	Ile	Asp	Gly	Ala	Met	Pro	Ser	Arg	Ala	Glu	Thr	Val	Lys	Gly	Tyr
				645					650					655	
Val	Gln	Ala	Met	His	Gln	Ser	Trp	Leu	Gln	Asp	Val	Ala	Ser	Arg	Gln
			660					665					670		
Ser	Thr	Pro	Ala	Ser	Gln	Ser	Gly	Leu	Met	Asn	Ile	Glu	Thr	Arg	Tyr
		675					680					685			
Arg	Tyr	Asn	Pro	Asp	Val	Lys	Ser	Leu	Pro	Ala	Ile	Val	Pro	Ala	Val
		690				695					700				
Ile	Pro	Leu	Leu	Leu	Met	Met	Ile	Pro	Ser	Met	Leu	Ser	Ala	Leu	Ser
705					710						715				720
Val	Val	Arg	Glu	Lys	Glu	Leu	Gly	Ser	Ile	Ile	Asn	Leu	Tyr	Val	Thr
				725						730				735	
Pro	Thr	Thr	Arg	Ser	Glu	Phe	Leu	Leu	Gly	Lys	Gln	Leu	Pro	Tyr	Ile
			740					745					750		
Ala	Leu	Gly	Met	Leu	Asn	Phe	Phe	Leu	Leu	Cys	Gly	Leu	Ser	Val	Phe
		755					760					765			
Val	Phe	Gly	Val	Pro	His	Lys	Gly	Ser	Phe	Leu	Thr	Leu	Thr	Leu	Ala
		770				775					780				
Ala	Leu	Leu	Tyr	Ile	Ile	Ile	Ala	Thr	Gly	Met	Gly	Leu	Leu	Ile	Ser
785					790						795				800
Thr	Phe	Met	Lys	Ser	Gln	Ile	Ala	Ala	Ile	Phe	Gly	Thr	Ala	Ile	Ile
				805						810				815	
Thr	Leu	Ile	Pro	Ala	Thr	Gln	Phe	Ser	Gly	Met	Ile	Asp	Pro	Val	Ala
			820					825					830		
Ser	Leu	Glu	Gly	Pro	Gly	Arg	Trp	Ile	Gly	Glu	Val	Tyr	Pro	Thr	Ser
		835					840					845			
His	Phe	Leu	Thr	Ile	Ala	Arg	Gly	Thr	Phe	Ser	Lys	Ala	Leu	Asp	Leu
		850				855					860				
Thr	Asp	Leu													

<210> 435

<211> 355

<212> PRT

<213> Escherichia coli

<400> 435

Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu

Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val
 20 25 30
 Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val
 35 40 45
 Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys
 50 55 60
 Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr
 65 70 75 80
 Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu
 85 90 95
 Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln
 100 105 110
 Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu
 115 120 125
 Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln
 130 135 140
 Arg Gly Ala Ile Ser Ala Gln Gln Leu Asp Asp Asp Arg Ala Ala Ala
 145 150 155 160
 Glu Ser Ala Arg Ala Ala Leu Glu Ser Ala Lys Ala Gln Val Ser Ala
 165 170 175
 Ser Lys Ala Ala Ile Glu Ala Ala Arg Thr Asn Ile Ile Gln Ala Gln
 180 185 190
 Thr Arg Val Glu Ala Ala Gln Ala Thr Glu Arg Arg Ile Ala Ala Asp
 195 200 205
 Ile Asp Asp Ser Glu Leu Lys Ala Pro Arg Asp Gly Arg Val Gln Tyr
 210 215 220
 Arg Val Ala Glu Pro Gly Glu Val Leu Ala Ala Gly Gly Arg Val Leu
 225 230 235 240
 Asn Met Val Asp Leu Ser Asp Val Tyr Met Thr Phe Phe Leu Pro Thr
 245 250 255
 Glu Gln Ala Gly Thr Leu Lys Leu Gly Gly Glu Ala Arg Leu Ile Leu
 260 265 270
 Asp Ala Ala Pro Asp Leu Arg Ile Pro Ala Thr Ile Ser Phe Val Ala
 275 280 285
 Ser Val Ala Gln Phe Thr Pro Lys Thr Val Glu Thr Ser Asp Glu Arg
 290 295 300
 Leu Lys Leu Met Phe Arg Val Lys Ala Arg Ile Pro Pro Glu Leu Leu
 305 310 315 320
 Gln Gln His Leu Glu Tyr Val Lys Thr Gly Leu Pro Gly Val Ala Trp
 325 330 335
 Val Arg Val Asn Glu Glu Leu Pro Trp Pro Asp Asp Leu Val Val Arg
 340 345 350
 Leu Pro Gln
 355

<210> 436

<211> 235

<212> PRT

<213> Escherichia coli

<400> 436

Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe
 1 5 10 15
 Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys
 20 25 30

Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys
35 40 45
Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln
50 55 60
Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val
65 70 75 80
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln
85 90 95
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr
100 105 110
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu
115 120 125
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly
130 135 140
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys
145 150 155 160
Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr
165 170 175
Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr
180 185 190
Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu
195 200 205
Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
210 215 220
Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser
225 230 235

<210> 437

<211> 480

<212> PRT

<213> Escherichia coli

<400> 437

Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro
1 5 10 15
Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala
20 25 30
Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys
35 40 45
Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His
50 55 60
Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr
65 70 75 80
Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu
85 90 95
Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile
100 105 110
Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu
115 120 125
Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met
130 135 140
Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys
145 150 155 160
Gly Ile Asn Lys Leu Gly Gly Gly Leu Ser Ala Glu Ala Leu Thr Glu
165 170 175
Lys Asp Lys Ala Asp Ile Lys Thr Ala Ala Leu Ile Gly Val Asp Tyr

245 250 255
 Tyr Arg Lys Ser Gln Asp Asp Glu Lys Leu Ser Thr Leu Ser His Ser
 260 265 270
 Trp Ser Gln Val Val Asp Val Ser Glu Val Leu Arg Asp Gly Thr Pro
 275 280 285
 Arg Arg Asp Glu Glu Ile Thr Ile Lys Asp Arg Leu Leu Leu Ile Asn
 290 295 300
 Thr Val Pro Val Arg Ser Asn Gly Val Ile Ile Gly Ala Ile Ser Thr
 305 310 315 320
 Phe Arg Asp Lys Thr Glu Val Arg Lys Leu Met Gln Arg Leu Asp Gly
 325 330 335
 Leu Val Asn Tyr Ala Asp Ala Leu Arg Glu Arg Ser His Glu Phe Met
 340 345 350
 Asn Lys Leu His Val Ile Leu Gly Leu Leu His Leu Lys Ser Tyr Lys
 355 360 365
 Gln Leu Glu Asp Tyr Ile Leu Lys Thr Ala Asn Asn Tyr Gln Glu Glu
 370 375 380
 Ile Gly Ser Leu Leu Gly Lys Ile Lys Ser Pro Val Ile Ala Gly Phe
 385 390 395 400
 Leu Ile Ser Lys Ile Asn Arg Ala Thr Asp Leu Gly His Thr Leu Ile
 405 410 415
 Leu Asn Ser Glu Ser Gln Leu Pro Asp Ser Gly Ser Glu Asp Gln Val
 420 425 430
 Ala Thr Leu Ile Thr Thr Leu Gly Asn Leu Ile Glu Asn Ala Leu Glu
 435 440 445
 Ala Leu Gly Pro Glu Pro Gly Gly Glu Ile Ser Val Thr Leu His Tyr
 450 455 460
 Arg His Gly Trp Leu His Cys Glu Val Asn Asp Asp Gly Pro Gly Ile
 465 470 475 480
 Ala Pro Asp Lys Ile Asp His Ile Phe Asp Lys Gly Val Ser Thr Lys
 485 490 495
 Gly Ser Glu Arg Gly Val Gly Leu Ala Leu Val Lys Gln Gln Val Glu
 500 505 510
 Asn Leu Gly Gly Ser Ile Ala Val Glu Ser Glu Pro Gly Ile Phe Thr
 515 520 525
 Gln Phe Phe Val Gln Ile Pro Trp Asp Gly Glu Arg Ser Asn Arg
 530 535 540

<210> 440

<211> 328

<212> PRT

<213> Escherichia coli

<400> 440

Met Ser Val Pro Leu Ser Thr Trp Asn Leu Leu Arg Tyr Asn Asn Ser
 1 5 10 15
 Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu
 20 25 30
 Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu
 35 40 45
 Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr
 50 55 60
 Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile
 65 70 75 80
 Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu
 85 90 95

<400>	442														
Met	Arg	Tyr	Asn	Gly	Leu	Asn	Asn	Met	Phe	Phe	Pro	Leu	Cys	Leu	Ile
1				5					10					15	
Asn	Asp	Asn	His	Ser	Val	Thr	Ser	Pro	Ser	His	Thr	Lys	Lys	Thr	Lys
			20					25					30		
Ser	Asp	Asn	Tyr	Ser	Lys	His	His	Lys	Asn	Thr	Leu	Ile	Asp	Asn	Lys
		35					40					45			
Ala	Leu	Ser	Leu	Phe	Lys	Met	Asp	Asp	His	Glu	Lys	Val	Ile	Gly	Leu
50						55					60				
Ile	Gln	Lys	Met	Lys	Arg	Ile	Tyr	Asp	Ser	Leu	Pro	Ser	Gly	Lys	Ile
65					70					75				80	
Thr	Lys	Glu	Thr	Asp	Arg	Lys	Ile	His	Lys	Tyr	Phe	Ile	Asp	Ile	Ala
				85					90					95	
Ser	His	Ala	Asn	Asn	Lys	Cys	Asp	Asp	Arg	Ile	Thr	Arg	Arg	Val	Tyr
			100					105					110		
Leu	Asn	Lys	Asp	Lys	Glu	Val	Ser	Ile	Lys	Val	Val	Tyr	Phe	Ile	Asn
		115					120					125			
Asn	Val	Thr	Val	His	Asn	Asn	Thr	Ile	Glu	Ile	Pro	Gln	Thr	Val	Asn
		130				135					140				
Gly	Gly	Tyr	Asp	Phe	Ser	His	Leu	Ser	Leu	Lys	Gly	Ile	Val	Ile	Lys
145					150					155				160	
Asp	Glu	Asp	Leu	Ser	Asn	Ser	Asn	Phe	Ala	Gly	Cys	Arg	Leu	Gln	Asn
				165					170					175	
Ala	Ile	Phe	Gln	Asp	Cys	Asn	Met	Tyr	Lys	Thr	Asn	Phe	Asn	Phe	Ala
			180					185					190		
Ile	Met	Glu	Lys	Ile	Leu	Phe	Asp	Asn	Cys	Ile	Leu	Asp	Asp	Ser	Asn
		195					200					205			
Phe	Ala	Gln	Ile	Lys	Met	Thr	Asp	Gly	Thr	Leu	Asn	Ser	Cys	Ser	Ala
		210					215				220				
Met	His	Val	Gln	Phe	Tyr	Asn	Ala	Thr	Met	Asn	Arg	Ala	Asn	Ile	Lys
225					230					235				240	
Asn	Thr	Phe	Leu	Asp	Tyr	Ser	Asn	Phe	Tyr	Met	Ala	Tyr	Met	Ala	Glu
				245					250					255	
Val	Asn	Leu	Tyr	Lys	Val	Ile	Ala	Pro	Tyr	Ile	Asn	Leu	Phe	Arg	Ala
			260					265					270		
Asp	Leu	Ser	Phe	Ser	Lys	Leu	Asp	Leu	Ile	Asn	Phe	Glu	His	Ala	Asp
		275					280					285			
Leu	Ser	Arg	Val	Asn	Leu	Asn	Lys	Ala	Thr	Leu	Gln	Asn	Ile	Asn	Leu
						295					300				
Ile	Asp	Ser	Lys	Leu	Phe	Phe	Thr	Arg	Leu	Thr	Asn	Thr	Phe	Leu	Glu
305					310					315					320
Met	Val	Ile	Cys	Thr	Asp	Ser	Asn	Met	Ala	Asn	Val	Asn	Phe	Asn	Asn
				325					330					335	
Ala	Asn	Leu	Ser	Asn	Cys	His	Phe	Asn	Cys	Ser	Val	Leu	Thr	Lys	Ala
			340</												

<210> 443
 <211> 883
 <212> PRT
 <213> Escherichia coli

<400> 443

Met	Asn	Glu	Gln	Tyr	Ser	Ala	Leu	Arg	Ser	Asn	Val	Ser	Met	Leu	Gly
1				5					10					15	
Lys	Val	Leu	Gly	Glu	Thr	Ile	Lys	Asp	Ala	Leu	Gly	Glu	His	Ile	Leu
			20					25					30		
Glu	Arg	Val	Glu	Thr	Ile	Arg	Lys	Leu	Ser	Lys	Ser	Ser	Arg	Ala	Gly
		35					40					45			
Asn	Asp	Ala	Asn	Arg	Gln	Glu	Leu	Leu	Thr	Thr	Leu	Gln	Asn	Leu	Ser
	50					55					60				
Asn	Asp	Glu	Leu	Leu	Pro	Val	Ala	Arg	Ala	Phe	Ser	Gln	Phe	Leu	Asn
65					70					75					80
Leu	Ala	Asn	Thr	Ala	Glu	Gln	Tyr	His	Ser	Ile	Ser	Pro	Lys	Gly	Glu
				85					90					95	
Ala	Ala	Ser	Asn	Pro	Glu	Val	Ile	Ala	Arg	Thr	Leu	Arg	Lys	Leu	Lys
			100					105					110		
Asn	Gln	Pro	Glu	Leu	Ser	Glu	Asp	Thr	Ile	Lys	Lys	Ala	Val	Glu	Ser
		115					120					125			
Leu	Ser	Leu	Glu	Leu	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Ile	Thr	Arg
	130					135					140				
Arg	Thr	Leu	Ile	His	Lys	Met	Val	Glu	Val	Asn	Ala	Cys	Leu	Lys	Gln
145					150					155					160
Leu	Asp	Asn	Lys	Asp	Ile	Ala	Asp	Tyr	Glu	His	Asn	Gln	Leu	Met	Arg
				165					170					175	
Arg	Leu	Arg	Gln	Leu	Ile	Ala	Gln	Ser	Trp	His	Thr	Asp	Glu	Ile	Arg
			180					185					190		
Lys	Leu	Arg	Pro	Ser	Pro	Val	Asp	Glu	Ala	Lys	Trp	Gly	Phe	Ala	Val
		195					200					205			
Val	Glu	Asn	Ser	Leu	Trp	Gln	Gly	Val	Pro	Asn	Tyr	Leu	Arg	Glu	Leu
	210					215					220				
Asn	Glu	Gln	Leu	Glu	Glu	Asn	Leu	Gly	Tyr	Lys	Leu	Pro	Val	Glu	Phe
225					230					235					240
Val	Pro	Val	Arg	Phe	Thr	Ser	Trp	Met	Gly	Gly	Asp	Arg	Asp	Gly	Asn
				245					250					255	
Pro	Asn	Val	Thr	Ala	Asp	Ile	Thr	Arg	His	Val	Leu	Leu	Leu	Ser	Arg
		260						265					270		
Trp	Lys	Ala	Thr	Asp	Leu	Phe	Leu	Lys	Asp	Ile	Gln	Val	Leu	Val	Ser
	275						280					285			
Glu	Leu	Ser	Met	Val	Glu	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Leu	Val	Gly
	290					295					300				
Glu	Glu	Gly	Ala	Ala	Glu	Pro	Tyr	Arg	Tyr	Leu	Met	Lys	Asn	Leu	Arg
305					310					315					320
Ser	Arg	Leu	Met	Ala	Thr	Gln	Ala	Trp	Leu	Glu	Ala	Arg	Leu	Lys	Gly
				325					330					335	
Glu	Glu	Leu	Pro	Lys	Pro	Glu	Gly	Leu	Leu	Thr	Gln	Asn	Glu	Glu	Leu
			340					345					350		
Trp	Glu	Pro	Leu	Tyr	Ala	Cys	Tyr	Gln	Ser	Leu	Gln	Ala	Cys	Gly	Met
		355					360					365			
Gly	Ile	Ile	Ala	Asn	Gly	Asp	Leu	Leu	Asp	Thr	Leu	Arg	Arg	Val	Lys
	370				375						380				
Cys	Phe	Gly	Val	Pro	Leu	Val	Arg	Ile	Asp	Ile	Arg	Gln	Glu	Ser	Thr
385					390					395					400
Arg	His	Thr	Glu	Ala	Leu	Gly	Glu	Leu	Thr	Arg	Tyr	Leu	Gly	Ile	Gly

405								410						415			
Asp	Tyr	Glu	Ser	Trp	Ser	Glu	Ala	Asp	Lys	Gln	Ala	Phe	Leu	Ile	Arg		
420								425						430			
Glu	Leu	Asn	Ser	Lys	Arg	Pro	Leu	Leu	Pro	Arg	Asn	Trp	Gln	Pro	Ser		
435								440						445			
Ala	Glu	Thr	Arg	Glu	Val	Leu	Asp	Thr	Cys	Gln	Val	Ile	Ala	Glu	Ala		
450								455						460			
Pro	Gln	Gly	Ser	Ile	Ala	Ala	Tyr	Val	Ile	Ser	Met	Ala	Lys	Thr	Pro		
465								470						475			
Ser	Asp	Val	Leu	Ala	Val	His	Leu	Leu	Leu	Lys	Glu	Ala	Gly	Ile	Gly		
485								490						495			
Phe	Ala	Met	Pro	Val	Ala	Pro	Leu	Phe	Glu	Thr	Leu	Asp	Asp	Leu	Asn		
500								505						510			
Asn	Ala	Asn	Asp	Val	Met	Thr	Gln	Leu	Leu	Asn	Ile	Asp	Trp	Tyr	Arg		
515								520						525			
Gly	Leu	Ile	Gln	Gly	Lys	Gln	Met	Val	Met	Ile	Gly	Tyr	Ser	Asp	Ser		
530								535						540			
Ala	Lys	Asp	Ala	Gly	Val	Met	Ala	Ala	Ser	Trp	Ala	Gln	Tyr	Gln	Ala		
545								550						555			
Gln	Asp	Ala	Leu	Ile	Lys	Thr	Cys	Glu	Lys	Ala	Gly	Ile	Glu	Leu	Thr		
565								570						575			
Leu	Phe	His	Gly	Arg	Gly	Gly	Ser	Ile	Gly	Arg	Gly	Gly	Ala	Pro	Ala		
580								585						590			
His	Ala	Ala	Leu	Leu	Ser	Gln	Pro	Pro	Gly	Ser	Leu	Lys	Gly	Gly	Leu		
595								600						605			
Arg	Val	Thr	Glu	Gln	Gly	Glu	Met	Ile	Arg	Phe	Lys	Tyr	Gly	Leu	Pro		
610								615						620			
Glu	Ile	Thr	Val	Ser	Ser	Leu	Ser	Leu	Tyr	Thr	Gly	Ala	Ile	Leu	Glu		
625								630						635			
Ala	Asn	Leu	Leu	Pro	Pro	Pro	Glu	Pro	Lys	Glu	Ser	Trp	Arg	Arg	Ile		
645								650						655			
Met	Asp	Glu	Leu	Ser	Val	Ile	Ser	Cys	Asp	Val	Tyr	Arg	Gly	Tyr	Val		
660								665						670			
Arg	Glu	Asn	Lys	Asp	Phe	Val	Pro	Tyr	Phe	Arg	Ser	Ala	Thr	Pro	Glu		
675								680						685			
Gln	Glu	Leu	Gly	Lys	Leu	Pro	Leu	Gly	Ser	Arg	Pro	Ala	Lys	Arg	Arg		
690								695						700			
Pro	Thr	Gly	Gly	Val	Glu	Ser	Leu	Arg	Ala	Ile	Pro	Trp	Ile	Phe	Ala		
705								710						715			
Trp	Thr	Gln	Asn	Arg	Leu	Met	Leu	Pro	Ala	Trp	Leu	Gly	Ala	Gly	Thr		
725								730						735			
Ala	Leu	Gln	Lys	Val	Val	Glu	Asp	Gly	Lys	Gln	Ser	Glu	Leu	Glu	Ala		
740								745						750			
Met	Cys	Arg	Asp	Trp	Pro	Phe	Phe	Ser	Thr	Arg	Leu	Gly	Met	Leu	Glu		
755								760						765			
Met	Val	Phe	Ala	Lys	Ala	Asp	Leu	Trp	Leu	Ala	Glu	Tyr	Tyr	Asp	Gln		
770								775						780			
Arg	Leu	Val	Asp	Lys	Ala	Leu	Trp	Pro	Leu	Gly	Lys	Glu	Leu	Arg	Asn		
785								790						795			
Leu	Gln	Glu	Glu	Asp	Ile	Lys	Val	Val	Leu	Ala	Ile	Ala	Asn	Asp	Ser		
805								810						815			
His	Leu	Met	Ala	Asp	Leu	Pro	Trp	Ile	Ala	Glu	Ser	Ile	Gln	Leu	Arg		
820								825						830			
Asn	Ile	Tyr	Thr	Asp	Pro	Leu	Asn	Val	Leu	Gln	Ala	Glu	Leu	Leu	His		
835								840						845			
Arg	Ser	Arg	Gln	Ala	Glu	Lys	Glu	Gly	Gln	Glu	Pro	Asp	Pro	Arg	Val		
850								855						860			

Glu Gln Ala Leu Met Val Thr Ile Ala Gly Ile Ala Ala Gly Met Arg
 865 870 875 880
 Asn Thr Gly

<210> 444
 <211> 663
 <212> PRT
 <213> Escherichia coli

<400> 444
 Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met
 1 5 10 15
 Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly
 20 25 30
 Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
 35 40 45
 Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
 50 55 60
 Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
 65 70 75 80
 Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
 85 90 95
 Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
 100 105 110
 Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile
 115 120 125
 Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
 130 135 140
 Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
 145 150 155 160
 Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
 165 170 175
 Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
 180 185 190
 Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
 195 200 205
 Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
 210 215 220
 Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
 225 230 235 240
 Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
 245 250 255
 Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
 260 265 270
 Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
 275 280 285
 Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300
 Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320
 Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335
 Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350
 Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe

355	360	365
Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro		
370	375	380
Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala		
385	390	395
Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala		400
	405	410
Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser		415
	420	425
Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala		430
	435	440
Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile		445
	450	455
Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala		460
465	470	475
Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln		480
	485	490
Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly		495
	500	505
Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg		510
	515	520
Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys		525
530	535	540
Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu		545
545	550	555
Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val		560
	565	570
Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln		575
	580	585
Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg		590
	595	600
Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly		605
	610	615
Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro		620
625	630	635
Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val		640
	645	650
Ala Lys Ala Lys Glu Leu Leu		655
	660	

<210> 445

<211> 152

<212> PRT

<213> Escherichia coli

<400> 445

Met Phe Arg Gly Ala Thr Leu Val Asn Leu Asp Ser Lys Gly Arg Leu	
1	5
Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly	
	10
	15
Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Leu Tyr	
	20
	25
Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser	
	30
	35
	40
	45
Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His	
	50
	55
	60
65	70
	75
	80

Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
85 90 95
Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
100 105 110
Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
115 120 125
Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
130 135 140
Glu Arg Leu Gln Asp Leu Ser Leu
145 150

<210> 446

<211> 313

<212> PRT

<213> Escherichia coli

<400> 446

Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val
1 5 10 15
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe
20 25 30
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu
35 40 45
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala
50 55 60
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser
65 70 75 80
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp
85 90 95
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala
100 105 110
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met
115 120 125
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu
130 135 140
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe
145 150 155 160
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro
165 170 175
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro
180 185 190
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val
195 200 205
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
210 215 220
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225 230 235 240
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
260 265 270
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300
Leu Arg Ile Ala Glu Arg Thr Asn Ala

305

310

<210> 447

<211> 121

<212> PRT

<213> Escherichia coli

<400> 447

Met	Ile	Ser	Arg	Val	Thr	Glu	Ala	Leu	Ser	Lys	Val	Lys	Gly	Ser	Met
1				5					10					15	
Gly	Ser	His	Glu	Arg	His	Ala	Leu	Pro	Gly	Val	Ile	Gly	Asp	Asp	Leu
			20					25					30		
Leu	Arg	Phe	Gly	Lys	Leu	Pro	Leu	Cys	Leu	Phe	Ile	Cys	Ile	Ile	Leu
		35					40					45			
Thr	Ala	Val	Thr	Val	Val	Thr	Thr	Ala	His	His	Thr	Arg	Leu	Leu	Thr
	50					55					60				
Ala	Gln	Arg	Glu	Gln	Leu	Val	Leu	Glu	Arg	Asp	Ala	Leu	Asp	Ile	Glu
65					70				75						80
Trp	Arg	Asn	Leu	Ile	Leu	Glu	Glu	Asn	Ala	Leu	Gly	Asp	His	Ser	Arg
			85					90					95		
Val	Glu	Arg	Ile	Ala	Thr	Glu	Lys	Leu	Gln	Met	Gln	His	Val	Asp	Pro
			100				105						110		
Ser	Gln	Glu	Asn	Ile	Val	Val	Gln	Lys							
		115					120								

<210> 448

<211> 588

<212> PRT

<213> Escherichia coli

<400> 448

Met	Lys	Ala	Ala	Ala	Lys	Thr	Gln	Lys	Pro	Lys	Arg	Gln	Glu	Glu	His
1				5					10					15	
Ala	Asn	Phe	Ile	Ser	Trp	Arg	Phe	Ala	Leu	Leu	Cys	Gly	Cys	Ile	Leu
			20					25					30		
Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gly	Arg	Val	Ala	Trp	Leu	Gln	Val	Ile
		35					40					45			
Ser	Pro	Asp	Met	Leu	Val	Lys	Glu	Gly	Asp	Met	Arg	Ser	Leu	Arg	Val
	50					55				60					
Gln	Gln	Val	Ser	Thr	Ser	Arg	Gly	Met	Ile	Thr	Asp	Arg	Ser	Gly	Arg
65					70				75						80
Pro	Leu	Ala	Val	Ser	Val	Pro	Val	Lys	Ala	Ile	Trp	Ala	Asp	Pro	Lys
			85					90					95		
Glu	Val	His	Asp	Ala	Gly	Gly	Ile	Ser	Val	Gly	Asp	Arg	Trp	Lys	Ala
		100					105						110		
Leu	Ala	Asn	Ala	Leu	Asn	Ile	Pro	Leu	Asp	Gln	Leu	Ser	Ala	Arg	Ile
		115					120					125			
Asn	Ala	Asn	Pro	Lys	Gly	Arg	Phe	Ile	Tyr	Leu	Ala	Arg	Gln	Val	Asn
	130					135				140					
Pro	Asp	Met	Ala	Asp	Tyr	Ile	Lys	Lys	Leu	Lys	Leu	Pro	Gly	Ile	His
145					150				155						160
Leu	Arg	Glu	Glu	Ser	Arg	Arg	Tyr	Tyr	Pro	Ser	Gly	Glu	Val	Thr	Ala
			165						170					175	
His	Leu	Ile	Gly	Phe	Thr	Asn	Val	Asp	Ser	Gln	Gly	Ile	Glu	Gly	Val
			180					185						190	

Glu Lys Ser Phe Asp Lys Trp Leu Thr Gly Gln Pro Gly Glu Arg Ile
195 200 205
Val Arg Lys Asp Arg Tyr Gly Arg Val Ile Glu Asp Ile Ser Ser Thr
210 215 220
Asp Ser Gln Ala Ala His Asn Leu Ala Leu Ser Ile Asp Glu Arg Leu
225 230 235 240
Gln Ala Leu Val Tyr Arg Glu Leu Asn Asn Ala Val Ala Phe Asn Lys
245 250 255
Ala Glu Ser Gly Ser Ala Val Leu Val Asp Val Asn Thr Gly Glu Val
260 265 270
Leu Ala Met Ala Asn Ser Pro Ser Tyr Asn Pro Asn Asn Leu Ser Gly
275 280 285
Thr Pro Lys Glu Ala Met Arg Asn Arg Thr Ile Thr Asp Val Phe Glu
290 295 300
Pro Gly Ser Thr Val Lys Pro Met Val Val Met Thr Ala Leu Gln Arg
305 310 315 320
Gly Val Val Arg Glu Asn Ser Val Leu Asn Thr Ile Pro Tyr Arg Ile
325 330 335
Asn Gly His Glu Ile Lys Asp Val Ala Arg Tyr Ser Glu Leu Thr Leu
340 345 350
Thr Gly Val Leu Gln Lys Ser Ser Asn Val Gly Val Ser Lys Leu Ala
355 360 365
Leu Ala Met Pro Ser Ser Ala Leu Val Asp Thr Tyr Ser Arg Phe Gly
370 375 380
Leu Gly Lys Ala Thr Asn Leu Gly Leu Val Gly Glu Arg Ser Gly Leu
385 390 395 400
Tyr Pro Gln Lys Gln Arg Trp Ser Asp Ile Glu Arg Ala Thr Phe Ser
405 410 415
Phe Gly Tyr Gly Leu Met Val Thr Pro Leu Gln Leu Ala Arg Val Tyr
420 425 430
Ala Thr Ile Gly Ser Tyr Gly Ile Tyr Arg Pro Leu Ser Ile Thr Lys
435 440 445
Val Asp Pro Pro Val Pro Gly Glu Arg Val Phe Pro Glu Ser Ile Val
450 455 460
Arg Thr Val Val His Met Met Glu Ser Val Ala Leu Pro Gly Gly Gly
465 470 475 480
Gly Val Lys Ala Ala Ile Lys Gly Tyr Arg Ile Ala Ile Lys Thr Gly
485 490 495
Thr Ala Lys Lys Val Gly Pro Asp Gly Arg Tyr Ile Asn Lys Tyr Ile
500 505 510
Ala Tyr Thr Ala Gly Val Ala Pro Ala Ser Gln Pro Arg Phe Ala Leu
515 520 525
Val Val Val Ile Asn Asp Pro Gln Ala Gly Lys Tyr Tyr Gly Gly Ala
530 535 540
Val Ser Ala Pro Val Phe Gly Ala Ile Met Gly Gly Val Leu Arg Thr
545 550 555 560
Met Asn Ile Glu Pro Asp Ala Leu Thr Thr Gly Asp Lys Asn Glu Phe
565 570 575
Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser
580 585

<210> 449

<211> 495

<212> PRT

<213> Escherichia coli

[illegible][illegible]

Thr Cys Ala Val Met Gln Ala Lys Glu Asn Asp Val Val Leu Val Ala
 450 455 460
 Gly Lys Gly His Glu Asp Tyr Gln Ile Val Gly Asn Gln Arg Leu Asp
 465 470 475 480
 Tyr Ser Asp Arg Val Thr Val Ala Arg Leu Leu Gly Val Ile Ala
 485 490 495

<210> 450

<211> 452

<212> PRT

<213> Escherichia coli

<400> 450

Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1 5 10 15
 Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
 20 25 30
 Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
 35 40 45
 Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
 50 55 60
 Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65 70 75 80
 Lys Asp Thr Arg Leu Ala Phe Gly Glu Leu Ala Ala Trp Val Arg Gln
 85 90 95
 Gln Val Pro Ala Arg Val Val Ala Leu Thr Gly Ser Ser Gly Lys Thr
 100 105 110
 Ser Val Lys Glu Met Thr Ala Ala Ile Leu Ser Gln Cys Gly Asn Thr
 115 120 125
 Leu Tyr Thr Ala Gly Asn Leu Asn Asn Asp Ile Gly Val Pro Met Thr
 130 135 140
 Leu Leu Arg Leu Thr Pro Glu Tyr Asp Tyr Ala Val Ile Glu Leu Gly
 145 150 155 160
 Ala Asn His Gln Gly Glu Ile Ala Trp Thr Val Ser Leu Thr Arg Pro
 165 170 175
 Glu Ala Ala Leu Val Asn Asn Leu Ala Ala Ala His Leu Glu Gly Phe
 180 185 190
 Gly Ser Leu Ala Gly Val Ala Lys Ala Lys Gly Glu Ile Phe Ser Gly
 195 200 205
 Leu Pro Glu Asn Gly Ile Ala Ile Met Asn Ala Asp Asn Asn Asp Trp
 210 215 220
 Leu Asn Trp Gln Ser Val Ile Gly Ser Arg Lys Val Trp Arg Phe Ser
 225 230 235 240
 Pro Asn Ala Ala Asn Ser Asp Phe Thr Ala Thr Asn Ile His Val Thr
 245 250 255
 Ser His Gly Thr Glu Phe Thr Leu Gln Thr Pro Thr Gly Ser Val Asp
 260 265 270
 Val Leu Leu Pro Leu Pro Gly Arg His Asn Ile Ala Asn Ala Leu Ala
 275 280 285
 Ala Ala Ala Leu Ser Met Ser Val Gly Ala Thr Leu Asp Ala Ile Lys
 290 295 300
 Ala Gly Leu Ala Asn Leu Lys Ala Val Pro Gly Arg Leu Phe Pro Ile
 305 310 315 320
 Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn
 325 330 335
 Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly

340 345 350
 Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser
 355 360 365
 Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile
 370 375 380
 Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala
 385 390 395 400
 Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg
 405 410 415
 Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys
 420 425 430
 Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu
 435 440 445
 Asn Gly Thr Cys
 450

<210> 451

<211> 360

<212> PRT

<213> Escherichia coli

<400> 451

Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe
 1 5 10 15
 Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr
 20 25 30
 Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu
 35 40 45
 Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser
 50 55 60
 His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu
 65 70 75 80
 Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro
 85 90 95
 Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly
 100 105 110
 Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu
 115 120 125
 Ile Ala Arg Trp Lys Tyr Phe Trp Met Ser Val Ile Ala Leu Gly Val
 130 135 140
 Ala Phe Ala Leu Tyr Leu Ala Gly Lys Asp Thr Pro Ala Thr Gln Leu
 145 150 155 160
 Val Val Pro Phe Phe Lys Asp Val Met Pro Gln Leu Gly Leu Phe Tyr
 165 170 175
 Ile Leu Leu Ala Tyr Phe Val Ile Val Gly Thr Gly Asn Ala Val Asn
 180 185 190
 Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Phe Val
 195 200 205
 Ala Gly Gly Phe Ala Leu Val Ala Trp Ala Thr Gly Asn Met Asn Phe
 210 215 220
 Ala Ser Tyr Leu His Ile Pro Tyr Leu Arg His Ala Gly Glu Leu Val
 225 230 235 240
 Ile Val Cys Thr Ala Ile Val Gly Ala Gly Leu Gly Phe Leu Trp Phe
 245 250 255
 Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
 260 265 270

290		295		300
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys				
305		310		320
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val				
	325		330	335
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp				
	340		345	350
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr				
	355		360	365
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val				
	370		375	380
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro				
385		390		400
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser				
	405		410	415
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg				
	420		425	430
Leu Ala Lys Glu Leu Gly				
435				

<210> 453
 <211> 414
 <212> PRT
 <213> Escherichia coli

<400> 453
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe
1 5 10 15
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
20 25 30
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu
35 40 45
Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr
50 55 60
Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe
65 70 75 80
Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala
85 90 95
Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala
100 105 110
Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val
115 120 125
Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu
130 135 140
Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile
145 150 155 160
Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg
165 170 175
Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu
180 185 190
Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr
195 200 205
Leu Ala Met Leu Phe Leu Ala Gly Ala Lys Leu Trp Gln Phe Ile Ala
210 215 220
Ile Ile Gly Met Gly Ile Ser Ala Val Val Leu Leu Ile Leu Ala Glu
225 230 235 240

Pro Tyr Arg Ile Arg Arg Val Thr Ala Phe Trp Asn Pro Trp Glu Asp
245 250 255
Pro Phe Gly Ser Gly Tyr Gln Leu Thr Gln Ser Leu Met Ala Phe Gly
260 265 270
Arg Gly Glu Leu Trp Gly Gln Gly Leu Gly Asn Ser Val Gln Lys Leu
275 280 285
Glu Tyr Leu Pro Glu Ala His Thr Asp Phe Ile Phe Ala Ile Ile Gly
290 295 300
Glu Glu Leu Gly Tyr Val Gly Val Val Leu Ala Leu Leu Met Val Phe
305 310 315 320
Phe Val Ala Phe Arg Ala Met Ser Ile Gly Arg Lys Ala Leu Glu Ile
325 330 335
Asp His Arg Phe Ser Gly Phe Leu Ala Cys Ser Ile Gly Ile Trp Phe
340 345 350
Ser Phe Gln Ala Leu Val Asn Val Gly Ala Ala Ala Gly Met Leu Pro
355 360 365
Thr Lys Gly Leu Thr Leu Pro Leu Ile Ser Tyr Gly Gly Ser Ser Leu
370 375 380
Leu Ile Met Ser Thr Ala Ile Met Met Leu Leu Arg Ile Asp Tyr Glu
385 390 395 400
Thr Arg Leu Glu Lys Ala Gln Ala Phe Val Arg Gly Ser Arg
405 410

<210> 454

<211> 355

<212> PRT

<213> Escherichia coli

<400> 454

Met Ser Gly Gln Gly Lys Arg Leu Met Val Met Ala Gly Gly Thr Gly
1 5 10 15
Gly His Val Phe Pro Gly Leu Ala Val Ala His His Leu Met Ala Gln
20 25 30
Gly Trp Gln Val Arg Trp Leu Gly Thr Ala Asp Arg Met Glu Ala Asp
35 40 45
Leu Val Pro Lys His Gly Ile Glu Ile Asp Phe Ile Arg Ile Ser Gly
50 55 60
Leu Arg Gly Lys Gly Ile Lys Ala Leu Ile Ala Ala Pro Leu Arg Ile
65 70 75 80
Phe Asn Ala Trp Arg Gln Ala Arg Ala Ile Met Lys Ala Tyr Lys Pro
85 90 95
Asp Val Val Leu Gly Met Gly Gly Tyr Val Ser Gly Pro Gly Gly Leu
100 105 110
Ala Ala Trp Ser Leu Gly Ile Pro Val Val Leu His Glu Gln Asn Gly
115 120 125
Ile Ala Gly Leu Thr Asn Lys Trp Leu Ala Lys Ile Ala Thr Lys Val
130 135 140
Met Gln Ala Phe Pro Gly Ala Phe Pro Asn Ala Glu Val Val Gly Asn
145 150 155 160
Pro Val Arg Thr Asp Val Leu Ala Leu Pro Leu Pro Gln Gln Arg Leu
165 170 175
Ala Gly Arg Glu Gly Pro Val Arg Val Leu Val Val Gly Gly Ser Gln
180 185 190
Gly Ala Arg Ile Leu Asn Gln Thr Met Pro Gln Val Ala Ala Lys Leu
195 200 205
Gly Asp Ser Val Thr Ile Trp His Gln Ser Gly Lys Gly Ser Gln Gln

210		215		220
Ser Val Glu Gln Ala Tyr	Ala Glu Ala Gly Gln	Pro Gln His Lys Val		
225	230	235		240
Thr Glu Phe Ile Asp	Asp Met Ala Ala Ala Tyr	Ala Trp Ala Asp Val		
	245	250		255
Val Val Cys Arg Ser Gly	Ala Leu Thr Val Ser	Glu Ile Ala Ala Ala		
	260	265		270
Gly Leu Pro Ala Leu Phe	Val Pro Phe Gln His Lys	Asp Arg Gln Gln		
	275	280		285
Tyr Trp Asn Ala Leu Pro	Leu Glu Lys Ala Gly	Ala Ala Lys Ile Ile		
	290	295		300
Glu Gln Pro Gln Leu Ser	Val Asp Ala Val Ala	Asn Thr Leu Ala Gly		
305	310	315		320
Trp Ser Arg Glu Thr Leu	Leu Thr Met Ala Glu	Arg Ala Arg Ala Ala		
	325	330		335
Ser Ile Pro Asp Ala Thr	Glu Arg Val Ala Asn	Glu Val Ser Arg Val		
	340	345		350
Ala Arg Ala				
355				

<210> 455
 <211> 491
 <212> PRT
 <213> Escherichia coli

<400> 455
Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met
1 5 10 15
Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met
20 25 30
Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly
35 40 45
Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly
50 55 60
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser
65 70 75 80
Val Val Val Val Ser Ser Ala Ile Ser Ala Asp Asn Pro Glu Ile Val
85 90 95
Ala Ala His Glu Ala Arg Ile Pro Val Ile Arg Arg Ala Glu Met Leu
100 105 110
Ala Glu Leu Met Arg Phe Arg His Gly Ile Ala Ile Ala Gly Thr His
115 120 125
Gly Lys Thr Thr Thr Thr Ala Met Val Ser Ser Ile Tyr Ala Glu Ala
130 135 140
Gly Leu Asp Pro Thr Phe Val Asn Gly Gly Leu Val Lys Ala Ala Gly
145 150 155 160
Val His Ala Arg Leu Gly His Gly Arg Tyr Leu Ile Ala Glu Ala Asp
165 170 175
Glu Ser Asp Ala Ser Phe Leu His Leu Gln Pro Met Val Ala Ile Val
180 185 190
Thr Asn Ile Glu Ala Asp His Met Asp Thr Tyr Gln Gly Asp Phe Glu
195 200 205
Asn Leu Lys Gln Thr Phe Ile Asn Phe Leu His Asn Leu Pro Phe Tyr
210 215 220
Gly Arg Ala Val Met Cys Val Asp Asp Pro Val Ile Arg Glu Leu Leu
225 230 235 240

Pro Arg Val Gly Arg Gln Thr Thr Thr Tyr Gly Phe Ser Glu Asp Ala
245 250 255
Asp Val Arg Val Glu Asp Tyr Gln Gln Ile Gly Pro Gln Gly His Phe
260 265 270
Thr Leu Leu Arg Gln Asp Lys Glu Pro Met Arg Val Thr Leu Asn Ala
275 280 285
Pro Gly Arg His Asn Ala Leu Asn Ala Ala Ala Val Ala Val Ala
290 295 300
Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser
305 310 315 320
Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu
325 330 335
Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr
340 345 350
Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala
355 360 365
Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe
370 375 380
Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln
385 390 395 400
Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro
405 410 415
Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg
420 425 430
Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu
435 440 445
Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly
450 455 460
Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu
465 470 475 480
Lys Pro Gln Thr Pro Glu Glu Glu Gln His Asp
485 490

<210> 456
<211> 306
<212> PRT
<213> Escherichia coli

<400> 456
Met Thr Asp Lys Ile Ala Val Leu Leu Gly Gly Thr Ser Ala Glu Arg
1 5 10 15
Glu Val Ser Leu Asn Ser Gly Ala Ala Val Leu Ala Gly Leu Arg Glu
20 25 30
Gly Gly Ile Asp Ala Tyr Pro Val Asp Pro Lys Glu Val Asp Val Thr
35 40 45
Gln Leu Lys Ser Met Gly Phe Gln Lys Val Phe Ile Ala Leu His Gly
50 55 60
Arg Gly Gly Glu Asp Gly Thr Leu Gln Gly Met Leu Glu Leu Met Gly
65 70 75 80
Leu Pro Tyr Thr Gly Ser Gly Val Met Ala Ser Ala Leu Ser Met Asp
85 90 95
Lys Leu Arg Ser Lys Leu Leu Trp Gln Gly Ala Gly Leu Pro Val Ala
100 105 110
Pro Trp Val Ala Leu Thr Arg Ala Glu Phe Glu Lys Gly Leu Ser Asp
115 120 125
Lys Gln Leu Ala Glu Ile Ser Ala Leu Gly Leu Pro Val Ile Val Lys

130		135		140
Pro Ser Arg Glu Gly	Ser Ser Val Gly Met	Ser Lys Val Val Ala Glu		
145	150	155	160	
Asn Ala Leu Gln Asp	Ala Leu Arg Leu Ala Phe	Gln His Asp Glu Glu		
165	170	175		
Val Leu Ile Glu Lys	Trp Leu Ser Gly Pro	Glu Phe Thr Val Ala Ile		
180	185	190		
Leu Gly Glu Glu Ile	Leu Pro Ser Ile Arg	Ile Gln Pro Ser Gly Thr		
195	200	205		
Phe Tyr Asp Tyr Glu	Ala Lys Tyr Leu Ser	Asp Glu Thr Gln Tyr Phe		
210	215	220		
Cys Pro Ala Gly Leu	Glu Ala Ser Gln Glu	Ala Asn Leu Gln Ala Leu		
225	230	235	240	
Val Leu Lys Ala Trp	Thr Thr Leu Gly Cys	Lys Gly Trp Gly Arg Ile		
245	250	255		
Asp Val Met Leu Asp	Ser Asp Gly Gln Phe	Tyr Leu Leu Glu Ala Asn		
260	265	270		
Thr Ser Pro Gly Met	Thr Ser His Ser	Leu Val Pro Met Ala Ala Arg		
275	280	285		
Gln Ala Gly Met Ser	Phe Ser Gln Leu Val	Val Arg Ile Leu Glu Leu		
290	295	300		
Ala Asp				
305				

<210> 457

<211> 201

<212> PRT

<213> Escherichia coli

<400> 457

Met Ala Leu His Asp	Glu Asn Val Val Trp	His Ser His Pro Val Thr
1	5	10 15
Val Gln Gln Arg Glu	Leu His His Gly His	Arg Gly Val Val Leu Trp
20	25	30
Phe Thr Gly Leu Ser	Gly Ser Gly Lys Ser	Thr Val Ala Gly Ala Leu
35	40	45
Glu Glu Ala Leu His	Lys Leu Gly Val Ser	Thr Tyr Leu Leu Asp Gly
50	55	60
Asp Asn Val Arg His	Gly Leu Cys Ser Asp	Leu Gly Phe Ser Asp Ala
65	70	75 80
Asp Arg Lys Glu Asn	Ile Arg Arg Val Gly	Glu Val Ala Asn Leu Met
85	90	95
Val Glu Ala Gly Leu	Val Val Leu Thr Ala	Phe Ile Ser Pro His Arg
100	105	110
Ala Glu Arg Gln Met	Val Arg Glu Arg Val	Gly Glu Gly Arg Phe Ile
115	120	125
Glu Val Phe Val Asp	Thr Pro Leu Ala Ile	Cys Glu Ala Arg Asp Pro
130	135	140
Lys Gly Leu Tyr Lys	Lys Ala Arg Ala Gly	Glu Leu Arg Asn Phe Thr
145	150	155 160
Gly Ile Asp Ser Val	Tyr Glu Ala Pro Glu	Ser Ala Glu Ile His Leu
165	170	175
Asn Gly Glu Gln Leu	Val Thr Asn Leu Val	Gln Gln Leu Leu Asp Leu
180	185	190
Leu Arg Gln Asn Asp	Ile Ile Arg Ser	
195	200	

<210> 458
 <211> 475
 <212> PRT
 <213> Escherichia coli

<400> 458

Met	Asn	Thr	Ala	Leu	Ala	Gln	Gln	Ile	Ala	Asn	Glu	Gly	Gly	Val	Glu
1				5					10					15	
Ala	Trp	Met	Ile	Ala	Gln	Gln	His	Lys	Ser	Leu	Leu	Arg	Phe	Leu	Thr
			20					25					30		
Cys	Gly	Ser	Val	Asp	Asp	Gly	Lys	Ser	Thr	Leu	Ile	Gly	Arg	Leu	Leu
		35					40					45			
His	Asp	Thr	Arg	Gln	Ile	Tyr	Glu	Asp	Gln	Leu	Ser	Ser	Leu	His	Asn
	50					55					60				
Asp	Ser	Lys	Arg	His	Gly	Thr	Gln	Gly	Glu	Lys	Leu	Asp	Leu	Ala	Leu
65					70					75					80
Leu	Val	Asp	Gly	Leu	Gln	Ala	Glu	Arg	Glu	Gln	Gly	Ile	Thr	Ile	Asp
				85					90					95	
Val	Ala	Tyr	Arg	Tyr	Phe	Ser	Thr	Glu	Lys	Arg	Lys	Phe	Ile	Ile	Ala
				100				105					110		
Asp	Thr	Pro	Gly	His	Glu	Gln	Tyr	Thr	Arg	Asn	Met	Ala	Thr	Gly	Ala
	115						120					125			
Ser	Thr	Cys	Glu	Leu	Ala	Ile	Leu	Leu	Ile	Asp	Ala	Arg	Lys	Gly	Val
	130					135					140				
Leu	Asp	Gln	Thr	Arg	Arg	His	Ser	Phe	Ile	Ser	Thr	Leu	Leu	Gly	Ile
145				150						155					160
Lys	His	Leu	Val	Val	Ala	Ile	Asn	Lys	Met	Asp	Leu	Val	Asp	Tyr	Ser
				165					170					175	
Glu	Glu	Thr	Phe	Thr	Arg	Ile	Arg	Glu	Asp	Tyr	Leu	Thr	Phe	Ala	Gly
			180					185					190		
Gln	Leu	Pro	Gly	Asn	Leu	Asp	Ile	Arg	Phe	Val	Pro	Leu	Ser	Ala	Leu
		195					200					205			
Glu	Gly	Asp	Asn	Val	Ala	Ser	Gln	Ser	Glu	Ser	Met	Pro	Trp	Tyr	Ser
	210					215					220				
Gly	Pro	Thr	Leu	Leu	Glu	Val	Leu	Glu	Thr	Val	Glu	Ile	Gln	Arg	Val
225					230					235					240
Val	Asp	Ala	Gln	Pro	Met	Arg	Phe	Pro	Val	Gln	Tyr	Val	Asn	Arg	Pro
				245					250					255	
Asn	Leu	Asp	Phe	Arg	Gly	Tyr	Ala	Gly	Thr	Leu	Ala	Ser	Gly	Arg	Val
			260					265					270		
Glu	Val	Gly	Gln	Arg	Val	Lys	Val	Leu	Pro	Ser	Gly	Val	Glu	Ser	Asn
		275					280					285			
Val	Ala	Arg	Ile	Val	Thr	Phe	Asp	Gly	Asp	Arg	Glu	Glu	Ala	Phe	Ala
					295						300				
Gly	Glu	Ala	Ile	Thr	Leu	Val	Leu	Thr	Asp	Glu	Ile	Asp	Ile	Ser	Arg
305					310					315					320
Gly	Asp	Leu	Leu	Leu	Ala	Ala	Asp	Glu	Ala	Leu	Pro	Ala	Val	Gln	Ser
				325					330					335	
Ala	Ser	Val	Asp	Val	Val	Trp	Met	Ala	Glu	Gln	Pro	Leu	Ser	Pro	Gly
			340					345					350		
Gln	Ser	Tyr	Asp	Ile	Lys	Ile	Ala	Gly	Lys	Lys	Thr	Arg	Ala	Arg	Val
		355					360					365			
Asp	Gly	Ile	Arg	Tyr	Gln	Val	Asp	Ile	Asn	Asn	Leu	Thr	Gln	Arg	Glu
370						375					380				
Val	Glu	Asn	Leu	Pro	Leu	Asn	Gly	Ile	Gly	Leu	Val	Asp	Leu	Thr	Phe


```

385          390          395          400
Asp Glu Pro Leu Val Leu Asp Arg Tyr Gln Gln Asn Pro Val Thr Gly
          405          410          415
Gly Leu Ile Phe Ile Asp Arg Leu Ser Asn Val Thr Val Gly Ala Gly
          420          425          430
Met Val His Glu Pro Val Ser Gln Ala Thr Ala Ala Pro Ser Glu Phe
          435          440          445
Ser Ala Phe Glu Leu Glu Leu Asn Ala Leu Val Arg Arg His Phe Pro
          450          455          460
His Trp Gly Ala Arg Asp Leu Leu Gly Asp Lys
465          470          475

```

<210> 459
 <211> 127
 <212> PRT
 <213> Escherichia coli

```

<400> 459
Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
  1          5          10          15
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
          20          25          30
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
          35          40          45
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
          50          55          60
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65          70          75          80
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
          85          90          95
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
          100          105          110
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu
          115          120          125

```

<210> 460
 <211> 329
 <212> PRT
 <213> Escherichia coli

```

<400> 460
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
  1          5          10          15
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
          20          25          30
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu
          35          40          45
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val
          50          55          60
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu
65          70          75          80
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp
          85          90          95
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala
          100          105          110

```

```

Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His
    115                      120                      125
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile
    130                      135                      140
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His
    145                      150                      155                      160
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys
    165                      170                      175
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val
    180                      185                      190
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn
    195                      200                      205
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu
    210                      215                      220
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro
    225                      230                      235                      240
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro
    245                      250                      255
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala
    260                      265                      270
Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu
    275                      280                      285
Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys
    290                      295                      300
Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn
    305                      310                      315                      320
Trp Pro Pro Ala Ser Ile Ala Asp Glu
    325

```

<210> 461
 <211> 206
 <212> PRT
 <213> Escherichia coli

```

<400> 461
Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly
  1          5          10          15
Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys
    20          25          30
Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu
    35          40          45
Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile
    50          55          60
Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala
    65          70          75          80
Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly
    85          90          95
Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala
    100         105         110
Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg
    115         120         125
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser
    130         135         140
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu
    145         150         155         160
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly

```


<210> 464
 <211> 460
 <212> PRT
 <213> Escherichia coli

<400> 464

Met	Thr	Gln	Leu	Thr	Met	Lys	Asp	Lys	Ile	Gly	Tyr	Gly	Leu	Gly	Asp
1				5					10					15	
Thr	Ala	Cys	Gly	Phe	Val	Trp	Gln	Ala	Thr	Met	Phe	Leu	Leu	Ala	Tyr
		20					25					30			
Phe	Tyr	Thr	Asp	Val	Phe	Gly	Leu	Ser	Ala	Gly	Ile	Met	Gly	Thr	Leu
		35					40					45			
Phe	Leu	Val	Ser	Arg	Val	Leu	Asp	Ala	Val	Thr	Asp	Pro	Leu	Met	Gly
	50					55					60				
Leu	Leu	Val	Asp	Arg	Thr	Arg	Thr	Arg	His	Gly	Gln	Phe	Arg	Pro	Phe
65					70					75					80
Leu	Leu	Trp	Gly	Ala	Ile	Pro	Phe	Gly	Ile	Val	Cys	Val	Leu	Thr	Phe
				85					90					95	
Tyr	Thr	Pro	Asp	Phe	Ser	Ala	Gln	Gly	Lys	Ile	Ile	Tyr	Ala	Cys	Val
			100					105					110		
Thr	Tyr	Ile	Leu	Leu	Thr	Leu	Val	Tyr	Thr	Phe	Val	Asn	Val	Pro	Tyr
		115					120					125			
Cys	Ala	Met	Pro	Gly	Val	Ile	Thr	Ala	Asp	Pro	Lys	Glu	Arg	His	Ala
	130					135					140				
Leu	Gln	Ser	Trp	Arg	Phe	Phe	Leu	Ala	Ala	Ala	Gly	Ser	Leu	Ala	Ile
145					150					155					160
Ser	Gly	Ile	Ala	Leu	Pro	Leu	Val	Ser	Ile	Ile	Gly	Lys	Gly	Asp	Glu
			165						170					175	
Gln	Val	Gly	Tyr	Phe	Gly	Ala	Met	Cys	Val	Leu	Gly	Leu	Ser	Gly	Val
			180					185					190		
Val	Leu	Leu	Tyr	Val	Cys	Phe	Phe	Thr	Thr	Lys	Glu	Arg	Tyr	Thr	Phe
	195						200					205			
Glu	Val	Gln	Pro	Gly	Ser	Ser	Val	Ala	Lys	Asp	Leu	Lys	Leu	Leu	Leu
	210					215					220				
Gly	Asn	Ser	Gln	Trp	Arg	Ile	Met	Cys	Ala	Phe	Lys	Met	Met	Ala	Thr
225					230					235					240
Cys	Ser	Asn	Val	Val	Arg	Gly	Gly	Ala	Thr	Leu	Tyr	Phe	Val	Lys	Tyr
			245						250					255	
Val	Met	Asp	His	Pro	Glu	Leu	Ala	Thr	Gln	Phe	Leu	Leu	Tyr	Gly	Ser
		260						265					270		
Leu	Ala	Thr	Met	Phe	Gly	Ser	Leu	Cys	Ser	Ser	Arg	Leu	Leu	Gly	Arg
	275						280					285			
Phe	Asp	Arg	Val	Thr	Ala	Phe	Lys	Trp	Ile	Ile	Val	Ala	Tyr	Ser	Leu
	290					295					300				
Ile	Ser	Leu	Leu	Ile	Phe	Val	Thr	Pro	Ala	Glu	His	Ile	Ala	Leu	Ile
305					310					315					320
Phe	Ala	Leu	Asn	Ile	Leu	Phe	Leu	Phe	Val	Phe	Asn	Thr	Thr	Thr	Pro
			325						330					335	
Leu	Gln	Trp	Leu	Met	Ala	Ser	Asp	Val	Val	Asp	Tyr	Glu	Glu	Ser	Arg
		340						345					350		
Ser	Gly	Arg	Arg	Leu	Asp	Gly	Leu	Val	Phe	Ser	Thr	Tyr	Leu	Phe	Ser
	355						360					365			
Leu	Lys	Ile	Gly	Leu	Ala	Ile	Gly	Gly	Ala	Val	Val	Gly	Trp	Ile	Leu
	370					375					380				
Ala	Tyr	Val	Asn	Tyr	Ser	Ala	Ser	Ser	Ser	Val	Gln	Pro	Val	Glu	Val
385					390					395					400
Leu	Thr	Thr	Ile	Lys	Ile	Leu	Phe	Cys	Val	Val	Pro	Val	Val	Leu	Tyr

Ala Ser Ser Leu Asp Pro Glu Leu Gln Thr Leu Arg Ile Pro Phe Asp
 340 345 350
 Asp Thr Leu Gly Ser Leu Thr Ala Arg Pro Gly Phe Leu Arg Leu Tyr
 355 360 365
 Gly Asn Asp Ser Leu Asn Ser Thr Phe Thr Gln Ser Thr Val Ala Arg
 370 375 380
 Arg Trp Gln His Phe Ala Phe Arg Ala Glu Thr Arg Met Glu Phe Ser
 385 390 395 400
 Pro Val His Phe Gln Gln Ser Ala Gly Leu Thr Cys Tyr Tyr Asn Ser
 405 410 415
 Lys Asn Trp Ser Tyr Cys Phe Val Asp Tyr Glu Glu Gly Gln Gly Arg
 420 425 430
 Thr Ile Lys Val Ile Gln Leu Asp His Asn Val Pro Ser Trp Pro Leu
 435 440 445
 His Glu Gln Pro Ile Pro Val Pro Glu His Ala Glu Ser Val Trp Leu
 450 455 460
 Arg Val Asp Val Asp Thr Leu Val Tyr Arg Tyr Ser Tyr Ser Phe Asp
 465 470 475 480
 Gly Glu Thr Trp His Thr Val Pro Val Thr Tyr Glu Ala Trp Lys Leu
 485 490 495
 Ser Asp Asp Tyr Ile Gly Gly Arg Gly Phe Phe Thr Gly Ala Phe Val
 500 505 510
 Gly Leu His Cys Glu Asp Ile Ser Gly Asp Gly Cys Tyr Ala Asp Phe
 515 520 525
 Asp Tyr Phe Thr Tyr Glu Pro Val
 530 535

<210> 466

<211> 325

<212> PRT

<213> Escherichia coli

<400> 466

Met His Met Lys Lys Ile Ile Phe Ala Phe Ile Ile Leu Phe Val Phe
 1 5 10 15
 Leu Leu Pro Met Ile Ile Phe Tyr Gln Pro Trp Val Asn Ala Leu Pro
 20 25 30
 Ser Thr Pro Arg His Ala Ser Pro Glu Gln Leu Glu Lys Thr Val Arg
 35 40 45
 Tyr Leu Thr Gln Thr Val His Pro Arg Ser Ala Asp Asn Ile Asp Asn
 50 55 60
 Leu Asn Arg Ser Ala Glu Tyr Ile Lys Glu Val Phe Val Ser Ser Gly
 65 70 75 80
 Ala Arg Val Thr Ser Gln Asp Val Pro Ile Thr Gly Gly Pro Tyr Lys
 85 90 95
 Asn Ile Val Ala Asp Tyr Gly Pro Ala Asp Gly Pro Leu Ile Ile Ile
 100 105 110
 Gly Ala His Tyr Asp Ser Ala Ser Ser Tyr Glu Asn Asp Gln Leu Thr
 115 120 125
 Tyr Thr Pro Gly Ala Asp Asp Asn Ala Ser Gly Val Ala Gly Leu Leu
 130 135 140
 Glu Leu Ala Arg Leu Leu His Gln Gln Val Pro Lys Thr Gly Val Gln
 145 150 155 160
 Leu Val Ala Tyr Ala Ser Glu Glu Pro Pro Phe Phe Arg Ser Asp Glu
 165 170 175
 Met Gly Ser Ala Val His Ala Ala Ser Leu Glu Arg Pro Val Lys Leu

Ile	Asn	Thr	Pro	Ile	Lys	Val	Ser	Ala	Glu	Pro	Asn	Gly	Ala	Arg	Leu
				245					250					255	
Val	Glu	Val	His	Gln	Pro	Leu	Ser	Glu	Lys	Ile	Asp	Asp	Asp	Pro	Gln
			260					265					270		
Leu	Leu	Pro	Ile	Thr	Leu	Asn	Ser	Ala	Met	Gln	Ser	Phe	Lys	Asp	Ala
		275					280					285			
Ala	Gln	Thr	Asp	Ala	Glu	Val	Met	Gln	His	Val	Met	Asp	Val	Arg	Ser
	290					295					300				
Gly	Met	Pro	Val	Asp	Val	Arg	Arg	His	Gln	Val	Ser	Pro	Gln	Thr	Leu
305					310					315					320

<210> 468

<211> 494

<212> PRT

<213> Escherichia coli

<400> 468

Met	Val	Ala	Ile	His	Leu	Leu	Pro	Val	Ser	Tyr	Asn	Ser	Ala	Thr	Ser
1				5					10					15	
Thr	Val	Asn	Ile	Ser	Ala	Arg	Ile	Ile	Pro	Leu	Leu	Ile	Ile	His	Gln
			20					25					30		
Arg	Tyr	Lys	Ile	Pro	Met	Pro	Lys	Val	Gln	Ala	Asp	Gly	Leu	Pro	Leu
		35					40					45			
Pro	Gln	Arg	Tyr	Gly	Ala	Ile	Leu	Thr	Ile	Val	Ile	Gly	Ile	Ser	Met
	50					55					60				
Ala	Val	Leu	Asp	Gly	Ala	Ile	Ala	Asn	Val	Ala	Leu	Pro	Thr	Ile	Ala
65					70					75					80
Thr	Asp	Leu	His	Ala	Thr	Pro	Ala	Ser	Ser	Ile	Trp	Val	Val	Asn	Ala
			85						90					95	
Tyr	Gln	Ile	Ala	Ile	Val	Ile	Ser	Leu	Leu	Ser	Phe	Ser	Phe	Leu	Gly
		100						105					110		
Asp	Met	Phe	Gly	Tyr	Arg	Arg	Ile	Tyr	Lys	Cys	Gly	Leu	Val	Val	Phe
		115					120					125			
Leu	Leu	Ser	Ser	Leu	Phe	Cys	Ala	Leu	Ser	Asp	Ser	Leu	Gln	Met	Leu
	130					135					140				
Thr	Leu	Ala	Arg	Val	Ile	Gln	Gly	Phe	Gly	Gly	Ala	Ala	Leu	Met	Ser
145					150					155					160
Val	Asn	Thr	Ala	Leu	Ile	Arg	Leu	Ile	Tyr	Pro	Gln	Arg	Phe	Leu	Gly
			165						170					175	
Arg	Gly	Met	Gly	Ile	Asn	Ser	Phe	Ile	Val	Ala	Val	Ser	Ser	Ala	Ala
		180					185						190		
Gly	Pro	Thr	Ile	Ala	Ala	Ala	Ile	Leu	Ser	Ile	Ala	Ser	Trp	Lys	Trp
	195						200					205			
Leu	Phe	Leu	Ile	Asn	Val	Pro	Leu	Gly	Ile	Ile	Ala	Leu	Leu	Leu	Ala
	210					215					220				
Met	Arg	Phe	Leu	Pro	Pro	Asn	Gly	Ser	Arg	Ala	Ser	Lys	Pro	Arg	Phe
225					230					235					240
Asp	Leu	Pro	Ser	Ala	Val	Met	Asn	Ala	Leu	Thr	Phe	Gly	Leu	Leu	Ile
				245					250					255	
Thr	Ala	Leu	Ser	Gly	Phe	Ala	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Ile	Ala
		260						265					270		
Ala	Glu	Leu	Val	Val	Met	Val	Val	Val	Gly	Ile	Phe	Phe	Ile	Arg	Arg
	275						280					285			
Gln	Leu	Ser	Leu	Pro	Val	Pro	Leu	Leu	Pro	Val	Asp	Leu	Leu	Arg	Ile
	290					295					300				
Pro	Leu	Phe	Ser	Leu	Ser	Ile	Cys	Thr	Ser	Val	Cys	Ser	Phe	Cys	Ala


```

305          310          315          320
Gln Met Leu Ala Met Val Ser Leu Pro Phe Tyr Leu Gln Thr Val Leu
          325          330          335
Gly Arg Ser Glu Val Glu Thr Gly Leu Leu Leu Thr Pro Trp Pro Leu
          340          345          350
Ala Thr Met Val Met Ala Pro Leu Ala Gly Tyr Leu Ile Glu Arg Val
          355          360          365
His Ala Gly Leu Leu Gly Ala Leu Gly Leu Phe Ile Met Ala Ala Gly
          370          375          380
Leu Phe Ser Leu Val Leu Leu Pro Ala Ser Pro Ala Asp Ile Asn Ile
385          390          395          400
Ile Trp Pro Met Ile Leu Cys Gly Ala Gly Phe Gly Leu Phe Gln Ser
          405          410          415
Pro Asn Asn His Thr Ile Ile Thr Ser Ala Pro Arg Glu Arg Ser Gly
          420          425          430
Gly Ala Ser Gly Met Leu Gly Thr Ala Arg Leu Leu Gly Gln Ser Ser
          435          440          445
Gly Ala Ala Leu Val Ala Leu Met Leu Asn Gln Phe Gly Asp Asn Gly
          450          455          460
Thr His Val Ser Leu Met Ala Ala Ala Ile Leu Ala Val Ile Ala Ala
465          470          475          480
Cys Val Ser Gly Leu Arg Ile Thr Gln Pro Arg Ser Arg Ala
          485          490

```

<210> 469

<211> 477

<212> PRT

<213> Escherichia coli

<400> 469

```

Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
  1          5          10          15
Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
          20          25          30
Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
          35          40          45
Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
          50          55          60
Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
65          70          75          80
Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
          85          90          95
Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg
          100          105          110
Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
          115          120          125
Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
          130          135          140
Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
          145          150          155          160
Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
          165          170          175
Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu
          180          185          190
Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr
          195          200          205

```


1					5					10					15
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp
			20				25						30		
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu
			35				40						45		
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr
			50				55						60		
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln
65				70						75			80		
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala
			85						90			95			
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu
			100						105			110			
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys
			115						120			125			
Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln
			130			135						140			
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu
145				150						155			160		
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn
			165						170			175			
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala
			180						185			190			
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys
			195						200			205			
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly
			210			215						220			
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu
225				230						235			240		
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala
			245						250			255			
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val
			260						265			270			
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu
			275			280						285			
Ala	Thr	Ile	Ala	Ser	Ala	Val	Ser	Ala	Val	Thr	Ala	Val	Tyr	Ser	Thr
			290			295						300			
Glu	Thr	Ala	Met	Ala	Lys	Leu	Ala	Leu	Thr	Glu	Trp	Leu	Val	Ser	Lys
305				310						315			320		
Ala	Trp	Gln	Pro	Phe	Leu	Asp	Ala	Lys	Ala	Gln	Gly	Lys	Ile	Ser	Asp
			325						330			335			
Ser	Phe	Lys	Arg	Phe	Ala	Asp	Ile	His	Leu	Ser	Arg	His	Ala	Ala	Glu
			340						345			350			
Leu	Lys	Ser	Val	Phe	Cys	Gln	Pro	Leu	Gly	Asp	Arg	Tyr	Arg	Asp	Gln
			355			360						365			
Leu	Pro	Arg	Leu	Thr	Arg	Asp	Ile	Asp	Ser	Ile	Leu	Leu	Leu	Ala	Gly
			370			375						380			
Tyr	Tyr	Asp	Pro	Val	Val	Ala	Gln	Ala	Trp	Leu	Glu	Asn	Trp	Gln	Gly
385				390						395			400		
Leu	His	His	Ala	Ile	Ala	Thr	Gly	Gln	Arg	Ile	Glu	Ile	Glu	His	Phe
			405						410			415			
Arg	Asn	Glu	Ala	Asn	Asn	Gln	Glu	Pro	Phe	Trp	Leu				

<210> 472
 <211> 207
 <212> PRT
 <213> Escherichia coli

<400> 472

Met	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Leu	Lys	Asp	Ala	Gly	Ile	Ser	Leu
1				5					10					15	
Thr	Asp	His	Gln	Lys	Asn	Gln	Leu	Ile	Ala	Tyr	Val	Asn	Met	Leu	His
			20					25					30		
Lys	Trp	Asn	Lys	Ala	Tyr	Asn	Leu	Thr	Ser	Val	Arg	Asp	Pro	Asn	Glu
		35					40					45			
Met	Leu	Val	Arg	His	Ile	Leu	Asp	Ser	Ile	Val	Val	Ala	Pro	Tyr	Leu
	50					55					60				
Gln	Gly	Glu	Arg	Phe	Ile	Asp	Val	Gly	Thr	Gly	Pro	Gly	Leu	Pro	Gly
65					70					75					80
Ile	Pro	Leu	Ser	Ile	Val	Arg	Pro	Glu	Ala	His	Phe	Thr	Leu	Leu	Asp
				85					90					95	
Ser	Leu	Gly	Lys	Arg	Val	Arg	Phe	Leu	Arg	Gln	Val	Gln	His	Glu	Leu
			100					105					110		
Lys	Leu	Glu	Asn	Ile	Glu	Pro	Val	Gln	Ser	Arg	Val	Glu	Glu	Phe	Pro
		115					120					125			
Ser	Glu	Pro	Pro	Phe	Asp	Gly	Val	Ile	Ser	Arg	Ala	Phe	Ala	Ser	Leu
	130					135					140				
Asn	Asp	Met	Val	Ser	Trp	Cys	His	His	Leu	Pro	Gly	Glu	Gln	Gly	Arg
145					150					155					160
Phe	Tyr	Ala	Leu	Lys	Gly	Gln	Met	Pro	Glu	Asp	Glu	Ile	Ala	Leu	Leu
				165					170					175	
Pro	Glu	Glu	Tyr	Gln	Val	Glu	Ser	Val	Val	Lys	Leu	Gln	Val	Pro	Ala
			180					185					190		
Leu	Asp	Gly	Glu	Arg	His	Leu	Val	Val	Ile	Lys	Ala	Asn	Lys	Ile	
		195					200					205			

<210> 473
 <211> 629
 <212> PRT
 <213> Escherichia coli

<400> 473

Met	Phe	Tyr	Pro	Asp	Pro	Phe	Asp	Val	Ile	Ile	Ile	Gly	Gly	Gly	His
1				5					10					15	
Ala	Gly	Thr	Glu	Ala	Ala	Met	Ala	Ala	Arg	Met	Gly	Gln	Gln	Thr	
			20					25					30		
Leu	Leu	Leu	Thr	His	Asn	Ile	Asp	Thr	Leu	Gly	Gln	Met	Ser	Cys	Asn
		35					40					45			
Pro	Ala	Ile	Gly	Gly	Ile	Gly	Lys	Gly	His	Leu	Val	Lys	Glu	Val	Asp
	50					55					60				
Ala	Leu	Gly	Gly	Leu	Met	Ala	Lys	Ala	Ile	Asp	Gln	Ala	Gly	Ile	Gln
65					70					75					80
Phe	Arg	Ile	Leu	Asn	Ala	Ser	Lys	Gly	Pro	Ala	Val	Arg	Ala	Thr	Arg
				85					90					95	
Ala	Gln	Ala	Asp	Arg	Val	Leu	Tyr	Arg	Gln	Ala	Val	Arg	Thr	Ala	Leu
			100					105					110		
Glu	Asn	Gln	Pro	Asn	Leu	Met	Ile	Phe	Gln	Gln	Ala	Val	Glu	Asp	Leu
		115					120					125			
Ile	Val	Glu	Asn	Asp	Arg	Val	Val	Gly	Ala	Val	Thr	Gln	Met	Gly	Leu

	130					135					140				
Lys 145	Phe	Arg	Ala	Lys	Ala 150	Val	Val	Leu	Thr	Val 155	Gly	Thr	Phe	Leu	Asp 160
Gly	Lys	Ile	His	Ile 165	Gly	Leu	Asp	Asn	Tyr 170	Ser	Gly	Gly	Arg	Ala 175	Gly
Asp	Pro	Pro	Ser 180	Ile	Pro	Leu	Ser	Arg	Arg 185	Leu	Arg	Glu	Leu	Pro 190	Leu
Arg	Val	Gly 195	Arg	Leu	Lys	Thr	Gly 200	Thr	Pro	Pro	Arg	Ile 205	Asp	Ala	Arg
Thr 210	Ile	Asp	Phe	Ser	Val	Leu 215	Ala	Gln	Gln	His	Gly 220	Asp	Asn	Pro	Met
Pro 225	Val	Phe	Ser	Phe	Met 230	Gly	Asn	Ala	Ser	Gln	His 235	Pro	Gln	Gln	Val
Pro	Cys	Tyr	Ile 245	Thr	His	Thr	Asn	Glu	Lys 250	Thr	His	Asp	Val	Ile 255	Arg
Ser	Asn	Leu	Asp 260	Arg	Ser	Pro	Met	Tyr 265	Ala	Gly	Val	Ile	Glu	Gly 270	Val
Gly	Pro	Arg	Tyr 275	Cys	Pro	Ser	Ile	Glu	Asp	Lys	Val	Met	Arg	Phe	Ala
Asp	Arg	Asn	Gln 290	His	Gln	Ile 295	Phe	Leu	Glu	Pro	Glu 300	Gly	Leu	Thr	Ser
Asn 305	Glu	Ile	Tyr	Pro	Asn 310	Gly	Ile	Ser	Thr	Ser	Leu 315	Pro	Phe	Asp	Val
Gln	Met	Gln	Ile 325	Val	Arg	Ser	Met	Gln	Gly 330	Met	Glu	Asn	Ala	Lys 335	Ile
Val	Arg	Pro	Gly 340	Tyr	Ala	Ile	Glu	Tyr 345	Asp	Phe	Phe	Asp	Pro	Arg	Asp
Leu	Lys	Pro 355	Thr	Leu	Glu	Ser	Lys 360	Phe	Ile	Gln	Gly	Leu 365	Phe	Phe	Ala
Gly	Gln	Ile 370	Asn	Gly	Thr	Thr 375	Gly	Tyr	Glu	Glu	Ala 380	Ala	Ala	Gln	Gly
Leu 385	Leu	Ala	Gly	Leu	Asn 390	Ala	Ala	Arg	Leu	Ser	Ala 395	Asp	Lys	Glu	Gly
Trp	Ala	Pro	Ala 405	Arg	Ser	Gln	Ala	Tyr	Leu	Gly	Val	Leu	Val	Asp	Asp
Leu	Cys	Thr 420	Leu	Gly	Thr	Lys	Glu	Pro	Tyr	Arg	Met	Phe	Thr	Ser	Arg
Ala	Glu	Tyr 435	Arg	Leu	Met	Leu	Arg	Glu	Asp	Asn	Ala	Asp	Leu	Arg	Leu
Thr	Glu	Ile 450	Gly	Arg	Glu	Leu	Gly	Leu	Val	Asp	Asp	Glu	Arg	Trp	Ala
Arg	Phe	Asn	Glu 465	Lys	Leu	Asn 470	Ile	Glu	Arg	Glu	Arg	Gln	Arg	Leu	Leu
Lys	Ser	Thr	Trp 485	Val	Thr	Pro	Ser	Ala	Glu	Ala	Ala	Ala	Glu	Val	Asn
Ala	His	Leu	Thr 500	Ala	Pro	Leu	Ser	Arg	Glu	Ala	Ser	Gly	Glu	Asp	Leu
Leu	Arg	Arg 515	Pro	Glu	Met	Thr	Tyr	Glu	Lys	Leu	Thr	Thr	Leu	Thr	Pro
Phe	Ala	Pro 530	Ala	Leu	Thr	Asp	Glu	Gln	Ala	Ala	Glu	Gln	Val	Glu	Ile
Gln	Val	Lys	Tyr 545	Glu	Gly	Tyr	Ile	Ala	Arg	Gln	Gln	Asp	Glu	Ile	Glu
Lys	Gln	Leu	Arg 565	Asn	Glu	Asn	Thr	Leu	Leu	Pro	Ala	Thr	Leu	Asp	Tyr
Arg	Gln	Val	Ser 580	Gly	Leu	Ser	Asn	Glu	Val	Ile	Ala	Lys	Leu	Asn	Asp

His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr
 595 600 605
 Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met
 610 615 620
 Leu Arg Arg Ser Ala
 625

<210> 474
 <211> 147
 <212> PRT
 <213> Escherichia coli

<400> 474
 Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu
 1 5 10 15
 Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr
 20 25 30
 Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly
 35 40 45
 Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp
 50 55 60
 Asn Leu Ser Pro Phe Tyr Glu Ala Leu Gln Glu Gln Lys Pro Asp Leu
 65 70 75 80
 Ser Ala Val Arg Phe Gly Ala Ile Gly Ile Gly Ser Arg Glu Tyr Asp
 85 90 95
 Thr Phe Cys Gly Ala Ile Asp Lys Leu Glu Ala Glu Leu Lys Asn Ser
 100 105 110
 Gly Ala Lys Gln Thr Gly Glu Thr Leu Lys Ile Asn Ile Leu Asp His
 115 120 125
 Asp Ile Pro Glu Asp Pro Ala Glu Glu Trp Leu Gly Ser Trp Val Asn
 130 135 140
 Leu Leu Lys
 145

<210> 475
 <211> 151
 <212> PRT
 <213> Escherichia coli

<400> 475
 Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
 1 5 10 15
 Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
 20 25 30
 Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser
 35 40 45
 Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
 50 55 60
 Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
 65 70 75 80
 Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
 85 90 95
 Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
 100 105 110
 Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser

115 120 125
 Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile
 130 135 140
 Leu Cys Ala Gly Val Thr Phe
 145 150

<210> 476
 <211> 501
 <212> PRT
 <213> Escherichia coli

<400> 476
 Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly
 1 5 10 15
 Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val
 20 25 30
 Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys
 35 40 45
 Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu
 50 55 60
 Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly
 65 70 75 80
 Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile
 85 90 95
 Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys
 100 105 110
 Ile Asp Trp Lys Thr Met Tyr Ala Glu Ala Asp Lys Leu Leu Ala Lys
 115 120 125
 Leu Asn Leu Arg Phe Lys Ser Asp Lys Leu Val Gly Asp Leu Ser Ile
 130 135 140
 Gly Asp Gln Gln Met Val Glu Ile Ala Lys Val Leu Ser Phe Glu Ser
 145 150 155 160
 Lys Val Ile Ile Met Asp Glu Pro Thr Asp Ala Leu Thr Asp Thr Glu
 165 170 175
 Thr Glu Ser Leu Phe Arg Val Ile Arg Glu Leu Lys Ser Gln Gly Arg
 180 185 190
 Gly Ile Val Tyr Ile Ser His Arg Met Lys Glu Ile Phe Glu Ile Cys
 195 200 205
 Asp Asp Val Thr Val Phe Arg Asp Gly Gln Phe Ile Ala Glu Arg Glu
 210 215 220
 Val Ala Ser Leu Thr Glu Asp Ser Leu Ile Glu Met Met Val Gly Arg
 225 230 235 240
 Lys Leu Glu Asp Gln Tyr Pro His Leu Asp Lys Ala Pro Gly Asp Ile
 245 250 255
 Arg Leu Lys Val Asp Asn Leu Cys Gly Pro Gly Val Asn Asp Val Ser
 260 265 270
 Phe Thr Leu Arg Lys Gly Glu Ile Leu Gly Val Ser Gly Leu Met Gly
 275 280 285
 Ala Gly Arg Thr Glu Leu Met Lys Val Leu Tyr Gly Ala Leu Pro Arg
 290 295 300
 Thr Ser Gly Tyr Val Thr Leu Asp Gly His Glu Val Val Thr Arg Ser
 305 310 315 320
 Pro Gln Asp Gly Leu Ala Asn Gly Ile Val Tyr Ile Ser Glu Asp Arg
 325 330 335
 Lys Arg Asp Gly Leu Val Leu Gly Met Ser Val Lys Glu Asn Met Ser
 340 345 350

Leu	Thr	Ala	Leu	Arg	Tyr	Phe	Ser	Arg	Ala	Gly	Gly	Ser	Leu	Lys	His
		355					360					365			
Ala	Asp	Glu	Gln	Gln	Ala	Val	Ser	Asp	Phe	Ile	Arg	Leu	Phe	Asn	Val
		370				375					380				
Lys	Thr	Pro	Ser	Met	Glu	Gln	Ala	Ile	Gly	Leu	Leu	Ser	Gly	Gly	Asn
385					390					395					400
Gln	Gln	Lys	Val	Ala	Ile	Ala	Arg	Gly	Leu	Met	Thr	Arg	Pro	Lys	Val
			405						410					415	
Leu	Ile	Leu	Asp	Glu	Pro	Thr	Arg	Gly	Val	Asp	Val	Gly	Ala	Lys	Lys
			420					425					430		
Glu	Ile	Tyr	Gln	Leu	Ile	Asn	Gln	Phe	Lys	Ala	Asp	Gly	Leu	Ser	Ile
		435				440						445			
Ile	Leu	Val	Ser	Ser	Glu	Met	Pro	Glu	Val	Leu	Gly	Met	Ser	Asp	Arg
		450				455					460				
Ile	Ile	Val	Met	His	Glu	Gly	His	Leu	Ser	Gly	Glu	Phe	Thr	Arg	Glu
465					470					475					480
Gln	Ala	Thr	Gln	Glu	Val	Leu	Met	Ala	Ala	Ala	Val	Gly	Lys	Leu	Asn
			485					490						495	
Arg	Val	Asn	Gln	Glu											
			500												

<210> 477

<211> 321

<212> PRT

<213> Escherichia coli

<400> 477

Met	Thr	Thr	Gln	Thr	Val	Ser	Gly	Arg	Arg	Tyr	Phe	Thr	Lys	Ala	Trp
1				5					10					15	
Leu	Met	Glu	Gln	Lys	Ser	Leu	Ile	Ala	Leu	Leu	Val	Leu	Ile	Ala	Ile
			20					25					30		
Val	Ser	Thr	Leu	Ser	Pro	Asn	Phe	Phe	Thr	Ile	Asn	Asn	Leu	Phe	Asn
		35				40					45				
Ile	Leu	Gln	Gln	Thr	Ser	Val	Asn	Ala	Ile	Met	Ala	Val	Gly	Met	Thr
	50				55					60					
Leu	Val	Ile	Leu	Thr	Ser	Gly	Ile	Asp	Leu	Ser	Val	Gly	Ser	Leu	Leu
65				70					75					80	
Ala	Leu	Thr	Gly	Ala	Val	Ala	Ala	Ser	Ile	Val	Gly	Ile	Glu	Val	Asn
			85					90					95		
Ala	Leu	Val	Ala	Val	Ala	Ala	Ala	Leu	Ala	Leu	Gly	Ala	Ala	Ile	Gly
		100					105					110			
Ala	Val	Thr	Gly	Val	Ile	Val	Ala	Lys	Gly	Arg	Val	Gln	Ala	Phe	Ile
		115				120					125				
Ala	Thr	Leu	Val	Met	Met	Leu	Leu	Arg	Gly	Val	Thr	Met	Val	Tyr	
	130				135					140					
Thr	Asn	Gly	Ser	Pro	Val	Asn	Thr	Gly	Phe	Thr	Glu	Asn	Ala	Asp	Leu
145				150					155					160	
Phe	Gly	Trp	Phe	Gly	Ile	Gly	Arg	Pro	Leu	Gly	Val	Pro	Thr	Pro	Val
			165					170						175	
Trp	Ile	Met	Gly	Ile	Val	Phe	Leu	Ala	Ala	Trp	Tyr	Met	Leu	His	His
		180					185					190			
Thr	Arg	Leu	Gly	Arg	Tyr	Ile	Tyr	Ala	Leu	Gly	Gly	Asn	Glu	Ala	Ala
		195				200						205			
Thr	Arg	Leu	Ser	Gly	Ile	Asn	Val	Asn	Lys	Ile	Lys	Ile	Ile	Val	Tyr
	210				215					220					
Ser	Leu	Cys	Gly	Leu	Leu	Ala	Ser	Leu	Ala	Gly	Ile	Ile	Glu	Val	Ala

225 230 235 240
 Arg Leu Ser Ser Ala Gln Pro Thr Ala Gly Thr Gly Tyr Glu Leu Asp
 245 250 255
 Ala Ile Ala Ala Val Val Leu Gly Gly Thr Ser Leu Ala Gly Gly Lys
 260 265 270
 Gly Arg Ile Val Gly Thr Leu Ile Gly Ala Leu Ile Leu Gly Phe Leu
 275 280 285
 Asn Asn Gly Leu Asn Leu Leu Gly Val Ser Ser Tyr Tyr Gln Met Ile
 290 295 300
 Val Lys Ala Val Val Ile Leu Leu Ala Val Leu Val Asp Asn Lys Lys
 305 310 315 320
 Gln

<210> 478
 <211> 296
 <212> PRT
 <213> Escherichia coli

<400> 478
 Met Asn Met Lys Lys Leu Ala Thr Leu Val Ser Ala Val Ala Leu Ser
 1 5 10 15
 Ala Thr Val Ser Ala Asn Ala Met Ala Lys Asp Thr Ile Ala Leu Val
 20 25 30
 Val Ser Thr Leu Asn Asn Pro Phe Val Ser Leu Lys Asp Gly Ala
 35 40 45
 Gln Lys Glu Ala Asp Lys Leu Gly Tyr Asn Leu Val Val Leu Asp Ser
 50 55 60
 Gln Asn Asn Pro Ala Lys Glu Leu Ala Asn Val Gln Asp Leu Thr Val
 65 70 75 80
 Arg Gly Thr Lys Ile Leu Leu Ile Asn Pro Thr Asp Ser Asp Ala Val
 85 90 95
 Gly Asn Ala Val Lys Met Ala Asn Gln Ala Asn Ile Pro Val Ile Thr
 100 105 110
 Leu Asp Arg Gln Ala Thr Lys Gly Glu Val Val Ser His Ile Ala Ser
 115 120 125
 Asp Asn Val Leu Gly Gly Lys Ile Ala Gly Asp Tyr Ile Ala Lys Lys
 130 135 140
 Ala Gly Glu Gly Ala Lys Val Ile Glu Leu Gln Gly Ile Ala Gly Thr
 145 150 155 160
 Ser Ala Ala Arg Glu Arg Gly Glu Gly Phe Gln Gln Ala Val Ala Ala
 165 170 175
 His Lys Phe Asn Val Leu Ala Ser Gln Pro Ala Asp Phe Asp Arg Ile
 180 185 190
 Lys Gly Leu Asn Val Met Gln Asn Leu Leu Thr Ala His Pro Asp Val
 195 200 205
 Gln Ala Val Phe Ala Gln Asn Asp Glu Met Ala Leu Gly Ala Leu Arg
 210 215 220
 Ala Leu Gln Thr Ala Gly Lys Ser Asp Val Met Val Val Gly Phe Asp
 225 230 235 240
 Gly Thr Pro Asp Gly Glu Lys Ala Val Asn Asp Gly Lys Leu Ala Ala
 245 250 255
 Thr Ile Ala Gln Leu Pro Asp Gln Ile Gly Ala Lys Gly Val Glu Thr
 260 265 270
 Ala Asp Lys Val Leu Lys Gly Glu Lys Val Gln Ala Lys Tyr Pro Val
 275 280 285

Asp Leu Lys Leu Val Val Lys Gln
 290 295

<210> 479
 <211> 309
 <212> PRT
 <213> Escherichia coli

<400> 479

Met Gln Asn Ala Gly Ser Leu Val Val Leu Gly Ser Ile Asn Ala Asp
 1 5 10 15
 His Ile Leu Asn Leu Gln Ser Phe Pro Thr Pro Gly Glu Thr Val Thr
 20 25 30
 Gly Asn His Tyr Gln Val Ala Phe Gly Gly Lys Gly Ala Asn Gln Ala
 35 40 45
 Val Ala Ala Gly Arg Ser Gly Ala Asn Ile Ala Phe Ile Ala Cys Thr
 50 55 60
 Gly Asp Asp Ser Ile Gly Glu Ser Val Arg Gln Gln Leu Ala Thr Asp
 65 70 75 80
 Asn Ile Asp Ile Thr Pro Val Ser Val Ile Lys Gly Glu Ser Thr Gly
 85 90 95
 Val Ala Leu Ile Phe Val Asn Gly Glu Gly Glu Asn Val Ile Gly Ile
 100 105 110
 His Ala Gly Ala Asn Ala Ala Leu Ser Pro Ala Leu Val Glu Ala Gln
 115 120 125
 Arg Glu Arg Ile Ala Asn Ala Ser Ala Leu Leu Met Gln Leu Glu Ser
 130 135 140
 Pro Leu Glu Ser Val Met Ala Ala Lys Ile Ala His Gln Asn Lys
 145 150 155 160
 Thr Ile Val Ala Leu Asn Pro Ala Pro Ala Arg Glu Leu Pro Asp Glu
 165 170 175
 Leu Leu Ala Leu Val Asp Ile Ile Thr Pro Asn Glu Thr Glu Ala Glu
 180 185 190
 Lys Leu Thr Gly Ile Arg Val Glu Asn Asp Glu Asp Ala Ala Lys Ala
 195 200 205
 Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
 210 215 220
 Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
 225 230 235 240
 Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
 245 250 255
 Phe Asn Gly Ala Leu Ile Thr Ala Leu Leu Glu Glu Lys Pro Leu Pro
 260 265 270
 Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ile Ala Val Thr Arg
 275 280 285
 Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe
 290 295 300
 Leu Asp Arg Gln Arg
 305

<210> 480
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Linker containing T7 terminator

<400> 480

gtctagcata accccttggg gcctctaaac gggtccttga ggggtttttt ga 52

<210> 481

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Linker containing T7 terminator

<400> 481

agcttcaaaa aaccctcaa ggaccggtt agaggcccca aggggttatg ctagactgca 60